

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:28:19 ; Search time 270.726 Seconds  
(without alignments)  
1213.978 Million cell updates/sec

Title: US-10-687-035-1  
Perfect score: 3945  
Sequence: 1 AAQARRARRTKLFTTHRSSV.....QKLISEDLMNMTGHHHHH 748

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3945	100.0	748	8	ADS94302
2	3904.5	99.0	809	8	ADS94303
3	3663	92.9	833	3	AB12554 Human ova
4	3663	92.9	833	5	ABP30898
5	3663	92.9	833	7	ADA08542
6	3663	92.9	833	7	ADF08885
7	3663	92.9	833	7	ADG46172
8	3663	92.9	833	3	ADX17768
9	3663	92.9	914	3	AB12552
10	3663	92.9	914	4	ABP30968
11	3663	92.9	914	5	ABP30968
12	3663	92.9	914	5	ABP30896
13	3663	92.9	914	5	ADU01425
14	3663	92.9	914	5	ADZ41689
15	3663	92.9	914	7	ADA08631
16	3663	92.9	914	7	ADA08465
17	3663	92.9	914	7	ADF08974
18	3663	92.9	914	7	ADF08808
19	3663	92.9	914	7	ADG46095
20	3663	92.9	914	8	ADN40451
21	3663	92.9	914	9	ADN40451
22	3663	92.9	914	9	ADN40451
23	3658	92.7	1889	6	ABE34700
24	3658	92.7	1890	5	ABG96381

98 1345 34.1 318 5 ABP31025  
99 1345 34.1 318 7 ADA08747  
100 1345 34.1 318 7 ADF09090

# ALIGNMENTS

RESULT 1  
ID ADS94302  
XX AC ADS94302;  
XX DT 02-DEC-2004 (first entry)  
XX DE CA 125/O772P 3-repeat amino acid sequence SEQ ID NO:1.  
XX KW antibody; antigen-binding antibody fragment;  
XX KW cell-associated CA 125/O772P; monoclonal antibody; cytostatic;  
XX KW immunostimulant; mediator of lysis; tumour; cell proliferative disorder;  
XX KW ovarian cancer; uterine cancer; breast cancer; lung cancer;  
XX OS Synthetic.  
XX FN WO2004035537-A2.  
XX PD 29-APR-2004.  
XX PF 15-OCT-2003; 2003WO-US032945.  
XX PR 16-OCT-2002; 2002US-0418828P.  
XX PA 10-JUL-2003; 2003US-0485986P.  
XX PI (EURO-) EUROCELTIQUE SA.  
XX PI Albone EF, Soltis DA;  
XX DR WPI; 2004-357171/33.  
XX PT Novel isolated antibody, or antigen-binding antibody fragment binding  
XX PT with cell-associated CA 125/O772P polypeptide relative to shed CA  
XX PT 125/O772P polypeptide, useful for ameliorating cervical or ovarian cancer.  
XX PS Example; SEQ ID NO 1; 153pp; English.

XX The present invention describes an isolated antibody, or an antigen-binding antibody fragment (I), that preferentially binds cell-associated CA 125/O772P polypeptide relative to shed CA 125/O772P polypeptide. Also described: (1) a monoclonal antibody (II) produced by hybridoma 4E7; (2) a monoclonal antibody that competes with binding of (II); (3) a hybridoma as deposited in (II); (4) an isolated nucleic acid molecule (III) comprising a nucleotide sequence that encodes a variable chain region of (I); (5) a pharmaceutical composition comprising an antibody or an antigen-binding antibody fragment that preferentially binds cell-associated CA 125/O772P polypeptide relative to shed CA 125/O772P polypeptide, and a carrier; (6) a pharmaceutical composition comprising a monoclonal antibody or an antigen-binding monoclonal antibody fragment that preferentially binds cell-associated CA 125/O772P polypeptide relative to shed CA 125/O772P polypeptide, and a carrier; (7) an article of manufacture (IV) comprising packaging material and a composition comprising an antibody, or an antigen-binding antibody fragment that preferentially binds cell-associated CA 125/O772P polypeptide relative to shed CA 125/O772P polypeptide, and a carrier; (8) a composition in a form suitable for administration to a subject; (9) a fusion polypeptide (V) comprising an antibody, or an antigen-binding antibody fragment, which preferentially binds cell-associated CA 125/O772P polypeptide relative to shed CA 125/O772P operably linked to a heterologous agent; (10) ameliorating (M1) a symptom of a CA 125/O772P-related disorder; (11) a monoclonal antibody (VI) chosen from 325.1, 621.1, 633.1, 654.1, 725.1, 8G9, 7F10, 8A1, 8AC3, 15C9, 8B5, 7G10, 16C7, 7C6, 7H1, 16H9, 7A11, 4E7, 117.1, 368.1, 446.1, 501.1, and 776.1 or its antigen-binding

CC antibody fragment; (11) an antibody or antigen binding antibody fragment that competes with (VI); and (12) a pharmaceutical composition comprising (VI) and a carrier. (I) has cytostatic activity, and can be used as an immunostimulant and a mediator of lysis of positive tumour cell. (II) is useful for ameliorating a symptom of a CA 125/O77P-related disorder which is a cell proliferative disorder such as cancer, cervical or uterine cancer, breast or lung cancer or ovarian cancer. (V) is useful diagnostically for monitoring the development or progression of cancer or tumour as part of clinical testing procedure. The present sequence represents the CA 125/O772P 3-repeat amino acid sequence, which is used in the exemplification of the present invention.

XX SQ Sequence 748 AA;

Query Match	100.0%;	Score 3945;	DB 8;	Length 748;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 748;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 AAQARRARRTKLFTHRSSVSTTSTPGTPVYLGASKTPASIFGPSAASHLLILFTLNFT 60  
DB 1 AAQARRARRTKLFTHRSSVSTTSTPGTPVYLGASKTPASIFGPSAASHLLILFTLNFT 60  
QY 61 ITNLYEENMWPGSRKFNFTTERRVQLGLRLPKNFTSVGPLYSGCRLTLLRPEKDGATGV 120  
DB 61 ITNLYEENMWPGSRKFNFTTERRVQLGLRLPKNFTSVGPLYSGCRLTLLRPEKDGATGV 120  
QY 121 DAICTHRPDPPTGDLREQLYELSQLTHSITELGPVTLDRDSLTYNGFTHRSSVPTTST 180  
DB 121 DAICTHRPDPPTGDLREQLYELSQLTHSITELGPVTLDRDSLTYNGFTHRSSVPTTST 180  
QY 181 GVSEEPFTLNFTINNLYRNADMGQPGSLAKFNITDNVMKLLSPLFORSSLGARYTCRV 240  
DB 181 GVSEEPFTLNFTINNLYRNADMGQPGSLAKFNITDNVMKLLSPLFORSSLGARYTCRV 240  
QY 241 IALRSVKNAGAEIVDILLCTYQLPSGGLPIKQVFHELSQLTHSITELGPVTLDRDSLTYNGFTHRSSVPTTST 300  
DB 241 IALRSVKNAGAEIVDILLCTYQLPSGGLPIKQVFHELSQLTHSITELGPVTLDRDSLTYNGFTHRSSVPTTST 300  
QY 301 NGYNEPGDEPPTTPKPAATFLPLSEATTAMGVHLKTLTNFTISNLQYSPDMGKGSAT 360  
DB 301 NGYNEPGDEPPTTPKPAATFLPLSEATTAMGVHLKTLTNFTISNLQYSPDMGKGSAT 360  
QY 361 FNSTEGVQLHLLRPLFOKSSMGPPYLGCGQLISLRPEKDGATGVDTTCTYHPDPVPGCLD 420  
DB 361 FNSTEGVQLHLLRPLFOKSSMGPPYLGCGQLISLRPEKDGATGVDTTCTYHPDPVPGCLD 420  
QY 421 IQQLYWELSQLTHGVTOLGPFVLDRLDSLFINGVAPQNLISIRGEYQINPHIVNWLSPDP 480  
DB 421 IQQLYWELSQLTHGVTOLGPFVLDRLDSLFINGVAPQNLISIRGEYQINPHIVNWLSPDP 480  
QY 481 TSSEYITLLRDIQDKVTLTKGSQLHDTFRCLVTNLTMDSVLTVKALFSSNLDPSLVE 540  
DB 481 TSSEYITLLRDIQDKVTLTKGSQLHDTFRCLVTNLTMDSVLTVKALFSSNLDPSLVE 540  
QY 541 QVFLDKTLNLSFWMLGSTYQLVDIHVTMESVSVQPTSSSSSTQHLYNFTITNLPYSQDK 600  
DB 541 QVFLDKTLNLSFWMLGSTYQLVDIHVTMESVSVQPTSSSSSTQHLYNFTITNLPYSQDK 600  
QY 601 AQPCTTNYQRNKRNIEDALNQLFNNSIKSYFSDQVSTFRSVNRRHHTGVDSLCNFSPL 660  
DB 601 AQPCTTNYQRNKRNIEDALNQLFNNSIKSYFSDQVSTFRSVNRRHHTGVDSLCNFSPL 660  
QY 661 ARRVDRVAIYEEFLRMTRNGTQLQNFITLDRSSVLVDGYSNPNRPLTGNADIOHSGGRS 720  
DB 661 ARRVDRVAIYEEFLRMTRNGTQLQNFITLDRSSVLVDGYSNPNRPLTGNADIOHSGGRS 720  
QY 721 SLEGPREFQKLISEEDLNMTGHHHHH 748  
DB 721 SLEGPREFQKLISEEDLNMTGHHHHH 748

RESULT 2  
ADS94303

ID ADS94303 standard; protein; 809 AA.  
 AC ADS94303;  
 XX  
 XX 02-DEC-2004 (first entry)  
 XX  
 XX CA 125/O772P 3-repeat TM amino acid sequence SEQ ID NO:2.  
 DE  
 XX antibody; antigen-binding antibody fragment;  
 KW cell-associated CA 125/O772P; monoclonal antibody; cytostatic;  
 KW immunostimulant; mediator of lysis; tumour; cell proliferative disorder;  
 KW cancer; cervical cancer; uterine cancer; breast cancer; lung cancer;  
 KW ovarian cancer.  
 XX  
 XX Synthetic.  
 XX  
 XX W02004035537-A2.  
 PN  
 XX  
 XX 29-APR-2004.  
 PD  
 XX  
 XX 15-OCT-2003; 2003WO-US032945.  
 PF  
 XX  
 XX 16-OCT-2002; 2002US-0418828P.  
 PR  
 XX  
 XX 10-JUL-2003; 2003US-0485986P.  
 XX  
 XX (EURO-) EUROCELTIQUE SA.  
 PA  
 XX  
 XX Albione EF, Soltis DA;  
 PI  
 XX WPI; 2004-357171/33.  
 DR  
 XX  
 XX Novel isolated antibody, or antigen-binding antibody fragment binding  
 PT with cell-associated CA 125/O772P polypeptide relative to shed CA  
 PT 125/O772 polypeptide, useful for ameliorating cervical or ovarian cancer.  
 PT  
 XX  
 XX Example; SEQ ID NO 2; 153pp; English.  
 PS  
 XX  
 XX The present invention describes an isolated antibody, or an antigen-  
 CC binding antibody fragment (I), that preferentially binds cell-associated  
 CC CA 125/O772P polypeptide relative to shed CA 125/O772 polypeptide. Also  
 CC described: (1) a monoclonal antibody (II) produced by hybridoma 4E7; (2)  
 CC a monoclonal antibody that competes with binding of (II); (3) a hybridoma  
 CC as deposited in (II); (4) an isolated nucleic acid molecule (III)  
 CC comprising a nucleotide sequence that encodes a variable chain region of  
 CC (I); (5) a pharmaceutical composition comprising an antibody or an  
 CC antigen-binding antibody fragment that preferentially binds cell-  
 CC associated CA 125/O772P polypeptide relative to shed CA 125/O772P  
 CC polypeptide, and a carrier; (6) a pharmaceutical composition comprising a  
 CC monoclonal antibody or an antigen-binding monoclonal antibody fragment  
 CC that preferentially binds cell-associated CA 125/O772P polypeptide  
 CC relative to shed CA 125/O772P polypeptide, and a carrier; (7) an article  
 CC of manufacture (IV) comprising packaging material and a composition  
 CC comprising an antibody, or an antigen-binding antibody fragment that  
 CC preferentially binds cell-associated CA 125/O772P relative to shed CA  
 CC 125/O772P, and a carrier contained within the packaging material, and  
 CC composition in a form suitable for administration to a subject; (8) a  
 CC fusion polypeptide (V) comprising an antibody, or an antigen-binding  
 CC antibody fragment, which preferentially binds cell-associated CA  
 CC 125/O772P relative to shed CA 125/O772P operably linked to a heterologous  
 CC agent; (9) ameliorating (VI) a symptom of CA 125/O772P-related disorder  
 CC; (10) a monoclonal antibody (VII) chosen from 325.1, 621.1, 633.1, 654.1,  
 CC 725.1, 8G9, 7F10, 8A1, 8AC3, 15C9, 8E3, 8B5, 7G10, 16C7, 7C6, 7H1, 16H9,  
 CC 7A11, 4E7, 117.1, 368.1, 446.1, 501.1, and 776.1 or its antigen-binding  
 CC antibody fragment; (11) an antibody or antigen binding antibody fragment  
 CC that competes with (VI); and (12) a pharmaceutical composition comprising  
 CC (VI) and a carrier. (I) has cytostatic activity, and can be used as an  
 CC immunostimulant and a mediator of lysis of positive tumour cell. (II) is  
 CC useful for ameliorating a symptom of a CA 125/O772P-related disorder which  
 CC is a cell proliferative disorder such as cancer, cervical or uterine  
 CC cancer, breast or lung cancer or ovarian cancer. (V) is useful  
 CC diagnostically for monitoring the development or progression of cancer or  
 CC tumour as part of clinical testing procedure. The present sequence  
 CC represents the CA 125/O772P 3-repeat TM amino acid sequence, which is

CC used in the exemplification of the present invention.

XX Sequence 809 AA;

Query Match 99.0%; Score 3904.5; DB 8; Length 809;  
 Best Local Similarity 92.5%; Pred. No. 0;  
 Matches 748; Conservative 0; Mismatches 0; Indels 61; Gaps 1;

QY 1 AAQARRARTKLFTHRSSVSTSTTGTPTVYLGASKTASIFGSAASHLLILFTLNFT 60

DB 1 AAQARRARTKLFTHRSSVSTSTTGTPTVYLGASKTASIFGSAASHLLILFTLNFT 60

QY 61 ITNLYEENWFGSRKFNTERVQLGLRPLKNTSVGLYSCRLTLLEPKDGEATGV 120

DB 61 ITNLYEENWFGSRKFNTERVQLGLRPLKNTSVGLYSCRLTLLEPKDGEATGV 120

QY 121 DAICTHRPPTGGLDREQLYLELSQLTHTSITELGPTTLDRLSLYVNGFTHRSSVPTTST 180

DB 121 DAICTHRPPTGGLDREQLYLELSQLTHTSITELGPTTLDRLSLYVNGFTHRSSVPTTST 180

QY 181 GVVSEPPFTLNFTINNLYMADMGQPSLKFNTIDNMKHLSPFLQSSLGARYTGCRV 240

DB 181 GVVSEPPFTLNFTINNLYMADMGQPSLKFNTIDNMKHLSPFLQSSLGARYTGCRV 240

QY 241 IALRSVNGAETRVDLLCTYLPQPSGLPIKQVFHELSQLTHGITHGIRLGPYSLDKDSL 300

DB 241 IALRSVNGAETRVDLLCTYLPQPSGLPIKQVFHELSQLTHGITHGIRLGPYSLDKDSL 300

QY 301 NGVNEPGDPPTTPKPAITTELPPLSEATTMGYHLKTLTNTFTISNLYQSPDMGKGSAT 360

DB 301 NGVNEPGDPPTTPKPAITTELPPLSEATTMGYHLKTLTNTFTISNLYQSPDMGKGSAT 360

QY 361 FNSTEGLVQLHRLPLFKSSMGPPFYLGCLISLRPEKDGAAATGVDTTCTYHPDPVPGGLD 420

DB 361 FNSTEGLVQLHRLPLFKSSMGPPFYLGCLISLRPEKDGAAATGVDTTCTYHPDPVPGGLD 420

QY 421 IQQLYWEISQLTHGVTQLGFFYVLDRLSLFNGVAPQNLSTIRGEYQINFIHVNWNLSPDP 480

DB 421 IQQLYWEISQLTHGVTQLGFFYVLDRLSLFNGVAPQNLSTIRGEYQINFIHVNWNLSPDP 480

QY 481 TSSEYITLARDIQDKVTLYKGSQHDTRFCLVNTLWDSVLVTVTKALFSSNLDPSLVE 540

DB 481 TSSEYITLARDIQDKVTLYKGSQHDTRFCLVNTLWDSVLVTVTKALFSSNLDPSLVE 540

QY 541 QVFLDKTLNASFWHLGSTYQLVDIHVTENESSVYQPTSSSTQHFYLNFTITNLPYSQDK 600

DB 541 QVFLDKTLNASFWHLGSTYQLVDIHVTENESSVYQPTSSSTQHFYLNFTITNLPYSQDK 600

QY 601 AQPSTNYQRNKRNIEDALNQLFRNSSIKSYSDCQVSTFRSVNRRHHTGVDSLCNFSPL 660

DB 601 AQPSTNYQRNKRNIEDALNQLFRNSSIKSYSDCQVSTFRSVNRRHHTGVDSLCNFSPL 660

QY 661 ARVRDVAIYEFLMTRNGTQLNFTLDRSSVLVDGYSPNRNEPLTG----- 708

DB 661 ARVRDVAIYEFLMTRNGTQLNFTLDRSSVLVDGYSPNRNEPLTG----- 708

QY 709 -----NSADIQHSQGR 719

DB 721 GLAGLLGLTCLICGLVTVTRRKKEGYVNVQOCQGYQSHLDLEDLQNSADIQHSQGR 780

QY 720 SSLEGPRPEQKLISEEDLNMTGHHHHH 748

DB 781 SSLEGPRPEQKLISEEDLNMTGHHHHH 809

RESULT 3

AAB12554

ID AAB12554 standard; protein; 833 AA.

XX AAB12554;

XX 07-NOV-2000 (first entry)

XX

DE Human ovarian carcinoma antigen O772P protein SEQ ID NO:389.  
XX Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;  
KW tumour antigen; identification; cytostatic; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN W0200036107-A2.  
XX  
XX 22-JUN-2000.  
XX  
XX 17-DEC-1999; 99WO-US030270.  
XX  
XX 17-DEC-1998; 98US-00215681.  
PR 17-DEC-1998; 98US-00216003.  
PR 23-JUN-1999; 99US-00338933.  
PR 24-SEP-1999; 99US-00404879.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Mitcham JL, King GE, Algate PA, Frudakis TN;  
PI  
XX WPI; 2000-431589/37.  
DR N-PSDB; AAA70075.  
XX  
XX Immunogenic portion of an ovarian carcinoma protein and the nucleic acid  
PT encoding it, useful for the diagnosis, prevention and treatment of  
PT cancer, preferably ovarian cancer.  
XX  
XX Example 2; Page 200-203; 299pp; English.  
XX  
XX The present invention describes an isolated polypeptide comprising an  
CC immunogenic portion of an ovarian carcinoma protein (or its variants).  
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have  
CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian  
CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful  
CC for the prevention, diagnosis and treatment of cancer, preferably ovarian  
CC cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human  
CC ovarian carcinoma polynucleotides and proteins used in the  
CC exemplification of the present invention  
XX  
XX Sequence 833 AA;  
SQ

Query Match 92.9%; Score 3663; DB 3; Length 833;  
Best Local Similarity 99.9%; Pred. No. 2.2e-315;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

14 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGSPSAASHLLILFTLNFTITNLRYEENWPG 73  
17 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGSPSAASHLLILFTLNFTITNLRYEENWPG 137  
74 SRKENTERVVLQGLLRPLPKNTSVGPLYSGCRLTLRLPEKDGATGVDATCTHRPDPGTP 133  
138 SRKENTERVVLQGLLRPLPKNTSVGPLYSGCRLTLRLPEKDGATGVDATCTHRPDPGTP 197  
134 GLDREQLYLELSQTHSTELGPTLDRDSLYVNGFTHRSSVPTSTGWSEEPFTLNFT 193  
198 GLDREQLYLELSQTHSTELGPTLDRDSLYVNGFTHRSSVPTSTGWSEEPFTLNFT 257  
194 INNLRVMADMGQPSGLKFNITDVMKLLSPFORSSIGARYTCRVIALRSVKNGAETR 253  
258 INNLRVMADMGQPSGLKFNITDVMKLLSPFORSSIGARYTCRVIALRSVKNGAETR 317  
254 VDLCTYLQPLSGPLPIKQVHFELSQTHGITLGPYSLDKSLYLNGVNEPDPBPPT 313  
318 VDLCTYLQPLSGPLPIKQVHFELSQTHGITLGPYSLDKSLYLNGVNEPDPBPPT 377  
314 TPXPATTFPLPLSEATTAMGWHKLTILNFTISNLQYSPDMKGSATFNSTEGVLOHLR 373  
378 TPXPATTFPLPLSEATTAMGWHKLTILNFTISNLQYSPDMKGSATFNSTEGVLOHLR 437  
374 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 433

Db 438 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 497  
Qy 434 GVTQLGFYVLDRLDSLFINGAPQNLISIRGEYQINFIHVNWNLSPDPPTSEYITLLRDIQ 493  
Db 498 GVTQLGFYVLDRLDSLFINGAPQNLISIRGEYQINFIHVNWNLSPDPPTSEYITLLRDIQ 557  
Qy 494 DKVTTLTKGSQLHDTFRFCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553  
Db 558 DKVTTLTKGSQLHDTFRFCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 617  
Qy 554 WLGSITQLVDIHVTENESSYQPTSSSTQHFVNLFTITNLPSYQDKAOPGTTNYQRNKR 613  
Db 618 WLGSITQLVDIHVTENESSYQPTSSSTQHFVNLFTITNLPSYQDKAOPGTTNYQRNKR 677  
Qy 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDSLCNFSPLARRVDRVAIYEFP 673  
Db 678 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVNRRHHTGVDSLCNFSPLARRVDRVAIYEFP 737  
Qy 674 LRMRNGTQLQNFTRDRSSVLVDGYSFNRNEPLTGNS 710  
Db 738 LRMRNGTQLQNFTRDRSSVLVDGYSFNRNEPLTGNS 774

RESULT 4  
ABP30898  
ID ABP30898 standard; protein; 833 AA.  
XX  
AC ABP30898;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE 0772P clone 21003.  
XX  
KW Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.  
XX  
OS Homo sapiens.  
XX  
PN W0200206317-A2.  
XX  
PD 24-JAN-2002.  
XX  
PF 17-JUL-2001; 2001WO-US022635.  
XX  
PR 17-JUL-2000; 2000US-00617747.  
PR 10-AUG-2000; 2000US-00636801.  
PR 20-SEP-2000; 2000US-00667857.  
PR 04-APR-2001; 2001US-00827271.  
PR 18-JUN-2001; 2001US-00884441.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Mitcham JL, King GE, Algate PA, Pling SP, Retter MW, Fanger GR;  
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;  
XX  
DR WPI; 2002-164781/21.  
XX  
XX N-PSDB; ABN72969.  
XX  
PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma  
PT protein or its variants, useful for stimulating an immune response in a  
PT patient and treating ovarian cancer.  
XX  
PS Example 2; Page 316-318; 408pp; English.  
XX  
CC This invention relates to polypeptides comprising an immunogenic portion  
CC of an ovarian carcinoma protein which acts as an immunostimulant and is  
CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion  
CC proteins, T cell populations and antigen presenting cells that express  
CC the polypeptides are useful for stimulating an immune response in a  
CC patient and treating ovarian cancer. This sequence represents protein  
CC related to the invention  
XX  
SQ Sequence 833 AA;



Query Match		92.9%; Score 3663; DB 5; Length 833;
Best Local Similarity		99.9%; Pred. No. 2.2e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	14	FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 73
DB	78	FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 137
QY	74	SRKFNTERVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDAICTHRPDPTGP 133
DB	138	SRKFNTERVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDAICTHRPDPTGP 197
QY	134	GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFLNFT 193
DB	198	GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFLNFT 257
QY	194	INNLRYMADMGQPSGLKFNITDNVMKHLSPLEFQSSLGARYTGCRIALRSVKNGAETR 253
DB	258	INNLRYMADMGQPSGLKFNITDNVMKHLSPLEFQSSLGARYTGCRIALRSVKNGAETR 317
QY	254	VDLLCTYLOPLSGPLPIKQVFHELSSQOHTGTRIGPYSLDKDSLTVNGFTHRSSVPTTSTGVVSEEPFLNFT 313
DB	318	VDLLCTYLOPLSGPLPIKQVFHELSSQOHTGTRIGPYSLDKDSLTVNGFTHRSSVPTTSTGVVSEEPFLNFT 377
QY	314	TPKPATTFPLPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
DB	378	TPKPATTFPLPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 437
QY	374	PLFQKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 433
DB	438	PLFQKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 497
QY	434	GVTLQGFVYLDRLDSLFINGYAPQNLISIRGEYQINPHIVNMNLSNPDPTSSSEYITLLRDIO 493
DB	498	GVTLQGFVYLDRLDSLFINGYAPQNLISIRGEYQINPHIVNMNLSNPDPTSSSEYITLLRDIO 557
RESULT 5		
ADA08542		
ID	ADA08542	standard; protein; 833 AA.
AC	ADA08542;	
DT	06-NOV-2003	(first entry)
XX	Human ovarian carcinoma antigen O772P #2.	
XX	human; gene therapy; ovarian cancer; cancer.	
XX	Homo sapiens.	
XX	US2003091580-A1.	
XX	15-MAY-2003.	
XX	17-JUL-2001; 2001US-00907969.	

PR	XX	19-JUN-2001; 2001US-00884441.
PA	(MITC/) MITCHAM J L.	
PA	(KING/) KING G E.	
PA	(ALGA/) ALGATE P A.	
PA	(FLIN/) FLING S P.	
PA	(RETT/) RETTER M W.	
PA	(FANG/) FANGER G R.	
PA	(REED/) REED S G.	
PA	(VEDV/) VEDVICK T S.	
PA	(CART/) CARTER D.	
PA	(HILL/) HILL P.	
PA	(ALBO/) ALBONE E.	
XX		
PI	Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR,	
PI	Reed SG, Vedvick TS, Carter D, Hill P, Albone E,	
XX	WPI; 2003-532352/50.	
DR	XX	New isolated O772P polypeptides and polynucleotides, useful in gene
PT	therapy, particularly for treating or diagnosing cancer, e.g. ovarian	
PT	cancer.	
XX		
PS	Example 2; SEQ ID NO 389; 371pp; English.	
XX		
CC	The invention relates to an isolated O772P polypeptide, which has the	
CC	structure fully defined in the specification. The composition containing	
CC	the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells	
CC	or antigen presenting cells are useful for stimulating an immune response	
CC	and treating ovarian cancer. Detecting the presence of the	
CC	polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian	
CC	carcinoma cDNAs and protein cDNAs were identified using microarray	
CC	technology. The present sequence represents a human ovarian carcinoma	
CC	antigen.	
XX		
SQ	Sequence 833 AA;	
Query Match		92.9%; Score 3663; DB 7; Length 833;
Best Local Similarity		99.9%; Pred. No. 2.2e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	14	FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 73
DB	78	FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 137
QY	74	SRKFNTERVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDAICTHRPDPTGP 133
DB	138	SRKFNTERVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDAICTHRPDPTGP 197
QY	134	GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFLNFT 193
DB	198	GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFLNFT 257
QY	194	INNLRYMADMGQPSGLKFNITDNVMKHLSPLEFQSSLGARYTGCRIALRSVKNGAETR 253
DB	258	INNLRYMADMGQPSGLKFNITDNVMKHLSPLEFQSSLGARYTGCRIALRSVKNGAETR 317
QY	254	VDLLCTYLOPLSGPLPIKQVFHELSSQOHTGTRIGPYSLDKDSLTVNGFTHRSSVPTTSTGVVSEEPFLNFT 313
DB	318	VDLLCTYLOPLSGPLPIKQVFHELSSQOHTGTRIGPYSLDKDSLTVNGFTHRSSVPTTSTGVVSEEPFLNFT 377
QY	314	TPKPATTFPLPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
DB	378	TPKPATTFPLPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 437
QY	374	PLFQKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 433
DB	438	PLFQKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 497
QY	434	GVTLQGFVYLDRLDSLFINGYAPQNLISIRGEYQINPHIVNMNLSNPDPTSSSEYITLLRDIO 493
DB	498	GVTLQGFVYLDRLDSLFINGYAPQNLISIRGEYQINPHIVNMNLSNPDPTSSSEYITLLRDIO 557

494 DKVTLLYKGSQHDHFRFCLVNTLMDSVLVTKALFSSNLDPSILVEQVFLDKTLNASFH 553  
 558 DKVTLLYKGSQHDHFRFCLVNTLMDSVLVTKALFSSNLDPSILVEQVFLDKTLNASFH 617  
 554 WLGSTYQLVDHVTMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 613  
 618 WLGSTYQLVDHVTMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 677  
 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLCNFPSPFLARRVDRVAIYEEF 673  
 678 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLCNFPSPFLARRVDRVAIYEEF 737  
 674 LMTTRNGTQLQNFITLDRSSVLVDGYSFNRNEPLTGN 710  
 738 LMTTRNGTQLQNFITLDRSSVLVDGYSFNRNEPLTGN 774

RESULT 6  
 ADF08885  
 ID ADF08885 standard; protein; 833 AA.  
 AC ADF08885;  
 XX  
 XX 12-FEB-2004 (first entry)  
 DT  
 XX  
 XX Secreted ovarian carcinoma antigen seqid 389.  
 XX  
 XX gene therapy; protein therapy; vaccine; antibody inhibition;  
 KW breast cancer; restorative therapy; diagnostic agent; immunoassay;  
 KW secreted ovarian carcinoma antigen.  
 XX  
 XX Homo sapiens.  
 XX  
 XX US2003124140-A1.  
 XX  
 XX 03-JUL-2003.  
 XX  
 XX 17-JUL-2002; 2002US-00198053.  
 XX  
 XX 17-DEC-1998; 98US-00215681.  
 XX 17-DEC-1998; 98US-00216003.  
 XX 23-JUN-1999; 99US-00338933.  
 XX 24-SEP-1999; 99US-00404879.  
 XX 17-JUL-2000; 2000US-00617747.  
 XX 10-AUG-2000; 2000US-00636801.  
 XX 20-SEP-2000; 2000US-00667857.  
 XX 04-APR-2001; 2001US-00827271.  
 XX 18-JUN-2001; 2001US-00884441.  
 XX 17-JUL-2001; 2001US-00907969.  
 XX  
 XX (CORI-) CORIXA CORP.  
 XX  
 XX Bangur CS, Retter MW, Fanger GR, Hill P;  
 XX  
 XX WPI; 2003-897152/82.  
 DR N-PSDB; ADF08882.  
 DR  
 XX  
 XX Oncogenic nucleic acids useful for the prevention, diagnosis and  
 PT treatment of breast cancer.  
 XX  
 XX Example 2; SEQ ID NO 389; 399pp; English.

The invention describes nucleic acids (I) and the polypeptides (II) they encode. The nucleic acids (I) may be used for preventing, diagnosing and treating diseases related to their aberrant expression i.e. breast cancers. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (II) by expressing inactive proteins or to supplement the patients own production of (II). Additionally, (I) may be used to produce (II), by inserting (I) into a host cell and culturing the cell to express the protein (II). (I) And its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in

CC samples, and therefore which patients may be in need of restorative  
 CC therapy. The host cell may also be used as antigens in the production of  
 CC antibodies against (ii) and in assays to identify modulators of (ii)'s  
 CC expression and activity. The anti-(ii) antibodies, agonists and  
 CC antagonists may be used to regulate expression and activity and as  
 CC diagnostic agents for detecting the presence of (ii) in samples (e.g. by  
 CC immunoassay). This sequence represents a secreted ovarian carcinoma  
 CC antigen.

XX  
 SQ Sequence 833 AA;  
 Query Match 92.9%; Score 3663; DB 7; Length 833;  
 Best Local Similarity 99.9%; Pred. No. 2.2e-315;  
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLFTTNLYEENMWPG 73  
 78 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLFTTNLYEENMWPG 137  
 74 SRKFNTTERTVLOGLLRPLPKNTSVGLYSGCCBLTLRPEKDGATGDAICTHRPDPGTP 133  
 138 SRKFNTTERTVLOGLLRPLPKNTSVGLYSGCCBLTLRPEKDGATGDAICTHRPDPGTP 197  
 134 GLDREQLYLELSQTHSITELGPTLDRDLSLVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193  
 198 GLDREQLYLELSQTHSITELGPTLDRDLSLVNGFTHRSSVPTTSTGVVSEEPFTLNFT 257  
 194 INNLRYMDWGPGLSKFNITDNVMKHLSPFORSSLGARYTGCVRVIALRSVNGAETR 253  
 258 INNLRYMDWGPGLSKFNITDNVMKHLSPFORSSLGARYTGCVRVIALRSVNGAETR 317  
 254 VDLLCTYLOPLSGPLPIKQVFHLSQOHTGITHGIPYSLDKSLVLYNGNEPDPDEPT 313  
 318 VDLLCTYLOPLSGPLPIKQVFHLSQOHTGITHGIPYSLDKSLVLYNGNEPDPDEPT 377  
 314 TPKPATFTPLSEATTAMGYHLKTLTNFTINLQYSPDMGKGSATFNSTEGVLQHLR 373  
 378 TPKPATFTPLSEATTAMGYHLKTLTNFTINLQYSPDMGKGSATFNSTEGVLQHLR 437  
 374 PLFOKSSMGPFYLGCCQLISLRPEKDGATGVDTTCTVHPDPVGPGLDIQQLYWLSQTH 433  
 438 PLFOKSSMGPFYLGCCQLISLRPEKDGATGVDTTCTVHPDPVGPGLDIQQLYWLSQTH 497  
 434 GVTQLGPFVLDRLSFLNGVAPQNLISIRGEYQINFHVNNLSNPDPTSSSYIILLRDIQ 493  
 498 GVTQLGPFVLDRLSFLNGVAPQNLISIRGEYQINFHVNNLSNPDPTSSSYIILLRDIQ 557  
 494 DKVTLLYKGSQHDHFRFCLVNTLMDSVLVTKALFSSNLDPSILVEQVFLDKTLNASFH 553  
 558 DKVTLLYKGSQHDHFRFCLVNTLMDSVLVTKALFSSNLDPSILVEQVFLDKTLNASFH 617  
 554 WLGSTYQLVDHVTMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 613  
 618 WLGSTYQLVDHVTMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 677  
 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLCNFPSPFLARRVDRVAIYEEF 673  
 678 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLCNFPSPFLARRVDRVAIYEEF 737  
 674 LMTTRNGTQLQNFITLDRSSVLVDGYSFNRNEPLTGN 710  
 738 LMTTRNGTQLQNFITLDRSSVLVDGYSFNRNEPLTGN 774

RESULT 7  
 ADG46172  
 ID ADG46172 standard; protein; 833 AA.  
 XX  
 XX ADG46172;  
 XX  
 XX 26-FEB-2004 (first entry)  
 DT  
 XX Human ovarian carcinoma polypeptide #3.  
 DE

XX Human; ovarian carcinoma; O8E; ovarian cancer; secreted tumour antigen;  
KW cytotatic; O772P.  
XX  
XX Homo sapiens.  
XX  
XX US2003165504-A1.  
XX  
XX 04-SEP-2003.  
XX  
XX 04-APR-2001; 2001US-00827271.  
XX  
XX 17-DEC-1998; 98US-00215681.  
XX 17-DEC-1998; 98US-00216003.  
XX 23-JUN-1999; 99US-00338933.  
XX 24-SEP-1999; 99US-00404879.  
XX 17-JUL-2000; 2000US-00617747.  
XX 20-SEP-2000; 2000US-00636801.  
XX 10-AUG-2000; 2000US-00667857.  
XX  
XX (RETT/) RETTER M W.  
XX (FANG/) FANGER G R.  
XX  
XX Retter MW, Fanger GR;  
XX  
XX WPI; 2003-898035/82.  
XX  
XX New isolated O8E or O772P polypeptides, useful for diagnosing,  
PT preventing, treating and monitoring cancer, e.g. ovarian cancer,  
PT stimulating the immune response in patient.  
XX  
XX Claim 5; SEQ ID NO 389; 290pp; English.  
XX  
XX The invention relates to human ovarian carcinoma polypeptides, designated  
CC O8E or O772P, and the polynucleotides encoding them. The invention also  
CC relates to methods for inhibiting the development of cancer, e.g. ovarian  
CC cancer in a patient, methods for stimulating and/or expanding T cells and  
CC methods for identifying secreted tumour antigens. The polypeptides,  
CC compositions, antibodies to the polypeptides and methods are useful for  
CC diagnosing, preventing, treating and monitoring cancer, e.g. ovarian  
CC cancer. The composition is particularly useful for stimulating an immune  
CC response in patient. This sequence represents a human ovarian carcinoma  
CC polypeptide of the invention.  
XX  
XX Sequence 833 AA;  
SQ  
Query Match 92.9%; Score 3663; DB 7; Length 833;  
Best Local Similarity 99.9%; Pred. No. 2.2e-315;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
14 FTHRSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTTNLYEENMWP 73  
78 FTHRSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTTNLYEENMWP 137  
74 SKFNTTERTVQLRLPLFNTSVGLYSGCRLTLRLPEKGEATGDAICTHRPDPTGP 133  
138 SKFNTTERTVQLRLPLFNTSVGLYSGCRLTLRLPEKGEATGDAICTHRPDPTGP 197  
134 GLDRQLVLELSQTHSITELGPYTLDRDSLXVNGFTHRSSVPTTSTGVSEPTLNFT 193  
198 GLDRQLVLELSQTHSITELGPYTLDRDSLXVNGFTHRSSVPTTSTGVSEPTLNFT 257  
194 INNLAYMDGQPGSLKFNITDNVKKHLLSPLFQSSILGARYTGCRVIALRSVKNGAETR 253  
258 INNLAYMDGQPGSLKFNITDNVKKHLLSPLFQSSILGARYTGCRVIALRSVKNGAETR 317  
254 VDLCTYLPQSGGLPIKQVPHLSQQTHGTRILGPYSLDKSLYLYNGYNEPGDEPPT 313  
318 VDLCTYLPQSGGLPIKQVPHLSQQTHGTRILGPYSLDKSLYLYNGYNEPGDEPPT 377  
314 TPKPATTLPPLSEATTAMGHLKTLTNFTISNLOYSFDMCKGSAATNSTEGVLOHLR 373  
378 TPKPATTLPPLSEATTAMGHLKTLTNFTISNLOYSFDMCKGSAATNSTEGVLOHLR 437

QY 374 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTCTTTHPDPVGPGLDIOQLYWELSQLTH 433  
Db 438 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTCTTTHPDPVGPGLDIOQLYWELSQLTH 497  
QY 434 GVTQLGFFVLDRLDPLFNGYAPQNLISIRGEYQINFIHVMNLSNPDPSTSEYITLLRDIQ 493  
Db 498 GVTQLGFFVLDRLDPLFNGYAPQNLISIRGEYQINFIHVMNLSNPDPSTSEYITLLRDIQ 557  
QY 494 DKVTTYLKGSQSLHDTFRCLVTNLTMDSVLVTVKALPSSNLDPSLVEQVFLDKTLNASPH 553  
Db 558 DKVTTYLKGSQSLHDTFRCLVTNLTMDSVLVTVKALPSSNLDPSLVEQVFLDKTLNASPH 617  
QY 554 WLGSSTYQLVDIHVTEMESSVYQPTSSSTQHFLYFNFTIITNLPYSQDKAOPGTTNYQRNKR 613  
Db 618 WLGSSTYQLVDIHVTEMESSVYQPTSSSTQHFLYFNFTIITNLPYSQDKAOPGTTNYQRNKR 677  
QY 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHTGVDSLGNFSPPLARRVDRVAIYEEF 673  
Db 678 NIEDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHTGVDSLGNFSPPLARRVDRVAIYEEF 737  
QY 674 LRWTRNGTOLQNFITLDRSSVLVDGYSPNREPLTGN 710  
Db 738 LRWTRNGTOLQNFITLDRSSVLVDGYSPNREPLTGN 774  
RESULT 8  
ADX17768  
ID ADX17768 standard; protein; 833 AA.  
XX  
AC ADX17768;  
XX  
DT 21-APR-2005 (first entry)  
XX Human ovarian carcinoma antigen cDNA O772P clone 21003 encoded protein.  
DE  
XX  
KW diagnosis; cytostatic; immunostimulant; gene therapy; tumor;  
KW ovarian tumor; cancer; carcinoma; antigen.  
XX  
OS Homo sapiens.  
XX  
PN US2005031634-A1.  
XX  
PD 10-FEB-2005.  
XX  
PP 02-JUN-2004; 2004US-00860790.  
XX  
PR 17-DEC-1998; 98US-00216003.  
PR 23-JUN-1999; 99US-00338933.  
PR 24-SEP-1999; 99US-00404879.  
PR 17-JUL-2000; 2000US-00617747.  
PR 10-AUG-2000; 2000US-00636801.  
PR 20-SEP-2000; 2000US-00667857.  
PR 04-APR-2001; 2001US-00827271.  
PR 18-JUN-2001; 2001US-00884441.  
PR 17-JUL-2001; 2001US-00907969.  
PR 17-JUL-2002; 2002US-00198053.  
XX (CORI-) CORIXA CORP.  
PA  
XX  
PI Bangur CS, Retter MW, Fanger GR, Hill P;  
XX  
XX WPI; 2005-151645/16.  
XX  
XX New ovarian carcinoma polynucleotides, preferably cDNAs, useful for  
PT diagnosing, preventing and treating diseases, such as ovarian cancer, and  
PT for eliciting humoral and/or cellular immune response.  
XX  
PS Example 2; SEQ ID NO 389; 398pp; English.  
XX  
CC The invention relates to an isolated polynucleotide comprising a sequence  
CC of, a sequence hybridizing under highly stringent conditions to, or  
CC having at least 75, or 90% identity to a 849 or 1399 bp, fully defined in

CC the specification, its complement or degenerate variants, or a sequence  
CC of at least 20 contiguous residues of the 849 or 1399 bp sequence. The  
CC polynucleotides and polypeptides are useful for diagnosing, preventing  
CC and treating diseases, such as ovarian cancer, and for eliciting humoral  
CC and/or cellular immune response. This sequence corresponds to an ovarian  
CC carcinoma antigen protein of the invention.

XX	Sequence 833 AA;	
QY	Query Match 92.9%; Score 3663; DB 9; Length 833;	
DB	Best Local Similarity 99.9%; Pred. No. 2.2e-315;	
QY	Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
DB	14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNFTINLYEENWMPG 73	
QY	78 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNFTINLYEENWMPG 137	
DB	74 SRKFNTERVLOGLLRPLFNTSVGLYSGCRLLTLRPEKGEATGVDAICTHRPDPTGP 133	
QY	138 SRKFNTERVLOGLLRPLFNTSVGLYSGCRLLTLRPEKGEATGVDAICTHRPDPTGP 197	
DB	134 GLDREQLYLELSQTHSITELGPTTLDRDLSLVNGFTHRSSVPTTGTGVSEEPFLNFT 193	
QY	198 GLDREQLYLELSQTHSITELGPTTLDRDLSLVNGFTHRSSVPTTGTGVSEEPFLNFT 257	
DB	194 INNLYMADMGQPSLKFNTIDNMVKHLLSPFORSSIGARYTCRVIALRSVKNGAETR 253	
QY	258 INNLYMADMGQPSLKFNTIDNMVKHLLSPFORSSIGARYTCRVIALRSVKNGAETR 317	
DB	254 VDLICTYLOPLSGPLPIKOVFHELSSQTHGTRGLPYSLDKSLYLVNGYNEPGDEPPT 313	
QY	318 VDLICTYLOPLSGPLPIKOVFHELSSQTHGTRGLPYSLDKSLYLVNGYNEPGDEPPT 377	
DB	314 TPKPATTFPLPSEATTAMGVHLKTLTLNFTISNLQVSPDMGKGSATFNSTEGVLOHLR 373	
QY	378 TPKPATTFPLPSEATTAMGVHLKTLTLNFTISNLQVSPDMGKGSATFNSTEGVLOHLR 437	
DB	374 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTTHPDVPGGLDIQOLYWELSOLTH 433	
QY	438 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTTHPDVPGGLDIQOLYWELSOLTH 497	
DB	434 GVTQLGFVLDRLDSLFNGVAPQNLISIRGEYQINFHIVNNWNLSPDPTSSSEYITLLRDIQ 493	
QY	498 GVTQLGFVLDRLDSLFNGVAPQNLISIRGEYQINFHIVNNWNLSPDPTSSSEYITLLRDIQ 557	
DB	494 DKVTTLYKGSQQLHDTFRCLVTNLTMDSVLTVKALFSSNLDPSLVQVFLDKTLNASFH 553	
QY	558 DKVTTLYKGSQQLHDTFRCLVTNLTMDSVLTVKALFSSNLDPSLVQVFLDKTLNASFH 617	
DB	554 WLSTYQLVDIHVTMESSVQPTSSSTQHFYLNFTINLYPSQDKAQCPTTNYQRNKR 613	
QY	618 WLSTYQLVDIHVTMESSVQPTSSSTQHFYLNFTINLYPSQDKAQCPTTNYQRNKR 677	
DB	614 NIEDALNQLFNSSIKSFSDQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF 673	
QY	678 NIEDALNQLFNSSIKSFSDQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF 737	
DB	674 LRMTFRNGTQLQNFTLDRSSVLVDGYSNPNRBLTGN 710	
QY	738 LRMTFRNGTQLQNFTLDRSSVLVDGYSNPNRBLTGN 774	

RESULT 9  
AAB12552  
ID AAB12552 standard; protein; 914 AA.  
XX  
AC AAB12552;  
XX  
DT 07-NOV-2000 (first entry)  
XX Human ovarian carcinoma antigen O772P protein SEQ ID NO:312.  
DE Human  
XX Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;  
KW

KW tumour antigen; identification; cytostatic; gene therapy; vaccine.  
XX Homo sapiens.  
OS WO200036107-A2.  
XX  
XX 22-JUN-2000.  
PD  
XX 17-DEC-1999; 99WO-US0302070.  
PF  
XX 17-DEC-1998; 98US-00215681.  
XX 17-DEC-1998; 98US-00216003.  
PR 23-JUN-1999; 99US-00338933.  
PR 24-SEP-1999; 99US-00404879.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Mitcham JL, King GE, Algate PA, Frudakis TN;  
PI WPI; 2000-431589/37.  
XX N-PSDB; AAA70001.  
DR  
XX Immunogenic portion of an ovarian carcinoma protein and the nucleic acid  
PT encoding it, useful for the diagnosis, prevention and treatment of  
PT cancer, preferably ovarian cancer.  
XX  
XX Example 2; Page 172-174; 299pp; English.  
XX  
XX The present invention describes an isolated polypeptide comprising an  
CC immunogenic portion of an ovarian carcinoma protein (or its variants).  
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have  
CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian  
CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful  
CC for the prevention, diagnosis and treatment of cancer, preferably ovarian  
CC cancer. AAA9691 to AAA70077 and AAB12552 to AAB12557 represent human  
CC ovarian carcinoma polynucleotides and proteins used in the  
CC exemplification of the present invention

XX	Sequence 914 AA;	
QY	Query Match 92.9%; Score 3663; DB 3; Length 914;	
DB	Best Local Similarity 99.9%; Pred. No. 2.5e-315;	
QY	Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
DB	14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNFTINLYEENWMPG 73	
QY	159 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNFTINLYEENWMPG 218	
DB	74 SRKFNTERVLOGLLRPLFNTSVGLYSGCRLLTLRPEKGEATGVDAICTHRPDPTGP 133	
QY	219 SRKFNTERVLOGLLRPLFNTSVGLYSGCRLLTLRPEKGEATGVDAICTHRPDPTGP 278	
DB	134 GLDREQLYLELSQTHSITELGPTTLDRDLSLVNGFTHRSSVPTTGTGVSEEPFLNFT 193	
QY	279 GLDREQLYLELSQTHSITELGPTTLDRDLSLVNGFTHRSSVPTTGTGVSEEPFLNFT 338	
DB	194 INNLYMADMGQPSLKFNTIDNMVKHLLSPFORSSIGARYTCRVIALRSVKNGAETR 253	
QY	339 INNLYMADMGQPSLKFNTIDNMVKHLLSPFORSSIGARYTCRVIALRSVKNGAETR 398	
DB	254 VDLICTYLOPLSGPLPIKOVFHELSSQTHGTRGLPYSLDKSLYLVNGYNEPGDEPPT 313	
QY	399 VDLICTYLOPLSGPLPIKOVFHELSSQTHGTRGLPYSLDKSLYLVNGYNEPGDEPPT 458	
DB	314 TPKPATTFPLPSEATTAMGVHLKTLTLNFTISNLQVSPDMGKGSATFNSTEGVLOHLR 373	
QY	459 TPKPATTFPLPSEATTAMGVHLKTLTLNFTISNLQVSPDMGKGSATFNSTEGVLOHLR 518	
DB	374 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTTHPDVPGGLDIQOLYWELSOLTH 433	
QY	519 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTTHPDVPGGLDIQOLYWELSOLTH 578	
DB	434 GVTQLGFVLDRLDSLFNGVAPQNLISIRGEYQINFHIVNNWNLSPDPTSSSEYITLLRDIQ 493	

Db 579 GVTQLGQYVLDRLDLSLFGVAPQNLIRGEYQINFIHVNWNLSPNDPTSEYITLLRDIQ 638  
Qy 494 DKVTLLYKGSQQLHDTFRFCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 553  
Db 639 DKVTLLYKGSQQLHDTFRFCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 698  
Qy 554 WLGSYQLVDIHVTEMESVYQPTSSSTQHFLYLNFTITNLPSYQDKAQPGTTNYQRNKR 613  
Db 699 WLGSYQLVDIHVTEMESVYQPTSSSTQHFLYLNFTITNLPSYQDKAQPGTTNYQRNKR 758  
Qy 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPNRHHTGVDSLGNFSPPLARRVDRVAIYEEF 673  
Db 759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPNRHHTGVDSLGNFSPPLARRVDRVAIYEEF 818  
Qy 674 LRMRNGTQLQNFLLDRSSVLDGYSNRPNEPLTGN 710  
Db 819 LRMRNGTQLQNFLLDRSSVLDGYSNRPNEPLTGN 855

RESULT 10  
AAB99203  
ID AAB99203 standard; protein; 914 AA.  
XX  
AC AAB99203;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Human ovarian tumour-derived antigen O772P.  
XX  
KW Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour;  
antigen; O772P.  
XX  
OS Homo sapiens.  
XX  
PN WO200140269-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 29-NOV-2000; 2000WO-US032520.  
XX  
PR 30-NOV-1999; 99US-00451651.  
PR 22-FEB-2000; 2000US-00510662.  
PR 10-MAR-2000; 2000US-00523586.  
PR 07-APR-2000; 2000US-00545068.  
PR 15-MAY-2000; 2000US-00571025.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Dillion DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;  
XX  
WPI; 2001-356154/37.  
XX  
N-PSDB; AAB99203.  
XX  
PT Breast tumor polypeptides and the nucleic acids that encode them, useful  
for the prevention, diagnosis and treatment of breast cancer.  
XX  
PS Example 3; Page 187-188; 221pp; English.  
XX  
CC The present invention relates to human breast tumour protein coding  
sequences (see AAB99203, AAB99203, AAB99203 and AAB99203-  
AAB99203). The breast tumour protein DNA sequences may be used in the  
prevention, diagnosis and treatment of diseases associated with  
inappropriate expression of the breast tumour protein e.g. breast cancer.  
CC The present sequence is a human ovarian tumour-derived antigen, which was  
used in an example from the present invention  
XX  
SQ Sequence 914 AA;

Query Match 92.9%; Score 3663; DB 4; Length 914;  
Best Local Similarity 99.9%; Pred. No. 2.5e-315;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTLNFTITNLRYEENWMPG 73  
Db 159 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTLNFTITNLRYEENWMPG 218  
Qy 74 SRKFNTERVLOGLLRPLPKNTSVGLYSYCRLLTLRPEKGEATGVDAICTHRPDTGP 133  
Db 219 SRKFNTERVLOGLLRPLPKNTSVGLYSYCRLLTLRPEKGEATGVDAICTHRPDTGP 278  
Qy 134 GLDREQLYLELSQTHSITELGPTVTLDRDLSLYNGFTHRSSVPTTSGVYSEEPFTLNFT 193  
Db 279 GLDREQLYLELSQTHSITELGPTVTLDRDLSLYNGFTHRSSVPTTSGVYSEEPFTLNFT 338  
Qy 194 INNLRYMADMGQPGSLKFNITDNMKHLLSPLRQSSLGARYTGCRRVIALRSVKNAGATR 253  
Db 339 INNLRYMADMGQPGSLKFNITDNMKHLLSPLRQSSLGARYTGCRRVIALRSVKNAGATR 398  
Qy 254 VDLCTYLOPLSGPGLPIKQVHFELSOQTHGIRLGPYSLDKSLYNGNEPDPDPPT 313  
Db 399 VDLCTYLOPLSGPGLPIKQVHFELSOQTHGIRLGPYSLDKSLYNGNEPDPDPPT 458  
Qy 314 TPKPATTFLPPLSEATTAMGYHLKTLTNTISNLOYSYPMGKGSATFNSSTEGVLOHLLR 373  
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTNTISNLOYSYPMGKGSATFNSSTEGVLOHLLR 518  
Qy 374 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTCTTTHPDPVGLDIOQLYWELSQLTH 433  
Db 519 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTCTTTHPDPVGLDIOQLYWELSQLTH 578  
Qy 434 GVTOLGPFYVLDRLDLSLFGVAPQNLIRGEYQINFIHVNWNLSPNDPTSEYITLLRDIQ 493  
Db 579 GVTOLGPFYVLDRLDLSLFGVAPQNLIRGEYQINFIHVNWNLSPNDPTSEYITLLRDIQ 638  
Qy 494 DKVTLLYKGSQQLHDTFRFCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 553  
Db 639 DKVTLLYKGSQQLHDTFRFCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 698  
Qy 554 WLGSYQLVDIHVTEMESVYQPTSSSTQHFLYLNFTITNLPSYQDKAQPGTTNYQRNKR 613  
Db 699 WLGSYQLVDIHVTEMESVYQPTSSSTQHFLYLNFTITNLPSYQDKAQPGTTNYQRNKR 758  
Qy 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPNRHHTGVDSLGNFSPPLARRVDRVAIYEEF 673  
Db 759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPNRHHTGVDSLGNFSPPLARRVDRVAIYEEF 818  
Qy 674 LRMRNGTQLQNFLLDRSSVLDGYSNRPNEPLTGN 710  
Db 819 LRMRNGTQLQNFLLDRSSVLDGYSNRPNEPLTGN 855

RESULT 11  
AAB99203  
ID AAB99203 standard; protein; 914 AA.  
XX  
AC AAB99203;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Hypothetical protein sequence for clone 0772P.  
XX  
KW Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.  
XX  
OS Homo sapiens.  
XX  
PN WO200206317-A2.  
XX  
PD 24-JAN-2002.  
XX  
PF 17-JUL-2001; 2001WO-US022635.  
XX  
PR 17-JUL-2000; 2000US-00617747.  
PR 10-AUG-2000; 2000US-00636801.  
PR 20-SEP-2000; 2000US-00667857.  
PR 04-APR-2001; 2001US-00827271.

18-JUN-2001; 2001US-00884441.  
(CORI-) CORIXA CORP.  
Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;  
Reed SG, Vedvick TS, Carter D, Hill P, Albone E;  
WPI; 2002-164781/21.  
N-PSDB; ABN72974.  
Polypeptides comprising an immunogenic portion of an ovarian carcinoma protein or its variants, useful for stimulating an immune response in a patient and treating ovarian cancer.  
Disclosure; Page 350-352; 408pp; English.  
This invention relates to polypeptides comprising an immunogenic portion of an ovarian carcinoma protein which acts as an immunostimulant and is cytostatic. The polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells that express the polypeptides are useful for stimulating an immune response in a patient and treating ovarian cancer. This sequence represents protein related to the invention  
SQ Sequence 914 AA;  
Query Match 92.9%; Score 3663; DB 5; Length 914;  
Best Local Similarity 99.9%; Pred. No. 2.5e-315;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 14 FTHRSSVSTTSTPGTPTVYLKNTSVGLYSGRLTLRLPEKDGATGVDAICTHRPDPGTP 73  
DB 159 FTHRSSVSTTSTPGTPTVYLKNTSVGLYSGRLTLRLPEKDGATGVDAICTHRPDPGTP 218  
QY 74 SRKFNTERVQLGLRLPLFKNTSVGLYSGRLTLRLPEKDGATGVDAICTHRPDPGTP 133  
DB 219 SRKFNTERVQLGLRLPLFKNTSVGLYSGRLTLRLPEKDGATGVDAICTHRPDPGTP 278  
QY 134 GLDRQLYLELSQLTHSITELGPTLDRDSLTVNGFTHRSSVPTTSTGVWSEEPFLNFT 193  
DB 279 GLDRQLYLELSQLTHSITELGPTLDRDSLTVNGFTHRSSVPTTSTGVWSEEPFLNFT 338  
QY 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSILGARYTCRVIALRSVKNGAETR 253  
DB 339 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSILGARYTCRVIALRSVKNGAETR 398  
QY 254 VDLICTVLOPLSGPLPIKQVHELSQLTHGITRLGYSGLDKDSLILNGYNEPGRDPPT 313  
DB 399 VDLICTVLOPLSGPLPIKQVHELSQLTHGITRLGYSGLDKDSLILNGYNEPGRDPPT 458  
QY 314 TPKEATTFPLPSEATTANGVHLKTLTLNFTISNLQYSPDMGKSATFNSTEGVLQHLR 373  
DB 459 TPKEATTFPLPSEATTANGVHLKTLTLNFTISNLQYSPDMGKSATFNSTEGVLQHLR 518  
QY 374 PLFQKSSMGPFYLGQILSLRPEKGAATGVDTTCTHHPDPVGPGLDIQQLYWLSQLTH 433  
DB 519 PLFQKSSMGPFYLGQILSLRPEKGAATGVDTTCTHHPDPVGPGLDIQQLYWLSQLTH 578  
QY 434 GVTQLGFVYLDRLSIFINGYAPONLSIRGEVQINPHIVNWLNSNPDPTSSSEVITLRLDIQ 493  
DB 579 GVTQLGFVYLDRLSIFINGYAPONLSIRGEVQINPHIVNWLNSNPDPTSSSEVITLRLDIQ 638  
QY 494 DKVTLYKGSOLHDFRCLVNTLMTDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH 553  
DB 639 DKVTLYKGSOLHDFRCLVNTLMTDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH 698  
QY 554 WLGSYQLVDIHVTEMSSSVQPTSSSTQHLYNFTITNLPYSQDKAQPGTNTYQRNKR 613  
DB 699 WLGSYQLVDIHVTEMSSSVQPTSSSTQHLYNFTITNLPYSQDKAQPGTNTYQRNKR 758  
QY 614 NIEDALNQLFRNSSIKSFESDCQVSTFRVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673  
DB 759 NIEDALNQLFRNSSIKSFESDCQVSTFRVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 818

674 LEWTRNGTOLQNFLLDRSSVLVDGYSPNREPLTGN 710  
819 LEWTRNGTOLQNFLLDRSSVLVDGYFPNREPLTGN 855  
RESULT 12  
ABP30896  
ID ABP30896 standard; protein; 914 AA.  
XX  
AC ABP30896;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE 0772P protein.  
XX  
KW Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.  
XX  
OS Homo sapiens.  
XX  
PN W0200206317-A2.  
XX  
PD 24-JAN-2002.  
XX  
PF 17-JUL-2001; 2001WO-US022635.  
XX  
PR 17-JUL-2000; 2000US-00617747.  
PR 10-AUG-2000; 2000US-00636801.  
PR 20-SEP-2000; 2000US-00667857.  
PR 04-APR-2001; 2001US-00827271.  
PR 18-JUN-2001; 2001US-00884441.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;  
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;  
XX  
DR WPI; 2002-164781/21.  
DR N-PSDB; ABN72895.  
XX  
PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma protein or its variants, useful for stimulating an immune response in a patient and treating ovarian cancer.  
XX  
PS Example 2; Page 291; 408pp; English.  
XX  
CC This invention relates to polypeptides comprising an immunogenic portion of an ovarian carcinoma protein which acts as an immunostimulant and is cytostatic. The polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells that express the polypeptides are useful for stimulating an immune response in a patient and treating ovarian cancer. This sequence represents protein related to the invention  
SQ Sequence 914 AA;  
Query Match 92.9%; Score 3663; DB 5; Length 914;  
Best Local Similarity 99.9%; Pred. No. 2.5e-315;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 14 FTHRSSVSTTSTPGTPTVYLKNTSVGLYSGRLTLRLPEKDGATGVDAICTHRPDPGTP 73  
DB 159 FTHRSSVSTTSTPGTPTVYLKNTSVGLYSGRLTLRLPEKDGATGVDAICTHRPDPGTP 218  
QY 74 SRKFNTERVQLGLRLPLFKNTSVGLYSGRLTLRLPEKDGATGVDAICTHRPDPGTP 133  
DB 219 SRKFNTERVQLGLRLPLFKNTSVGLYSGRLTLRLPEKDGATGVDAICTHRPDPGTP 278  
QY 134 GLDRQLYLELSQLTHSITELGPTLDRDSLTVNGFTHRSSVPTTSTGVWSEEPFLNFT 193  
DB 279 GLDRQLYLELSQLTHSITELGPTLDRDSLTVNGFTHRSSVPTTSTGVWSEEPFLNFT 338  
QY 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSILGARYTCRVIALRSVKNGAETR 253

Db 339 INNLRYMADMGQPSGLKFNITDNVMKHLSPFQSSSLGARYTGCRVIALRSVKNAGETR 398  
QY 254 VDLCTYQLQPSGLPIKQVPHLSQOOTHGIRLGPYSLDKDSLYLNGVNEBPGDEPPT 313  
Db 399 VDLCTYQLQPSGLPIKQVPHLSQOOTHGIRLGPYSLDKDSLYLNGVNEBPGDEPPT 458  
QY 314 TPKPATTFLPPLSEATTAMGYHLKTLTILNFTISNLQYSPDMGKGSATFNSGVLQHLR 373  
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTILNFTISNLQYSPDMGKGSATFNSGVLQHLR 518  
QY 374 PLFQKSSMGPPYLGCOLISLRPEKGAATGVDCTCTHYHDPVCPGLDIOQLYELSLQTH 433  
Db 519 PLFQKSSMGPPYLGCOLISLRPEKGAATGVDCTCTHYHDPVCPGLDIOQLYELSLQTH 578  
QY 434 GVTQLGFVYLDRLSDFNGVAPQNLISIRGEYQINFNHIVNWNLSNPPTSSSEYITLLRDQ 493  
Db 579 GVTQLGFVYLDRLSDFNGVAPQNLISIRGEYQINFNHIVNWNLSNPPTSSSEYITLLRDQ 638  
QY 494 DKVTTLKGSQSLHDTFRFCLVNTLMTDSVLVTVKALFSSNLDPSLVEQVPLDKTLNASFH 553  
Db 639 DKVTTLKGSQSLHDTFRFCLVNTLMTDSVLVTVKALFSSNLDPSLVEQVPLDKTLNASFH 698  
QY 554 WLGSTYQLVDIHVTMESSYVQPTSSSTQHFLNFTITNLQYSPDMGKGSATFNSGVLQHLR 613  
Db 699 WLGSTYQLVDIHVTMESSYVQPTSSSTQHFLNFTITNLQYSPDMGKGSATFNSGVLQHLR 758  
QY 614 NIEDALNQLFRNSSIKSYSDCOVSTFRSPVNRHHTGVDSLCNFSPLARRVDRVAIYEEF 673  
Db 759 NIEDALNQLFRNSSIKSYSDCOVSTFRSPVNRHHTGVDSLCNFSPLARRVDRVAIYEEF 818  
QY 674 LRMRNGTQLQNFLLDRSSVLVDGYSFNRNEPLTGN 710  
Db 819 LRMRNGTQLQNFLLDRSSVLVDGYSFNRNEPLTGN 855  
RESULT 13  
ID ADU01425  
XX ADU01425 standard; protein; 914 AA.  
XX AC ADU01425;  
XX DT 30-DEC-2004 (first entry)  
XX DE Breast cancer associated polypeptide seqid 206.  
XX KW cytostatic; gene therapy; vaccine; breast cancer; cancer; tumour;  
XX KW immune response; O8E; vaccine.  
XX OS Homo sapiens.  
XX PN US2002081609-A1.  
XX PD 27-JUN-2002.  
XX PF 20-JUL-2001; 2001US-00910689.  
XX PR 30-NOV-1999; 99US-00451651.  
XX PR 22-FEB-2000; 2000US-00510662.  
XX PR 10-MAR-2000; 2000US-00523586.  
XX PR 07-APR-2000; 2000US-00545068.  
XX PR 15-MAY-2000; 2000US-00571025.  
XX PR 06-FEB-2001; 2001US-00778320.  
XX PA (DILL/) DILLON D C.  
XX PA (DAYC/) DAY C H.  
XX PA (JIAN/) JIANG Y.  
XX PA (HOUG/) HOUGHTON R L.  
XX PA (MITC/) MITCHAM J L.  
XX PA (WANG/) WANG T.  
XX PA (MCNE/) MCNEILL P D.  
XX PA (HARL/) HARLOCKER S L.  
XX

PI Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang T;  
PI McNeill PD, Harlocker SL;  
XX WPI; 2002-657500/70.  
DR N-PSDB; ADU01424.  
XX  
PT Novel breast cancer polynucleotides and polypeptides encoded by the  
PT polynucleotides, useful for detecting the presence of breast cancer in  
PT patient, and in pharmaceutical compositions, for treating breast cancer.  
XX  
PS Claim 2; SEQ ID NO 206; 159pp; English.  
XX  
CC The invention describes an isolated breast cancer polynucleotide (I)  
CC comprising a sequence (S1) selected from the 249 nucleotide sequences  
CC fully defined in the specification, complements of S1, a sequence that  
CC comprising at least 20 contiguous residues of S1, a sequence that  
CC hybridise to S1, under moderately stringent conditions, a sequence having  
CC at least 75%, preferably 90% identity to S1, or degenerate variants of  
CC S1. Also described are: an isolated polypeptide (II) encoded by (I), or  
CC sequences having at least 70%, preferably 90% identity to (I); an  
CC expression vector (III); a host cell (IV) transformed or transfected with  
CC (III); an isolated antibody (Ab) that specifically binds to (II);  
CC detecting (M1) the presence of cancer in a patient; a fusion protein (V)  
CC comprising (II); an oligonucleotide (VI) that hybridises to S1;  
CC stimulating and/or expanding (M2) T cells specific for a tumour protein;  
CC a composition (C) comprising physiologically acceptable carriers and  
CC immunostimulants as first component, and a second component selected from  
CC (I), (II), Ab, (VI), (VII) and antigen presenting cells that express (II);  
CC and inhibiting (M3) the development of a cancer in a patient. (C) is  
CC useful for stimulating immune response in a patient, and for treating  
CC cancer in a patient. (VI) is useful for determining the presence of  
CC cancer in a patient, by obtaining a biological sample from the patient,  
CC contacting the biological sample with a monoclonal antibody that bind to  
CC O8E, isolating cells that bind to the antibody that binds to O8E,  
CC isolating polynucleotides from the isolated cells, and contacting the  
CC polynucleotides with (VI), detecting an amount of polynucleotides that  
CC hybridise to the oligonucleotide, and comparing the amount of  
CC polynucleotides that hybridise to the oligonucleotide to a predetermined  
CC cut-off value, and thus determining the presence of cancer in the  
CC patient. (I) and (II) are useful in pharmaceutical compositions, e.g.  
CC vaccines. (I) is useful in the design and preparation of ribozyme  
CC molecules for inhibiting expression of the tumour polypeptides and  
CC proteins in tumour cells. (I) is useful as marker to indicate the  
CC presence or absence of a cancer such as breast cancer. (C) is useful for  
CC inhibiting the development of breast cancer in a patient, and for  
CC removing tumour cells from a biological sample. Ab (binding agent for  
CC (I)) is useful for detecting the presence of cancer in a patient. This  
CC sequence represents a breast cancer associated protein.  
XX  
SQ Sequence 914 AA;  
Query Match 92.9%; Score 3663; DB 5; Length 914;  
Best Local Similarity 99.9%; Pred. No. 2.5e-315; Indels 0; Gaps 0;  
Matches 696; Conservative 0; Mismatches 1;  
QY 14 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNTITNLRYEENWPG 73  
Db 159 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNTITNLRYEENWPG 218  
QY 74 SRKFNTTERTVLOGLLPLFNKTSVGLYSGCRLLTLRPEKDGATGDAICTHRPDTGP 133  
Db 219 SRKFNTTERTVLOGLLPLFNKTSVGLYSGCRLLTLRPEKDGATGDAICTHRPDTGP 278  
QY 134 GLDREQLYLELSQTHSITELGPYTLDRDLSLVNGFTHRSSVPTTGTGVVSEBPFLLNFT 193  
Db 279 GLDREQLYLELSQTHSITELGPYTLDRDLSLVNGFTHRSSVPTTGTGVVSEBPFLLNFT 338  
QY 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFQSSSLGARYTGCRVIALRSVKNAGETR 253  
Db 339 INNLRYMADMGQPSGLKFNITDNVMKHLSPFQSSSLGARYTGCRVIALRSVKNAGETR 398  
QY 254 VDLCTYQLQPSGLPIKQVPHLSQOOTHGIRLGPYSLDKDSLYLNGVNEBPGDEPPT 313



Db 399 VDLLCTYLQPLSGPLPIKQVHFLSQTHGTRGLRPSYSLDKSLYNGYNEPGDPPT 458  
Qy 314 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSATFSTEGVQLHLR 373  
Db 459 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSATFSTEGVQLHLR 518  
Qy 374 PLFKSSMGPFYLGCLISLRPEKGAATGVDTTCTVHPDPVPGGLDIQQLYWELSLTH 433  
Db 519 PLFKSSMGPFYLGCLISLRPEKGAATGVDTTCTVHPDPVPGGLDIQQLYWELSLTH 578  
Qy 434 GVTQLGPFVLDRLDSLFNGYAPQNLISIRGEYQINFIHVNWNLNPDPTSEYITLLRDIQ 493  
Db 579 GVTQLGPFVLDRLDSLFNGYAPQNLISIRGEYQINFIHVNWNLNPDPTSEYITLLRDIQ 638  
Qy 494 DKVTTLKGSQQLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553  
Db 639 DKVTTLKGSQQLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698  
Qy 554 WLGSYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAQPGLTNYQRNKR 613  
Db 699 WLGSYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAQPGLTNYQRNKR 758  
Qy 614 NIEDALNQLFRNSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF 673  
Db 759 NIEDALNQLFRNSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF 818  
Qy 674 LRMTNQTQLNFTLDRSSVLVDGYSNRPNEPLTGN 710  
Db 819 LRMTNQTQLNFTLDRSSVLVDGYSNRPNEPLTGN 855

RESULT 14  
ADZ41689  
ID ADZ41689 standard; protein; 914 AA.  
XX  
AC ADZ41689;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE Human breast cancer associated protein SEQ ID NO 206.  
XX  
KW cytostatic; gene therapy; vaccine; diagnosis; cancer; pharmaceutical; cancer;  
KW neoplasm; breast tumor; endocrine disease; gynecology and obstetrics.  
OS Homo sapiens.  
XX  
PN W0200262203-A2.  
XX  
PD 15-AUG-2002.  
XX  
PF 04-FEB-2002; 2002WO-US003332.  
XX  
PR 06-FEB-2001; 2001US-00778320.  
PR 20-JUL-2001; 2001US-00910689.  
PR 30-NOV-2001; 2001US-00010742.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Dillion DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang T;  
PI McNeill PD, Harlocker SL, Bennington AA, Zehentner B, Fanger GR;  
PI Retter MW;  
XX  
DR WPI; 2002-657500/70.  
DR N-PSDB; ADZ41688.  
XX  
XX Novel breast cancer polynucleotides and polypeptides encoded by the  
PT polynucleotides, useful for detecting the presence of breast cancer in  
PT patient, and in pharmaceutical compositions, for treating breast cancer.  
XX  
XX Claim 2; SEQ ID NO 206; 237pp; English.  
PS  
XX The invention describes an isolated breast cancer polynucleotide (I)  
CC comprising a sequence (S1) selected from the 249 nucleotide sequences

CC fully defined in the specification, complements of S1, a sequence  
CC comprising at least 20 contiguous residues of S1, a sequence that  
CC hybridize to S1, under moderately stringent conditions, a sequence having  
CC at least 75%, preferably 90% identity to S1, or degenerate variants of  
CC S1. Also described are: an isolated polypeptide (II) comprising a  
CC sequence (S2) selected from any one of the 11 sequences mentioned in the  
CC specification, sequences encoded by (I), or sequences having at least  
CC 70%, preferably 90% identity to (I); an expression vector (III)  
CC comprising (II) operably linked to an expression control sequence; a host  
CC cell (IV) transformed or transfected with (III); an isolated antibody  
CC (Ab) or its antigen-binding fragment, that specifically binds to (II);  
CC detecting (M1) the presence of cancer in a patient; a fusion protein (V)  
CC comprising (II); an oligonucleotide (VI) that hybridizes to S1;  
CC stimulating and/or expanding (M2) T cells specific for a tumor protein;  
CC an isolated T cell population (VII), comprising T cells prepared by (M2);  
CC a composition (C) comprising physiologically acceptable carriers and  
CC immunostimulants as first component, and a second component selected from  
CC (I), (II), Ab, (V), (VII) and antigen presenting cells that express (II);  
CC a diagnostic kit (VIII) comprising (VI), or Ab and a detection reagent  
CC comprising a reporter group; and inhibiting (M3) the development of a  
CC cancer in a patient, by incubating CD4+ and/or CD8+ T cells isolated from  
CC a patient with (I), (II) or antigen presenting cells that express (II), the  
CC so that T cell proliferate, administering the proliferated T cells to the  
CC patient, and therefore inhibiting the development of a cancer in the  
CC patient. The following are disclosed: monitoring the progression of  
CC cancer; fragments of (II); (xenogeneic) variants of (I); polynucleotide  
CC compositions comprising antisense oligonucleotide; and kit for use in  
CC diagnostic methods. (C) is useful for stimulating immune response in a  
CC patient, and for treating cancer in a patient. (VI) is useful for  
CC determining the presence of cancer in a patient. (I) and (II) are useful  
CC in pharmaceutical compositions, e.g. vaccines. (I) is useful in the  
CC design and preparation of ribozyme molecules for inhibiting expression of  
CC the tumor polypeptides and proteins in tumor cells. (I) is useful as  
CC marker to indicate the presence or absence of a cancer such as breast  
CC cancer. (C) is useful for inhibiting the development of breast cancer in  
CC a patient, and for removing tumor cells from a biological sample. Ab  
CC (binding agent for (I)) is useful for detecting the presence of cancer in  
CC a patient. This is the amino acid sequence of a breast cancer associated  
CC protein. Note: This sequence has been extracted from the sequence listing  
CC of a corrected version of the specification published on the 3rd of March  
CC 2005.  
XX

## Sequence 914 AA;

Query Match 92.9%; Score 3663; DB 5; Length 914;  
Best Local Similarity 99.9%; Pred. No. 2.5e-315;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 14 FTHRSSVSTSTPGTPTVILGASKTPASIFGPSAASHLLILFTLFTITNLRYEENMWPG 73  
Db 159 FTHRSSVSTSTPGTPTVILGASKTPASIFGPSAASHLLILFTLFTITNLRYEENMWPG 218  
Qy 74 SRKFNTTERTVQLGLRLPLFKNTSVGLYSGRITLLRPEKDGATGVDAICTHRPDTGP 133  
Db 219 SRKFNTTERTVQLGLRLPLFKNTSVGLYSGRITLLRPEKDGATGVDAICTHRPDTGP 278  
Qy 134 GLDREQLYELSLQTHSITELGPVTLDRDLSLYNGFTHRSSVPTTSVGVSEEPFTLNFT 193  
Db 279 GLDREQLYELSLQTHSITELGPVTLDRDLSLYNGFTHRSSVPTTSVGVSEEPFTLNFT 338  
Qy 194 INNLRYMADMGQPSGLKFNITDNVMKLLSPLFORSSLGARYTGCRIALRSVNGAETR 253  
Db 339 INNLRYMADMGQPSGLKFNITDNVMKLLSPLFORSSLGARYTGCRIALRSVNGAETR 398  
Qy 254 VDLLCTYLQPLSGPLPIKQVHFLSQTHGTRGLRPSYSLDKSLYNGYNEPGDPPT 313  
Db 399 VDLLCTYLQPLSGPLPIKQVHFLSQTHGTRGLRPSYSLDKSLYNGYNEPGDPPT 458  
Qy 314 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSATFSTEGVQLHLR 373  
Db 459 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKSATFSTEGVQLHLR 518  
Qy 374 PLFKSSMGPFYLGCLISLRPEKGAATGVDTTCTVHPDPVPGGLDIQQLYWELSLTH 433



|||||  
519 PLFKSSMGPFYLGQCLISLRPEKGAAGTCTTCTHYHDPVGPGLDIQOLYWELSQLTH 578  
QY 434 GVTQLGPFYVLDRLSLFNGVAPQNLISIRGEYQINFIHVNWNLNPNPPTSSSEYITLLRDIQ 493  
Db 579 GVTQLGPFYVLDRLSLFNGVAPQNLISIRGEYQINFIHVNWNLNPNPPTSSSEYITLLRDIQ 638  
QY 494 DKVTTLTKGSQLHDTFRFCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553  
Db 639 DKVTTLTKGSQLHDTFRFCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698  
QY 554 WLGSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTITNLPYSQDKAOPGTTNYQRNKR 613  
Db 699 WLGSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTITNLPYSQDKAOPGTTNYQRNKR 758  
QY 614 NIEDALNQLFRNSSIKSYSDCCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673  
Db 759 NIEDALNQLFRNSSIKSYSDCCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 818  
QY 674 LRMRNGTQLQNTLDRSSVLVDGYSPNRNEPLTGNS 710  
Db 819 LRMRNGTQLQNTLDRSSVLVDGYSPNRNEPLTGNS 855

## RESULT 15

ADA08631  
ID ADA08631 standard; protein; 914 AA.

AC ADA08631;

DT 06-NOV-2003 (first entry)

DE Human O772P partial protein #1.

EX human; gene therapy; ovarian cancer; cancer.

OS Homo sapiens.

PN US2003091580-A1.

XX 15-MAY-2003.

PF 17-JUL-2001; 2001US-00907969.

XX 18-JUN-2001; 2001US-00884441.

PA (MITC/) MITCHAM J L.

PA (KING/) KING G E.

PA (ALGA/) ALGATE P A.

PA (FLIN/) FLING S P.

PA (RETT/) RETTER M W.

PA (FANG/) FANGER G R.

PA (REED/) REED S G.

PA (VEDV/) VEDVICK T S.

PA (CART/) CARTER D.

PA (HILL/) HILL P.

PA (ALBO/) ALBONE E.

XX Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;

PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;

XX WPI; 2003-532352/50.

XX New isolated O772P polypeptides and polynucleotides, useful in gene

PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian

PT cancer.

CC and treating ovarian cancer. Detecting the presence of the  
CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian  
CC carcinoma and protein cDNAs were identified using microarray  
CC technology. The present sequence represents a human ovarian carcinoma  
CC antigen.  
XX  
SQ Sequence 914 AA;

## Query Match

Best Local Similarity 92.9%; Score 3663; DB 7; Length 914;

Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 PTHRVSSTSTPGPTTVYLGASKTPASIFGSAASHLLILFTLNTITNLRYEENWPG 73  
Db 159 PTHRVSSTSTPGPTTVYLGASKTPASIFGSAASHLLILFTLNTITNLRYEENWPG 218

QY 74 SRKFNTERVLOGLRLPLFNKTSVGLYSGCRLLTLRPEKGEATGVDAICTHRPDPGP 133  
Db 219 SRKFNTERVLOGLRLPLFNKTSVGLYSGCRLLTLRPEKGEATGVDAICTHRPDPGP 278

QY 134 GLDREQLYLELSQLTHSITELGPTTLDRDSLTVNGFTHRSSVPTTSTGVVSEFPPTLNPT 193  
Db 279 GLDREQLYLELSQLTHSITELGPTTLDRDSLTVNGFTHRSSVPTTSTGVVSEFPPTLNPT 338

QY 194 INNLRYMADMGQPSGLKFNITDNVMKHLISPLFORSSLGARTGCRVIALRSVNGAETR 253  
Db 339 INNLRYMADMGQPSGLKFNITDNVMKHLISPLFORSSLGARTGCRVIALRSVNGAETR 398

QY 254 VDLCTYQLPLSGPGLPIKQVFHELSQOHTGTRGLGPSYLDKDSLTVNGVNEGPDPPT 313  
Db 399 VDLCTYQLPLSGPGLPIKQVFHELSQOHTGTRGLGPSYLDKDSLTVNGVNEGPDPPT 458

QY 314 TPKPATTFLPPLSEATTAMGYHLKTLITLNTISNLOQSPDMGKGSATFNSTEGVLOHLR 373  
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLITLNTISNLOQSPDMGKGSATFNSTEGVLOHLR 518

QY 374 PLFQKSSMGPFYLGQCLISLRPEKGAAGTCTTCTHYHDPVGPGLDIQOLYWELSQLTH 433  
Db 519 PLFQKSSMGPFYLGQCLISLRPEKGAAGTCTTCTHYHDPVGPGLDIQOLYWELSQLTH 578

QY 434 GVTQLGPFYVLDRLSLFNGVAPQNLISIRGEYQINFIHVNWNLNPNPPTSSSEYITLLRDIQ 493  
Db 579 GVTQLGPFYVLDRLSLFNGVAPQNLISIRGEYQINFIHVNWNLNPNPPTSSSEYITLLRDIQ 638

QY 494 DKVTTLTKGSQLHDTFRFCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553  
Db 639 DKVTTLTKGSQLHDTFRFCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698

QY 554 WLGSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTITNLPYSQDKAOPGTTNYQRNKR 613  
Db 699 WLGSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTITNLPYSQDKAOPGTTNYQRNKR 758

QY 614 NIEDALNQLFRNSSIKSYSDCCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673  
Db 759 NIEDALNQLFRNSSIKSYSDCCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 818

QY 674 LRMRNGTQLQNTLDRSSVLVDGYSPNRNEPLTGNS 710

Db 819 LRMRNGTQLQNTLDRSSVLVDGYSPNRNEPLTGNS 855

## RESULT 16

ADA08465

ID ADA08465 standard; protein; 914 AA.

XX ADA08465;

XX 06-NOV-2003 (first entry)

DE Human ovarian carcinoma antigen O772P.

XX human; gene therapy; ovarian cancer; cancer.

XX

```

OS Homo sapiens.
XX US2003091580-A1.
XX
XX PD 15-MAY-2003.
XX
XX PF 17-JUL-2001; 2001US-00907969.
XX
XX PR 18-JUN-2001; 2001US-00884441.
XX
XX PA (MITC/) MITCHAM J L.
XX PA (KING/) KING G E.
XX PA (ALGA/) ALGATE P A.
XX PA (FLIN/) FLING S P.
XX PA (RETT/) RETTER M W.
XX PA (FANG/) FANGER G R.
XX PA (REED/) REED S G.
XX PA (VEDV/) VEDVICK T S.
XX PA (CART/) CARTER D.
XX PA (HILL/) HILL P.
XX PA (ALBO/) ALBONE E.
XX
XX PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
XX PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
XX DR WPI; 2003-532352/50.
XX DR N-PSDB; ADA09060.
XX
XX PT New isolated O772P polypeptides and polynucleotides, useful in gene
XX PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
XX PT cancer.
XX
XX PS Example 2; SEQ ID NO 312; 371pp; English.
XX
XX CC The invention relates to an isolated O772P polypeptide, which has the
XX CC structure fully defined in the specification. The composition containing
XX CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
XX CC or antigen presenting cells are useful for stimulating an immune response
XX CC and treating ovarian cancer. Detecting the presence of the
XX CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
XX CC carcinoma cDNAs and protein cDNAs were identified using microarray
XX CC technology. The present sequence represents a human ovarian carcinoma
XX CC antigen.
XX
XX SQ Sequence 914 AA;

Query Match          92.9%; Score 3663; DB 7; Length 914;
Best Local Similarity 99.9%; Pred. No. 2.5e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 73
DB 159 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 218
QY 74 SRKENTTERTVLQGLRLPLFKNTSGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPTGP 133
DB 219 SRKENTTERTVLQGLRLPLFKNTSGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPTGP 278
QY 134 GLDREQLYLELSQLTSHSTITELGPTLDRDLSLYNNGFTHRSSVPTTSTGVSEEPFTLNFT 193
DB 279 GLDREQLYLELSQLTSHSTITELGPTLDRDLSLYNNGFTHRSSVPTTSTGVSEEPFTLNFT 338
QY 194 INNLRYMADMGQPSGLKFNITDNNMKHLLSPLFORSSIGARYTCGRVIALRSVKNGAETR 253
DB 339 INNLRYMADMGQPSGLKFNITDNNMKHLLSPLFORSSIGARYTCGRVIALRSVKNGAETR 398
QY 254 VDLCLTVLQPLSGPLPTKQVFHELSQOQTGITRLGPVSLDKSLYLNGYNEPGRDPPT 313
DB 399 VDLCLTVLQPLSGPLPTKQVFHELSQOQTGITRLGPVSLDKSLYLNGYNEPGRDPPT 458
QY 314 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSMDMGKGSATFNSTGVQLHLR 373
DB 459 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSMDMGKGSATFNSTGVQLHLR 518

```

## RESULT 17

ADFO8974

ID ADF08974 standard; protein; 914 AA.

AC ADF08974;

DT 12-FEB-2004 (first entry)

XX Secreted ovarian carcinoma antigen seqid 478.

XX gene therapy; protein therapy; vaccine; antibody inhibition;

XX breast cancer; restorative therapy; diagnostic agent; immunoassay;

XX secreted ovarian carcinoma antigen.

XX Homo sapiens.

XX US2003124140-A1.

XX 03-JUL-2003.

XX 17-JUL-2002; 2002US-00198053.

XX 17-DEC-1998; 98US-00215681.

XX 17-DEC-1998; 98US-00216003.

XX 23-JUN-1999; 99US-00338933.

XX 24-SEP-1999; 99US-00404879.

XX 17-JUL-2000; 2000US-00617747.

XX 10-AUG-2000; 2000US-00636801.

XX 20-SEP-2000; 2000US-00667857.

XX 04-APR-2001; 2001US-00827271.

XX 18-JUN-2001; 2001US-00884441.

XX 17-JUL-2001; 2001US-00907969.

XX (CORI-) CORIXA CORP.

XX Bangor CS, Retter MW, Fanger GR, Hill P;

XX WPI; 2003-897152/82.

XX Oncogenic nucleic acids useful for the prevention, diagnosis and treatment of breast cancer.

XX Example 13; SEQ ID NO 478; 399pp; English.

XX The invention describes nucleic acids (I) and the polypeptides (II) they encode. The nucleic acids (I) may be used for preventing, diagnosing and treating diseases related to their aberrant expression i.e. breast

CC cancers. For example, (I) and (II) may be used to treat disorders  
CC associated with decreased expression by rectifying mutations or deletions  
CC in a patient's genome that affect the activity of (II) by expressing  
CC inactive proteins or to supplement the patients own production of (II).  
CC Additionally, (I) may be used to produce (II), by inserting (I) into a  
CC host cell and culturing the cell to express the protein (II). (I) And its  
CC complementary sequences may also be used as DNA probes in diagnostic  
CC assays to detect and quantitate the presence of similar nucleic acids in  
CC samples, and therefore which patients may be in need of restorative  
CC therapy. The host cell may also be used as antigens in the production of  
CC antibodies against (II) and in assays to identify modulators of (II)'s  
CC expression and activity. The anti-(II) antibodies, agonists and  
CC antagonists may be used to regulate expression and activity and as  
CC diagnostic agents for detecting the presence of (II) in samples (e.g. by  
CC immunoassay). This sequence represents a secreted ovarian carcinoma  
CC antigen.  
XX  
SQ Sequence 914 AA;

Query Match 92.9%; Score 3663; DB 7; Length 914;  
Best Local Similarity 99.9%; Pred. NO. 2.5e-315;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSAASHLLILFTLNFTLNRYEENWPG 73  
DB 159 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSAASHLLILFTLNFTLNRYEENWPG 218

QY 74 SRKFNTTERTVQLGLLPFNKTSVGLYSGSCRITLLRPEKDGATGVDALCTHRPPTGP 133  
DB 219 SRKFNTTERTVQLGLLPFNKTSVGLYSGSCRITLLRPEKDGATGVDALCTHRPPTGP 278

QY 134 GLDRQLYLSELSQTHSITELGPTTLDRLSYNGFTHRSSVPTTSTGVVSEPPFTLNFT 193  
DB 279 GLDRQLYLSELSQTHSITELGPTTLDRLSYNGFTHRSSVPTTSTGVVSEPPFTLNFT 338

QY 194 INNLRYMADMGQPSLKFNITDNNMKHLLSPLRQSSLGARYTGCRIALRSYKGAETR 253  
DB 339 INNLRYMADMGQPSLKFNITDNNMKHLLSPLRQSSLGARYTGCRIALRSYKGAETR 398

QY 254 VDLCTYLOPLSGPGLPIKQVHELSSQTHGIRLGPYSIDKSLYNGVNEPDEPPT 313  
DB 399 VDLCTYLOPLSGPGLPIKQVHELSSQTHGIRLGPYSIDKSLYNGVNEPDEPPT 458

QY 314 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 373  
DB 459 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 518

QY 374 PLFQKSMGPFYLGCOLISLRPEKGAATGVDCTTCTHDPVCPGLDIOQLYWELSLTH 433  
DB 519 PLFQKSMGPFYLGCOLISLRPEKGAATGVDCTTCTHDPVCPGLDIOQLYWELSLTH 578

QY 434 GVTOLGFYVLDRLSLFNGVAPQNLISIRGEYQINFIHVNWNLNPDPTSEYITLLRDIO 493  
DB 579 GVTOLGFYVLDRLSLFNGVAPQNLISIRGEYQINFIHVNWNLNPDPTSEYITLLRDIO 638

QY 494 DKVTLLYKGSQSLHDTFRCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553  
DB 639 DKVTLLYKGSQSLHDTFRCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698

QY 554 WLGSTVQLVDIHVTMESSYQPTSSSTQHFYLNFTITNLPYSQKAGPTTNYQRKR 613  
DB 699 WLGSTVQLVDIHVTMESSYQPTSSSTQHFYLNFTITNLPYSQKAGPTTNYQRKR 758

QY 614 NIEDALNQLFRNSSIKSYSDCOVSTFRSPNRRHTGVDLSLNFSPARRVDRVAIYERF 673  
DB 759 NIEDALNQLFRNSSIKSYSDCOVSTFRSPNRRHTGVDLSLNFSPARRVDRVAIYERF 818

QY 674 LRMRNGTQLONFTRDLRSSVLVDGYSFNRNEPLTGN 710  
DB 819 LRMRNGTQLONFTRDLRSSVLVDGYSFNRNEPLTGN 855

RESULT 18

ADF08808  
ID ADF08808 standard; protein; 914 AA.  
XX  
AC ADF08808;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Secreted ovarian carcinoma antigen seqid 312.  
XX  
KW gene therapy; protein therapy; vaccine; antibody inhibition;  
KW breast cancer; restorative therapy; diagnostic agent; immunoassay;  
KW secreted ovarian carcinoma antigen.  
XX  
OS Homo sapiens.  
XX  
PN US2003124140-A1.  
XX  
PD 03-JUL-2003.  
XX  
PF 17-JUL-2002; 2002US-00198053.  
XX  
PR 17-DEC-1998; 98US-00215681.  
PR 17-DEC-1998; 98US-00216003.  
PR 23-JUN-1999; 99US-00338933.  
PR 24-SEP-1999; 99US-00404879.  
PR 17-JUL-2000; 2000US-00617747.  
PR 10-AUG-2000; 2000US-00636801.  
PR 20-SEP-2000; 2000US-00667857.  
PR 04-APR-2001; 2001US-00827271.  
PR 18-JUN-2001; 2001US-00884441.  
PR 17-JUL-2001; 2001US-00907969.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Bangur CS, Retter MW, Fanger GR, Hill P;  
XX  
XX WPI; 2003-897152/82.  
DR N-PSDB; ADF08807.  
XX  
PT Oncogenic nucleic acids useful for the prevention, diagnosis and  
XX treatment of breast cancer.  
PS Example 2; SEQ ID NO 312; 399pp; English.  
XX  
CC The invention describes nucleic acids (I) and the polypeptides (II) they  
CC encode. The nucleic acids (I) may be used for preventing, diagnosing and  
CC treating diseases related to their aberrant expression in breast  
CC cancers. For example, (I) and (II) may be used to treat disorders  
CC associated with decreased expression by rectifying mutations or deletions  
CC in a patient's genome that affect the activity of (II) by expressing  
CC inactive proteins or to supplement the patients own production of (II).  
CC Additionally, (I) may be used to produce (II), by inserting (I) into a  
CC host cell and culturing the cell to express the protein (II). (I) And its  
CC complementary sequences may also be used as DNA probes in diagnostic  
CC assays to detect and quantitate the presence of similar nucleic acids in  
CC samples, and therefore which patients may be in need of restorative  
CC therapy. The host cell may also be used as antigens in the production of  
CC antibodies against (II) and in assays to identify modulators of (II)'s  
CC expression and activity. The anti-(II) antibodies, agonists and  
CC antagonists may be used to regulate expression and activity and as  
CC diagnostic agents for detecting the presence of (II) in samples (e.g. by  
CC immunoassay). This sequence represents a secreted ovarian carcinoma  
CC antigen.  
XX  
SQ Sequence 914 AA;

Query Match 92.9%; Score 3663; DB 7; Length 914;  
Best Local Similarity 99.9%; Pred. NO. 2.5e-315;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSAASHLLILFTLNFTLNRYEENWPG 73  
DB 159 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSAASHLLILFTLNFTLNRYEENWPG 218

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QY 74 SRKFNTERVLOGLLRPLFKNTSVGLYSGRLTLRPEKDGATGVDALCTHRPDTGP 133
Db 219 SRKFNTERVLOGLLRPLFKNTSVGLYSGRLTLRPEKDGATGVDALCTHRPDTGP 278
QY 134 GLDREQLYLELSQTHSITELGPTVTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPTVTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
QY 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTCRVIARLSVKNAGETR 253
Db 339 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTCRVIARLSVKNAGETR 398
QY 254 VDLCTVLOPLSGPLPIKOVFHELSSQTHGIRLGPVSLDKDSLTVNGNEGPDEPPT 313
Db 399 VDLCTVLOPLSGPLPIKOVFHELSSQTHGIRLGPVSLDKDSLTVNGNEGPDEPPT 458
QY 314 TPKPATTFLLPPLSEATTAMGYHLKTLTLNFTISNLQVSPDMGKGSATFNSSTEGVLQHLR 373
Db 459 TPKPATTFLLPPLSEATTAMGYHLKTLTLNFTISNLQVSPDMGKGSATFNSSTEGVLQHLR 518
QY 374 PLFOKSSMGPPYLGQQLISLRPEKDGATGVDTTCTVHPDPVGPGLDIQQLYWELSQLTH 433
Db 519 PLFOKSSMGPPYLGQQLISLRPEKDGATGVDTTCTVHPDPVGPGLDIQQLYWELSQLTH 578
QY 434 GVTOLGFFVLDRLSLFNGVAPQNLISIRGEVQINFIHVNWNLSPDPTSSSEYITLLRDIQ 493
Db 579 GVTOLGFFVLDRLSLFNGVAPQNLISIRGEVQINFIHVNWNLSPDPTSSSEYITLLRDIQ 638
QY 494 DKVTLLYKGSQQLHDTFRFCLVTNLTMDSVLTVKALFSSNLDPSLVQVFLDKTLNASFH 553
Db 639 DKVTLLYKGSQQLHDTFRFCLVTNLTMDSVLTVKALFSSNLDPSLVQVFLDKTLNASFH 698
QY 554 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPSYQDKAQPCTTNYQRNKR 613
Db 699 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPSYQDKAQPCTTNYQRNKR 758
QY 614 NIEDALNQLFNSSIKSYFSDCQVSTFRSPNRRHGTGVDSLCNFSPPLARRVDRVAIYEEF 673
Db 759 NIEDALNQLFNSSIKSYFSDCQVSTFRSPNRRHGTGVDSLCNFSPPLARRVDRVAIYEEF 818
QY 674 LRWTRNGTQLQNFILDRSSVLVDGYSNPNRNEPLTGNS 710
Db 819 LRWTRNGTQLQNFILDRSSVLVDGYSNPNRNEPLTGNS 855
RESULT 19
ADG46095
ID ADG46095 standard; protein; 914 AA.
XX AC ADG46095;
XX AC ADG46095;
DT 26-FEB-2004 (first entry)
XX XX Human ovarian carcinoma polypeptide #1.
XX DE Human; ovarian carcinoma; O8E; ovarian cancer; secreted tumour antigen;
XX KW cytosolic; O772P.
XX OS Homo sapiens.
XX FN US2003165504-A1.
XX PD 04-SEP-2003.
XX PF 04-APR-2001; 2001US-00827271.
XX PR 17-DEC-1998; 98US-00215691.
XX PR 17-DEC-1998; 98US-00216003.
XX PR 23-JUN-1999; 99US-00338933.
XX PR 24-SEP-1999; 99US-00404879.
XX PR 17-JUL-2000; 2000US-00617747.
XX PR 10-AUG-2000; 2000US-00636801.
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PR 20-SEP-2000; 2000US-00667857.
XX (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
XX Retter MW, Fanger GR;
XX WPI: 2003-898035/82.
XX N-PSDB; ADG46555.
XX New isolated O8E or O772P polypeptides, useful for diagnosing,
PT preventing, treating and monitoring cancer, e.g. ovarian cancer,
PT stimulating the immune response in patient.
XX Claim 5; SEQ ID NO 312; 290pp; English.
XX The invention relates to human ovarian carcinoma polypeptides, designated
CC O8E or O772P, and the polynucleotides encoding them. The invention also
CC relates to methods for inhibiting the development of cancer, e.g. ovarian
CC cancer in a patient, methods for stimulating and/or expanding T cells and
CC methods for identifying secreted tumour antigens. The polypeptides,
CC compositions, antibodies to the polypeptides and methods are useful for
CC diagnosing, preventing, treating and monitoring cancer, e.g. ovarian
CC cancer. The composition is particularly useful for stimulating an immune
CC response in patient. This sequence represents a human ovarian carcinoma
CC polypeptide of the invention.
XX Sequence 914 AA;
```

```
Query Match 92.9%; Score 3663; DB 7; Length 914;
Best Local Similarity 99.9%; Pred. No. 2.5e-315;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 FTHRSSVSTTSTGTPVTLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 73
Db 159 FTHRSSVSTTSTGTPVTLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218
QY 74 SRKFNTERVLOGLLRPLFKNTSVGLYSGRLTLRPEKDGATGVDALCTHRPDTGP 133
Db 219 SRKFNTERVLOGLLRPLFKNTSVGLYSGRLTLRPEKDGATGVDALCTHRPDTGP 278
QY 134 GLDREQLYLELSQTHSITELGPTVTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPTVTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
QY 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTCRVIARLSVKNAGETR 253
Db 339 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTCRVIARLSVKNAGETR 398
QY 254 VDLCTVLOPLSGPLPIKOVFHELSSQTHGIRLGPVSLDKDSLTVNGNEGPDEPPT 313
Db 399 VDLCTVLOPLSGPLPIKOVFHELSSQTHGIRLGPVSLDKDSLTVNGNEGPDEPPT 458
QY 314 TPKPATTFLLPPLSEATTAMGYHLKTLTLNFTISNLQVSPDMGKGSATFNSSTEGVLQHLR 373
Db 459 TPKPATTFLLPPLSEATTAMGYHLKTLTLNFTISNLQVSPDMGKGSATFNSSTEGVLQHLR 518
QY 374 PLFOKSSMGPPYLGQQLISLRPEKDGATGVDTTCTVHPDPVGPGLDIQQLYWELSQLTH 433
Db 519 PLFOKSSMGPPYLGQQLISLRPEKDGATGVDTTCTVHPDPVGPGLDIQQLYWELSQLTH 578
QY 434 GVTOLGFFVLDRLSLFNGVAPQNLISIRGEVQINFIHVNWNLSPDPTSSSEYITLLRDIQ 493
Db 579 GVTOLGFFVLDRLSLFNGVAPQNLISIRGEVQINFIHVNWNLSPDPTSSSEYITLLRDIQ 638
QY 494 DKVTLLYKGSQQLHDTFRFCLVTNLTMDSVLTVKALFSSNLDPSLVQVFLDKTLNASFH 553
Db 639 DKVTLLYKGSQQLHDTFRFCLVTNLTMDSVLTVKALFSSNLDPSLVQVFLDKTLNASFH 698
QY 554 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPSYQDKAQPCTTNYQRNKR 613
Db 699 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPSYQDKAQPCTTNYQRNKR 758
```

QY 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673  
Db 759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 818  
QY 674 LRMTNGTQLQNFRTLDSSVLVDGYSNPNRNEPLTGNS 710  
Db 819 LRMTNGTQLQNFRTLDSSVLVDGYPFNRNEPLTGNS 855

RESULT 20

ADN40451  
ID ADN40451 standard; protein; 914 AA.  
XX AC ADN40451;  
XX DT 12-AUG-2004 (first entry)  
XX DE Human breast cancer associated polypeptide sequence #4.  
XX KW Human; breast cancer; T cell; tumour protein; antigen presenting cell;  
KW immune response; CD4+; CD8+; cytostatic.  
XX OS Homo sapiens.  
XX PN US2004101899-A1.  
XX PD 27-MAY-2004.  
XX PF 13-NOV-2003; 2003US-00714389.  
XX PR 30-NOV-1999; 99US-00451651.  
PR 22-FEB-2000; 2000US-00510662.  
PR 10-MAR-2000; 2000US-00523586.  
PR 07-APR-2000; 2000US-00545068.  
PR 15-MAY-2000; 2000US-00571025.  
PR 06-FEB-2001; 2001US-00778320.  
XX PA (CORI-) CORIXA CORP.  
XX PI Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang T;  
PI McNeill PD;  
XX WPI; 2004-399689/37.  
DR N-PSDB; ADN40450.

XX New polynucleotides, useful for treating and diagnosing cancer,  
PT particularly breast cancer by stimulating immune response in a patient  
PT and inhibiting the development of cancer.  
XX Claim 2; SEQ ID NO 206; 151pp; English.  
XX The present invention relates to polynucleotide and polypeptide sequences  
CC associated with breast cancer. Also disclosed are expression vectors  
CC comprising the polynucleotide sequences of the invention operably linked  
CC to an expression control sequence, host cells comprising the vector,  
CC antibodies (or antigen binding fragments of antibodies) specifically  
CC binding the polypeptides of the invention, fusion proteins comprising at  
CC least one of the polypeptides, stimulating and/or expanding T cells  
CC specific for a tumour protein. The polynucleotide sequences, polypeptide  
CC sequences, and antigen presenting cells can be administered  
CC therapeutically/prophylactically to induce an immune response. They can  
CC be included with a physiological carrier/immunostimulant in compositions  
CC such as vaccines, particularly to treat or prevent cancers such as breast  
CC cancer. They can also be used to inhibit the development of cancer by  
CC incubating one or more of them with CD4+ and/or CD8+ T cells isolated  
CC from a patient, such that the T cells proliferate, and administering the  
CC proliferated T cells to the patient. The polynucleotide sequences are  
CC useful for detecting cancer in a patient, producing fusion proteins,  
CC producing T cell populations and antigen presenting cells. The present  
CC sequence represents a polypeptide sequence of the invention.

Sequence 914 AA;

Query Match 92.9%; Score 3663; DB 8; Length 914;  
Best Local Similarity 99.9%; Pred. No. 2.5e-315;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 14 FTHRSSVSTSTPGPTVYLGASKTPASIFGSPASASHLLILFTLTNTITNLRYEENWMPG 73  
Db 159 FTHRSSVSTSTPGPTVYLGASKTPASIFGSPASASHLLILFTLTNTITNLRYEENWMPG 218  
QY 74 SRKFNTTTERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 133  
Db 219 SRKFNTTTERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 278  
QY 134 GLDREQLYLELSQLTHSITELGPYTLDRSLYNGFTHRSSVPTTGTGVVSEEPFTLNFT 193  
Db 279 GLDREQLYLELSQLTHSITELGPYTLDRSLYNGFTHRSSVPTTGTGVVSEEPFTLNFT 338  
QY 194 INNRYMADMGOPGSLKFNTIDNVKHLISPLFORSSLCGARYTGCRIALRSVKNGAETR 253  
Db 339 INNRYMADMGOPGSLKFNTIDNVKHLISPLFORSSLCGARYTGCRIALRSVKNGAETR 398  
QY 254 VDLCTYLOPLSGPLPIKQVFHELSQOQTHGTRIGPYSLDKDSLNGYNEPGEPPPT 313  
Db 399 VDLCTYLOPLSGPLPIKQVFHELSQOQTHGTRIGPYSLDKDSLNGYNEPGEPPPT 458  
QY 314 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLTQYSPDMGKGSATFNSTEGVLOHLLR 373  
Db 459 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLTQYSPDMGKGSATFNSTEGVLOHLLR 518  
QY 374 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTCTYHPDPVGPGLDIOOLYWELSQTH 433  
Db 519 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTCTYHPDPVGPGLDIOOLYWELSQTH 578  
QY 434 GVTQLGFYVLDRLSIFINGYAPQNLISIRGEYQINFHIVMNLNSNPDPTSEYITLLRDIQ 493  
Db 579 GVTQLGFYVLDRLSIFINGYAPQNLISIRGEYQINFHIVMNLNSNPDPTSEYITLLRDIQ 638  
QY 494 DKVTLYKGSQQLHDTFRFCLVNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASEPH 553  
Db 639 DKVTLYKGSQQLHDTFRFCLVNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASEPH 698  
QY 554 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFVLAFTITNLPYSODKAQPGTINYORNRK 613  
Db 699 WLGSTYQLVDIHVTMESSVYQPTSSSTQHFVLAFTITNLPYSODKAQPGTINYORNRK 758  
QY 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673  
Db 759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 818  
QY 674 LRMTNGTQLQNFRTLDSSVLVDGYSNPNRNEPLTGNS 710  
Db 819 LRMTNGTQLQNFRTLDSSVLVDGYPFNRNEPLTGNS 855

Search completed: March 20, 2006, 07:35:37  
Job time : 277.726 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: March 20, 2006, 07:28:38 ; Search time 140.158 Seconds  
(without alignments)  
3765.293 Million cell updates/sec

Title: US-10-687-035-1  
Perfect score: 3945  
Sequence: 1 AAQPARARRTKLTHRSSV.....QKLISEDLNMTGHHHHH 748

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3655	92.9	6995	2	Q96RK2_HUMAN
2	3649	92.5	22152	2	Q8WX17_HUMAN
3	3642	92.3	1148	2	Q9H7S7_HUMAN
4	1562.5	39.6	867	2	Q6ZQW5_HUMAN
5	736.5	18.7	258	2	Q9D1H1_MOUSE
6	144.5	3.7	1408	2	Q27557_MOUSE
7	143.5	3.6	656	2	Q7R3F3_GIALA
8	141.5	3.6	5010	2	Q4MT18_BACCE
9	138	3.5	3443	2	Q8JZM8_MOUSE
10	136	3.4	605	2	Q94K06_ARATH
11	135.5	3.4	1117	1	YN96_YEAST
12	134.5	3.4	1526	2	Q6BL58_DEBHA
13	132.5	3.4	797	2	Q54E23_DICDI
14	131	3.3	1230	2	Q54E54_DICDI
15	131	3.3	1447	2	Q54JR7_DICDI
16	128	3.2	879	2	Q4J6T1_SULAC
17	128	3.2	5017	2	Q81F10_BACCR
18	127	3.2	1166	2	Q4UDD4_THERAN
19	127	3.2	1364	2	Q86AL8_DICDI
20	126.5	3.2	885	2	Q54V40_DICDI
21	126.5	3.2	2340	2	Q8U227_9POTY
22	126	3.2	1056	2	Q4VNF3_9HERP
23	126	3.2	1818	2	Q54HY5_DICDI
24	125.5	3.2	1011	2	Q5T0W9_HUMAN
25	125.5	3.2	5017	2	Q81SNO_BACAN
26	125	3.2	1084	2	Q8EUS5_MYCPE
27	125	3.2	5572	2	Q7QSA1_GIALA
28	125	3.2	10791	2	Q7U7M8_SYNPX
29	124.5	3.2	1012	2	Q6FQ05_CANGA
30	124.5	3.2	2121	2	Q733G8_BACCI
31	124.5	3.2	2535	2	Q755B8_ASHYA

## ALIGNMENTS

32	124.5	3.2	5017	2	Q63DF3_BACCZ
33	124	3.1	856	2	Q6FXG3_CANGA
34	124	3.1	1442	2	Q96YH5_SULTO
35	123.5	3.1	1837	2	Q9N5F6_CABEL
36	123.5	3.1	2477	1	FINC_RAT
37	123.5	3.1	2520	2	Q4NM6_BACCE
38	123	3.1	1085	2	Q54B86_DICDI
39	123	3.1	2959	2	Q5UPY0_MIMIV
40	123	3.1	3441	2	Q89PB9_BRAJA
41	122.5	3.1	393	2	Q59Q37_CANAL
42	122.5	3.1	767	2	Q5W2S2_SULIS
43	122.5	3.1	1206	2	Q5CHP8_CRYHO
44	122.5	3.1	1260	2	Q4UILL_THERAN
45	122.5	3.1	1390	2	Q8PX84_METMA
46	122.5	3.1	2520	2	Q6HFE0_BACHK
47	122	3.1	1608	2	Q8PVI0_METMA
48	122	3.1	2319	2	Q5CTK9_CRYPV
49	122	3.1	2520	2	Q637G8_BACCZ
50	122	3.1	8591	2	Q81B94_PLAF7
51	121.5	3.1	1377	2	Q5SVH8_MOUSE
52	121.5	3.1	1475	1	NUI5K3_HUMAN
53	121.5	3.1	2471	2	Q9YTK3_9HERP
54	121.5	3.1	5005	2	Q9PP25_UREPA
55	121	3.1	1131	1	ADG3_SCHPO
56	121	3.1	1632	2	Q8T141_METAC
57	120.5	3.1	936	2	Q66853_ADEGX
58	120.5	3.1	1322	2	Q4UET5_THERAN
59	120.5	3.1	1377	1	CBPD_MOUSE
60	120.5	3.1	1380	2	Q556L7_DICDI
61	120.5	3.1	1921	2	Q4M222_THERA
62	120.5	3.1	2833	2	Q9VP13_DROME
63	120.5	3.1	3080	2	Q5EGP2_HUMAN
64	120.5	3.1	5017	2	Q6HKW5_BACHK
65	120	3.0	651	2	Q6CNL5_KLULA
66	120	3.0	1093	2	Q8SV69_MYCPE
67	120	3.0	1397	1	CID_DROME
68	120	3.0	1447	2	Q5CFG8_CRYHO
69	120	3.0	1449	2	Q9U112_DROME
70	120	3.0	1836	2	Q54KW5_DICDI
71	120	3.0	2409	2	Q960G6_DROME
72	119.5	3.0	631	2	Q99K60_MOUSE
73	119.5	3.0	846	2	Q54HL8_DICDI
74	119.5	3.0	1111	2	Q5AMQ6_CANAL
75	119.5	3.0	1225	2	Q5A849_CANAL
76	119.5	3.0	2306	2	Q4SEE4_TETNG
77	119.5	3.0	11696	2	Q5CV09_CRYPV
78	119	3.0	957	2	Q9UKN0_HUMAN
79	119	3.0	2206	2	Q95FJ4_9PICO
80	119	3.0	2392	1	YCF2_ANTFO
81	118.5	3.0	738	2	Q41980_GIBZE
82	118.5	3.0	967	2	Q4J9K1_SULAC
83	118.5	3.0	1463	2	Q70320_CAVPO
84	118.5	3.0	1941	2	Q54JEL_DICDI
85	118.5	3.0	2193	2	Q6WZM7_HUMAN
86	118.5	3.0	2267	2	Q68DP9_HUMAN
87	118.5	3.0	2283	2	Q8VQ99_STAAU
88	118.5	3.0	2477	1	FINC_MOUSE
89	118.5	3.0	3229	2	Q63UE4_BURPS
90	118.5	3.0	9439	2	Q8CF76_STAEP
91	118.5	3.0	10203	2	Q5HPA2_STAEP
92	118	3.0	699	2	Q5KFX2_CRYNE
93	118	3.0	1804	2	Q66IN2_XENLA
94	118	3.0	5010	2	Q81CV2_BACCR
95	117.5	3.0	668	2	Q7QWQ2_GIALA
96	117.5	3.0	704	2	Q6COT3_KLULA
97	117.5	3.0	729	2	Q8DKG0_SYNEL
98	117.5	3.0	870	2	Q4N9G2_THERA
99	117.5	3.0	1045	2	Q76037_HUMAN
100	117.5	3.0	1136	2	Q5LGX7_BACFN

Q63df3 bacillus ce  
Q6fxg3 candida gla  
Q96yh5 sulfolobus  
Q9n5f6 caenorhabdi  
P04937 rattus norv  
Q4nm6 bacillus ce  
Q54b86 dictyosteli  
Q5upy0 mimivirus  
Q89pb9 bradyrhizob  
Q59q37 candida alb  
Q5w2s2 sulfolobus  
Q5chp8 cryptospori  
Q4uill thelleria a  
Q8px84 methanosarc  
Q6hfe0 bacillus th  
Q8pvi0 methanosarc  
Q5ctk9 cryptospori  
Q637g8 bacillus ce  
Q5svh8 mus musculu  
P49790 homo sapien  
Q9ytk3 ateline her  
Q9pp25 ureaplasma  
Q74851 schizosacch  
Q8t141 methanosarc  
Q66853 avian adeno  
Q4uet5 thelleria a  
Q89001 mus musculu  
Q556l7 dictyosteli  
Q4m222 thelleria p  
Q9vp13 drosophila  
Q5egp2 homo sapien  
Q6hkw5 bacillus th  
Q6cnl5 kluyveromyc  
Q8sv69 mycoplasma  
P19338 drosophila  
Q5cfgh cryptospori  
Q9u112 drosophila  
Q54kw5 dictyosteli  
Q960g6 drosophila  
Q99k60 mus musculu  
Q54hl8 dictyosteli  
Q5amq6 candida alb  
Q5a849 candida alb  
Q4see4 tetraodon n  
Q5cv09 cryptospori  
Q9ukn0 homo sapien  
Q95fj4 porcine tes  
Q859w7 antoceros  
Q41980 gibberella  
Q4j9k1 sulfolobus  
Q70320 cavia porce  
Q54jel dictyosteli  
Q6wzm7 homo sapien  
Q68dp9 homo sapien  
Q8vq99 staphylococ  
P11276 mus musculu  
Q63ue4 burkholderi  
Q8cf76 staphylococ  
Q5hpa2 staphylococ  
Q5kfx2 cryptococcu  
Q66in2 xenopus lae  
Q81cv2 bacillus ce  
Q7qwq2 giardia lam  
Q6cot3 kluyveromyc  
Q8dkg0 synechococc  
Q4n9g2 thelleria p  
Q76037 homo sapien  
Q5lgx7 bacteroides

RESULT 1	
Q96RK2_HUMAN	Q96RK2_HUMAN PRELIMINARY; PRT; 6995 AA.
ID	Q96RK2_HUMAN PRELIMINARY; PRT; 6995 AA.
AC	Q96RK2_HUMAN PRELIMINARY; PRT; 6995 AA.
DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Mucin 16 (Fragment).
GN	Name=MUC16;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC	Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=21347965; PubMed=11369781; DOI=10.1074/jbc.M103554200;
RA	Yin B.W., Lloyd K.O.,
RT	"Molecular cloning of the cal25 ovarian cancer antigen. identification
RT	as a new mucin, muc16.";
RL	J. Biol. Chem. 276:27371-27375 (2001).
RN	[2]
RP	NUCLEOTIDE SEQUENCE.
RA	Lloyd K.O., Yin B.W.T.;
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF361486; AAK74120.3; -; mRNA.
DR	HSP; Q9D1H1; IIVZ.
DR	SMR; Q96RK2; 6803-6922.
DR	Ensembl; ENSG00000181143; Homo sapiens.
DR	InterPro; IPR000194; ATPase_a/bcentre.
DR	InterPro; IPR000082; SEA.
DR	Pfam; PF01390; SEA; 20.
DR	SMART; SM00200; SEA; 10.
DR	PROSITE; PS00152; ATPase ALPHA_BETA; UNKNOWN_1.
DR	PROSITE; PS50024; SEA; 6.
FT	NON TER
SQ	SEQUENCE 6995 AA; 744958 MW; 80C797DBDBF33A2B CRC64;
Query Match 92.9%; Score 3665; DB 2; Length 6995;	
Best Local Similarity 99.9%; Pred. No. 2.7e-237;	
Matches 696; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Qy	14 FTHRSSVSTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLYEENMWPG 73
Db	6240 FTHRSSVSTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLYEENMWPG 6299
Qy	74 SRKFTTERTVQLGLRLPLFKNTSVGPLYSGCRLTLRPEKDGATGVDAICTHRPDPTGP 133
Db	6300 SRKFTTERTVQLGLRLPLFKNTSVGPLYSGCRLTLRPEKDGATGVDAICTHRPDPTGP 6359
Qy	134 GLDREQLYLELSQTHSITELGPYTLDRDSLIVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db	6360 GLDREQLYLELSQTHSITELGPYTLDRDSLIVNGFTHRSSVPTTSTGVVSEEPFTLNFT 6419
Qy	194 INNLYRMADMGQPSGLKFNITDNWKLLSLPFRSSIGARYTCRVIALRSVKGAEFR 253
Db	6420 INNLYRMADMGQPSGLKFNITDNWKLLSLPFRSSIGARYTCRVIALRSVKGAEFR 6479
Qy	254 VDLACTVQLPUSGGLPLTKQVFHLSQTHGTRIGLPGVSLDKSLVNGYNEPDPDPPT 313
Db	6480 VDLACTVQLPUSGGLPLTKQVFHLSQTHGTRIGLPGVSLDKSLVNGYNEPDPDPPT 6539
Qy	314 TPKEATTFPLPLSEATTAMGYHLKTLTLNFTISNLQSPDMGKGSATFNSFTEGVQLHLR 373
Db	6540 TPKEATTFPLPLSEATTAMGYHLKTLTLNFTISNLQSPDMGKGSATFNSFTEGVQLHLR 6599
Qy	374 PLFKSSMGPIYLGCLISLPEKDGATGVDTCTTHPDPVGPGLDIDQLYWLSQLTH 433
Db	6600 PLFKSSMGPIYLGCLISLPEKDGATGVDTCTTHPDPVGPGLDIDQLYWLSQLTH 6659
Qy	434 GVTQLGFVLDRLDSLIFNGYAPQNLISIRGEYQINFIHVMNLSNPDPSTSEYITLLRDIQ 493
Query Match 92.5%; Score 3649; DB 2; Length 22152;	
Best Local Similarity 99.7%; Pred. No. 1.9e-235;	
Matches 695; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	14 FTHRSSVSTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLYEENMWPG 73
Db	21397 FTHRSSVSTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLYEENMWPG 21456
Qy	74 SRKFTTERTVQLGLRLPLFKNTSVGPLYSGCRLTLRPEKDGATGVDAICTHRPDPTGP 133
Db	21457 SRKFTTERTVQLGLRLPLFKNTSVGPLYSGCRLTLRPEKDGATGVDAICTHRPDPTGP 21516
Qy	134 GLDREQLYLELSQTHSITELGPYTLDRDSLIVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db	21517 GLDREQLYLELSQTHSITELGPYTLDRDSLIVNGFTHRSSVPTTSTGVVSEEPFTLNFT 21576



194 INNRYMADMGQPSGLKFNITDNNMKHLLSPLFORSSIGARYTCRCVIALRSVKNAGETR 253  
21577 INNRYMADMGQPSGLKFNITDNNMKHLLSPLFORSSIGARYTCRCVIALRSVKNAGETR 21636  
254 VDLCTYQLPSGLPIKOVFHELSOOTHGIRLPGYSIDKSLYNGNEGPDPPT 313  
21637 VDLCTYQLPSGLPIKOVFHELSOOTHGIRLPGYSIDKSLYNGNEGPDPPT 21696  
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21697 TPKPATTFLPPLSEATTAMGYHLKTLTNTFNISNLYSPDMGKGSATFNSSTEGVLOHLR 21756  
374 PLFQKSSMGPFYLGQCLISLRPEKGAATGVTCTTHPDPVPGGLDIOQLYWELSLTH 433  
21757 PLFQKSSMGPFYLGQCLISLRPEKGAATGVTCTTHPDPVPGGLDIOQLYWELSLTH 21816  
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21817 GVTQLGYVLDRLSPLFNGVAPQNLISIRGEYQINFNHVNLSNPDPSTSEYITLLRDIO 21876  
494 DKVTTLKGSQSLDHTFRCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVLDKTLNASFH 553  
21877 DKVTTLKGSQSLDHTFRCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVLDKTLNASFH 21936  
554 WLGSYVQLVDIHVTMESSYVQPTSSSTQHFYLNFTITNLYSQDKAQPGTTNYQRNR 613  
21937 WLGSYVQLVDIHVTMESSYVQPTSSSTQHFYLNFTITNLYSQDKAQPGTTNYQRNR 21996  
614 NIEDALNQLFRNSSIKSYFSDQVSTFRSPNRRHTGVDSLCNFSPLARRVDRVAIYEEF 673  
21997 NIEDALNQLFRNSSIKSYFSDQVSTFRSPNRRHTGVDSLCNFSPLARRVDRVAIYEEF 22056  
674 LRWTRNGTQONFTLDRSSVLVDGYSNRPNEPLTGN 710  
22057 LRWTRNGTQONFTLDRSSVLVDGYSNRPNEPLTGN 22093

RESULT 3  
Q9H7S7 HUMAN  
ID Q9H7S7 HUMAN PRELIMINARY; PRT; 1148 AA.  
AC Q9H7S7  
DT 01-MAR-2001 (T-EMBLrel. 16, Created)  
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
DE Hypothetical protein FLJ14303.  
OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Placenta;  
RX PubMed=14702039; DOI=10.1038/ng1285;  
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Iehi S.,  
RA Yamanoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,  
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,  
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,  
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
RA Omura Y., Abe K., Kamihara K., Katsuma N., Sato K., Tanikawa M.,  
RA Yamazaki M., Ninomiya K., Iehibashi T., Yamashita H., Murakawa K.,  
RA Fujinori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,  
RA Ishida S., Oho Y., Takiguchi S., Watanabe S., Yoshida M., Hotsu T.,  
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,  
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,  
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
RA Yoshihara Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,  
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

Fujimori Y., Komiya M., Tashiro H., Tanigami A., Fujiwara T.,  
Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamaguchi R.,  
Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
RT "Complete sequencing and characterization of 21,243 full-length human  
cDNAs";  
RL Nat. Genet. 36:40-45(2004).  
DR ENBL; AK024365; BAB14899.1; -; mRNA.  
DR HSSP; Q9D1H1; 11VZ.  
DR SNR; Q9H7S7; 956-1075.  
DR InterPro; IPR000082; SEA.  
DR Pfam; PF01390; SEA: 7.  
DR PROSITE; P55004; SEA: 3.  
SQ SEQUENCE 1148 AA; 127957 MW; 386180D5EFD8ABC CRC64;  
Query Match 92.3%; Score 3642; DB 2; Length 1148;  
Best Local Similarity 99.6%; Pred. No. 6.4e-237; Indels 0; Gaps 0;  
Matches 694; Conservative 0; Mismatches 3;  
14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTNFTITNLYEENWPG 73  
393 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTNFTITNLYEENWPG 452  
74 SRKFNTERVLOGLLRPLFKNTSVGLYSGRLTLRPEKDGATGDAICTHRPDP 133  
453 SRKFNTERVLOGLLRPLFKNTSVGLYSGRLTLRPEKDGATGDAICTHRPDP 512  
134 GLDREQLYLELSOLTHSITELGPTLDRDLSLVNGFTHRSSVPTTGTGVVSEFP 193  
513 GLDREQLYLELSOLTHSITELGPTLDRDLSLVNGFTHRSSVPTTGTGVVSEFP 572  
194 INNRYMADMGQPSGLKFNITDNNMKHLLSPLFORSSIGARYTCRCVIALRSVKNAGETR 253  
573 INNRYMADMGQPSGLKFNITDNNMKHLLSPLFORSSIGARYTCRCVIALRSVKNAGETR 632  
254 VDLCTYQLPSGLPIKOVFHELSOOTHGIRLPGYSIDKSLYNGNEGPDPPT 313  
633 VDLCTYQLPSGLPIKOVFHELSOOTHGIRLPGYSIDKSLYNGNEGPDPPT 692  
314 TPKPATTFLPPLSEATTAMGYHLKTLTNTFNISNLYSPDMGKGSATFNSSTEGVLOHLR 373  
693 TPKPATTFLPPLSEATTAMGYHLKTLTNTFNISNLYSPDMGKGSATFNSSTEGVLOHLR 752  
374 PLFQKSSMGPFYLGQCLISLRPEKGAATGVTCTTHPDPVPGGLDIOQLYWELSLTH 433  
753 PLFQKSSMGPFYLGQCLISLRPEKGAATGVTCTTHPDPVPGGLDIOQLYWELSLTH 812  
434 GVTQLGYVLDRLSPLFNGVAPQNLISIRGEYQINFNHVNLSNPDPSTSEYITLLRDIO 493  
813 GVTQLGYVLDRLSPLFNGVAPQNLISIRGEYQINFNHVNLSNPDPSTSEYITLLRDIO 872  
494 DKVTTLKGSQSLDHTFRCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVLDKTLNASFH 553  
873 DKVTTLKGSQSLDHTFRCLVTLNLTWDSVLVTKALFSSNLDPSLVEQVLDKTLNASFH 932  
554 WLGSYVQLVDIHVTMESSYVQPTSSSTQHFYLNFTITNLYSQDKAQPGTTNYQRNR 613  
933 WLGSYVQLVDIHVTMESSYVQPTSSSTQHFYLNFTITNLYSQDKAQPGTTNYQRNR 992  
614 NIEDALNQLFRNSSIKSYFSDQVSTFRSPNRRHTGVDSLCNFSPLARRVDRVAIYEEF 673  
993 NIEDALNQLFRNSSIKSYFSDQVSTFRSPNRRHTGVDSLCNFSPLARRVDRVAIYEEF 1052  
674 LRWTRNGTQONFTLDRSSVLVDGYSNRPNEPLTGN 710  
1053 LRWTRNGTQONFTLDRSSVLVDGYSNRPNEPLTGN 1089

Qy 492 IQKVVTLYKGSQSLHDTFRCLVTNL--TWDSVLVTVTKALPSSNLDPSLV-----EQVELD 548  
Db 639 LOGLLRPLFNFTSVGPLYSGSCRLTALPEKDGAEATGDAICTHRPDPGPGDLRQLYLE 698  
Qy 546 -KTLNASFHWLGS--TYQLVDIHWTEMSSVYQPTSSS---STQHFYLNFTTINLPYSQDK 600  
Db 699 LSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSGVVSSEPTFLNFTINLRYMADM 758  
Qy 601 AQPQTWYQNRKNIEDALNQLFRNSIKSVFSCQVSTFRFVNRHHTGVDSLCNF--SP 659  
Db 759 GQPGSLKFNITDNVMQHLSPFLFORSSILGARYTCGRVIALRSVNGAETRVDDLCTYLQP 818  
Qy 660 LA-RRDRVAIYEFLRMWTNGTQLQNTLDRSSVLVDGYSPPNEPLT 707  
Db 819 LSGPLPIQVHFELSQOOTHGTRLGPYSLDKDSLYLNGHHTLQOQSTT 867

RESULT 5

Q9D1H1\_MOUSE

ID Q9D1H1\_MOUSE PRELIMINARY; PRT; 258 AA.

AC Q9D1H1;

CD 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:110008114 product:hypothetical SEA domain containing protein, full insert sequence.

DE DE

GN Name=1110008114Rik;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RL [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Whole body;

RX MEDLINE=92729253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RL [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Whole body;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H., Kuehl P., Lewis S., Matsuo Y., Nkaido I., Pesole G., Quackenbush J., Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RL [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Whole body;

RA The FANTOM Consortium,

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).



QY 557 -STYQLVDIHVTEMESVYQP-----TSSSTQHFLYNLNET-----ITNLPYSQDKAQPCT 605  
DB 923 PASITSLDLRT--PSSGFLPITATATARTNGEVDGNTAVLYINGLADEKNVTGVA 980  
QY 606 TNYQRNKRNIETDALNQLFRNSSI-----KSYFSDCOVSTFRSVP-----NRHHT 649  
DB 981 -----GRSVQAFNHTIENAGIYLAGISLTPLDVRLVSEPALNSLSATPLTGVSPHRI 1034  
QY 650 GVDSLCNFS-----PLARRVDRVAIYEBFLMRNGTOLQNTFLDRS-----SVLVGG 697  
DB 1035 IVTALVSTTEEGSGNYTAGLYIDGVNVQNRVTRVTPGSGVLVSFTADISBGEHQVTNS 1094  
QY 698 YSP 700  
DB 1095 LSP 1097  
RESULT 7  
Q7R3F3\_GIALA  
ID Q7R3F3\_GIALA PRELIMINARY; PRT; 656 AA.  
AC Q7R3F3;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE GUP\_158\_79919 77949.  
OS Giardia lamblia ATCC 50803.  
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.  
OX NCBI\_TaxID=184922;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=WB C6;  
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,  
RA Olsen G.J., Sogin M.L.;  
RT "Draft sequence of the Giardia lamblia genome.";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AACB01000015; EAA41889.1; -; Genomic\_DNA.  
DR HSP; P10081; 17UK.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR InterPro; IPR001410; DEAD.  
DR InterPro; IPR011545; DEAD/DEAH\_N.  
DR Pfam; PF00270; DEAD; 1.  
DR Pfam; PF00271; Helicase C; 1.  
SQ SEQUENCE 656 AA; 73379 MW; EBF73D219C01978B CRC64;  
Query Match 3.6%; Score 143.5; DB 2; Length 656;  
Best Local Similarity 21.1%; Pred. No. 0.7;  
Matches 114; Conservative 63; Mismatches 185; Indels 179; Gaps 24;  
QY 271 IKQV-----FHELSQOHTGIRLGPYSLDKDSLYN-----GYNEPGDEPTTPKPAITP 321  
DB 116 IKEVAPIATPDLRSRE-----PFLLDPE-VYQNTVRAKYQPTPIQKHALP----- 160  
QY 322 LPPLSEATTAGYHLKTL-----TLNFTLSNQ-----YSPDMG----- 355  
DB 161 -----TGMVGYDLACSGTSGSKTCAFIPIILHRTATEKLYTMSPGHEDRFRN 213  
QY 356 -KGSATFNSTEGVLQHLRLPILQKSMGPFYLGQCLISLRPKDGAATGVDVTTCTYHPDP 414  
DB 214 AKGSRAPFC--IIMSPTRVLQQTAKASWML-----SYGTSILTRVAYGDP 259  
QY 415 VPGGLDQQLYELWSQLTHG-----VTQLGFYVLDL--DSLFIINGYAFQNLISIR 461  
DB 260 SGQORDALQMGCDILVATPGRLDPIKQGVVETTVRVFVFECDRLMDMGFEQIRDIL 319  
QY 462 GEYQINFIHNNWLSNPDPTSEVITLLRDIQDKVITLYKGSQQLHDTFRFCLVNLNLTWD- 520

DB 320 HELPPIHHSVQ-DPSNPDIHQ-----IERQTLFSATFPKE-----IKNLAMEF 363  
QY 521 -----SVLYTKALFSSNLDPSLVEQVFLDKTNASFHMLGSTYQLVDIHVTEMESVYQ 575  
DB 364 LRQDLRLSVITGVIGSSN--PNLAQRVLVRSNDKRLLL----- 401  
QY 576 PTSSTSTQHFLYNLFTITNLPYSQDKAQPCTTNYQRNKRNIETDALNQLFRNSSIKSYFSDC 635  
DB 402 -TEYITQGNADLNMLIEV-YGTDKEQ-----DPSLSTVSSSTAGISEEFNEA 446  
QY 636 QVSTFRSPVNRHHTGVDSL-----CNFSPLARVV-----DRVAIYEEFL 674  
DB 447 MNATY---PDSHAARDHTLNKOGIIQVQTVTFNFKSEADRIFRYFDMDRYRVAVIHGM 503  
QY 675 RMTNRGTOLQNTFLDRSSVLVDGYSNPR-----NEPLTGSADIQHSGRSSL 723  
DB 504 TOKERENNLKYFKAGRTNLTIGTVAQGLDIPNRLVLNLDPLGNVDDYTHRIGRTGRA 563  
QY 724 G 724  
DB 564 G 564  
RESULT 8  
Q4MT18\_BACCE  
ID Q4MT18\_BACCE PRELIMINARY; PRT; 5010 AA.  
AC Q4MT18;  
DT 13-SRP-2005 (TrEMBLrel. 31, Created)  
DT 13-SRP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SRP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Cell surface protein.  
GN ORFNames=BCE\_G9241\_1620;  
OS Bacillus cereus G9241.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_TaxID=269801;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=G9241;  
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;  
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,  
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,  
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,  
RA Rilstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,  
RA Popovic I., Fraser C.M.;  
RT "Identification of anthrax toxin genes in a Bacillus cereus associated  
RT with an illness resembling inhalation anthrax.";  
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AABK01000008; EAL15315.1; -; Genomic DNA.  
SQ SEQUENCE 5010 AA; 521891 MW; B00914651BF832DD CRC64;  
Query Match 3.6%; Score 141.5; DB 2; Length 5010;  
Best Local Similarity 18.5%; Pred. No. 21;  
Matches 153; Conservative 123; Mismatches 328; Indels 223; Gaps 36;  
QY 10 RTKLFTHRSSVSTSTPGTPTVYLGASKTSPASIPGSAASHLLILFTLNTLRYEEN 69  
DB 3658 QAOLITKTSNPTTDIGGTILYISEVKNIGV-----DAINIIFT-----D 3699  
QY 70 MWPGSRKFNTERVLOGLRP---LFXNTSVGLYSGRLTL-----RPEKDEATG- 119  
DB 3700 SIPAGTTTFVSPDSTVINGVLOPDTPNENGISIGTIPSSSKTILFQVOTNNPPTTEIVNQ 3759  
QY 120 VDAICTHRPPTGPGGLDR-----EQLYELSQ-----LTHSITEL 154  
DB 3760 SSAMQVSVISPTAPPVNRSATSNIVTSLQVANIISIKQADVTFSIGQNTITYNTLQNI 3819  
QY 155 GPVTLT-----RDSLYNGFTHRSSVP-----TTSTGVVSEBPTTFNTINN 196  
DB 3820 GTVPANNTLFDNIPEGTIFIEDSLSNVNNVQPGANPENGITLGTIQDPTVTSFQVL 3879



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Db 2094 DTGHSVTITTHGSLATTQVSLTPSSQNMSTVSMPTSSSQELTSLPQOHTG--SMETSS 2151
Qy 659 PLARRVDRAIYEFEFLMTNRGTQLQNFLLDRSS 692
Db 2152 QPQNITPTVTVTSTLLSFSRSGSTELQTMWGTS 2185

RESULT 10
Q94K06_ARATH PRELIMINARY; PRT; 605 AA.
AC Q94K06;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-FEB-2005 (T-EMBLrel. 29, Last annotation update)
DE TRNA adenylyltransferase-like protein.
GN Name=r22J18.17; Synonyms=Atlg22660;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF370489; AAK43866.1; -; mRNA.
DR EMBL; BT000361; AAN15680.1; -; mRNA.
DR GO; GO:0005739; C-mitochondrion; IDA.
DR InterPro; IPR012222; PAP_CCA.
DR InterPro; IPR012277; Poly(A).
DR InterPro; IPR002646; PolyA_pol_reg.
DR PANTHER; PTHR13734; PolyA_pol.1.
DR Pfam; PF01743; PolyA_pol.1.
DR PIRSF; PIRSF00814; PolyA_pol.1.
DR Nucleotide; Nucleotide; RNA-binding; Transferase.
SQ SEQUENCE 605 AA; 68953 MW; 2DB2778EA9368A18 CRC64;

Query Match 3.4%; Score 136; DB 2; Length 605;
Best Local Similarity 20.6%; Pred. No. 2;
Matches 99; Conservative 67; Mismatches 185; Indels 130; Gaps 20;

Qy 113 KGEATGDAICTHRPPTGPGCLDRQLYLSELSLTHSITELGPTLDRSLYNGGTHR 172
Db 152 RDEEVQG-DTVIERNPD-----QSKHLETAKL-----RIYDQWIDFVNLSEERYTEN 197
Qy 173 SSVPTSTGVSEPPFTLNFTNNLRNLYMADMGQPSL-KFNITDNVKKHLLSPFLFRSS- 230
Db 198 SRITPMFGTAKDAFRDLTINSLFYNNINGAVEDLTERGIDDLKSGKIVTLPKATPF 257
Qy 231 -----LGARYTGCRVIALRSVKNAGETRVDLLCTLYQLPSGLPIKQVFHEL 278
Db 258 LDDPLRLVLRVFRGARFGFTLDEELKEAASSEVRVAL-----GEKISRERIGNEI 308
Qy 279 SQQTHG-----ITRLGPYSLDKSLYNGVNEPGDEP-----PTTPKP 317
Db 309 DLMTSGNGPVSATVYSLDKLFSVVFPALPSSAEPSPENCGSLSQSYLEAMWSLLKTPRP 368
Qy 318 -----ATTFLP-----PLSEATTAMGYHLK 337
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Db 369 GKFSGEORRLALVAMFLPFRKTVYKDTGKKSIPVNVNHFKFSMKRKTSDAETVMNIHOT 428
Qy 338 TLTLNFTTISNLQYSPDMGKGSATFNSTEGVLOH-----LLRPLFKSSMGPFYLGCOLIS 392
Db 429 TERFRSLIPSLEVKDVELDELTW--AADILEHWKSIITLNDPVPATSKIRVLGT---FL 483
Qy 393 LRPEKD---GAATGVDITCTYHPDPVPGCLDTQQLYWLSQL--THGVTLQGLFVYVLD 446
Db 484 LRDIKDFWRVSLTSLTLLSATV--DGSNDHODIGQLDFOLERNRETYTLTVEATITHELGLD 541
Qy 447 SLF-----INGYAPQNLIS-IRG-----EYQINPHVNNLSNPDPTSSSYITLLRIQD 494
Db 542 KIWDAKPLVNGREIMQIAELKGGSLRIREWQK--LLTWLAYPNGTGAERCKEWMRDKA 599
Qy 495 K 495
Db 600 K 600

RESULT 11
YN96_YEAST STANDARD; PRT; 1117 AA.
ID YN96_YEAST AC PS3753;
DT 01-OCT-1996 (Rel. 34, Created)
DT 10-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical 121.1 kDa protein in BIO3-HXT17 intergenic region
DE precursor.
GN OrderedLocusNames=YNR067C; ORFNames=N3547;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OC NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=97313269; PubMed=9169873;
RA Hegenann J.H., Obermaier B., Urrestarazu L.A., Aert R., Albermann K.,
RA Altmann R., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M.,
RA Beinbauer J.D., Boskovic J., Buitrago M.J., Bussereau F., Coster F.,
RA Crouzet M., D'Angelo M., Dal Pero F., De Antoni A., del Rey F.,
RA Doignon F., Domdey H., Dubois E., Fiedler T.A., Fleig U., Floeth M.,
RA Fritz C., Gaillardin C., Garcia-Cantalejo J.M., Glansdorff N.,
RA Gaffeau A., Guellder U., Herbert C.J., Heumann K., Heuss-Neitzel D.,
RA Hilbert H., Himi K., Iraqui Houssaini I., Jacquet M., Jimenez A.,
RA Jonnaux J.-L., Karpfinger-Hartl L., Lanfranchi G., Lepingle A.,
RA Levesque H., Lyck R., Mattahi M., Mallet L., Maurer C.T.C.,
RA Messenguy F., Mewes H.-W., Moestl D., Nasr F., Nicaud J.-M.,
RA Niedenthal R.K., Pandolfo D., Pierard A., Piravandi E., Planta R.J.,
RA Pohl T.M., Purnelle B., Rebischung C., Remacha M.A., Revuelta J.L.,
RA Rinke M., Saiz J.E., Sartorello F., Scherens B., Sen-Gupta M.,
RA Soler-Mira A., Urbanus J.H.M., Valle G., Van Dyck L., Verhasselt P.,
RA Vierendeels F., Vissers S., Voet M., Volckaert G., Wach A.,
RA Wambutt R., Wedler H., Zollner A., Hani J.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIV
and its evolutionary implications.";
RL Nature 387:93-98(1997).
CC CC
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 81 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; Z71682; CAA96349.1; -; Genomic_DNA.
CC PIR; S63399; S63399.
CC GenOnline; 143412.
CC Ensembl; YNR067C; Saccharomyces cerevisiae.
CC SGD; S000005350; D8E4.
CC DR GO; GO:0030428; C:cell septum; IDA.
CC DR GO; GO:0009277; C:cell wall (sensu Fungi); IDA.
CC DR GO; GO:0007109; P:cytokinesis, completion of separation; IEP.
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DR InterPro; IPR005200; Glyco hydro 81.  
DR Pfam; PF03639; Glyco hydro 81; 1.  
KW Complete proteome; Glycoprotein; Glycosidase; Hydrolase;  
KW Hypothetical protein; Signal  
FT SIGNAL 1 16 Potential.  
FT CHAIN 17 1117 Hypothetical protein YNR067C.  
FT COMPBIAS 342 345 Poly-Ser.  
FT COMPBIAS 365 370 Poly-Ser.  
FT COMPBIAS 376 383 Poly-Ser.  
FT CARBOHYD 138 138 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 186 186 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 223 223 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 259 259 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 280 280 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 303 303 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 307 307 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 393 393 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 533 533 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 886 886 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 1117 AA; 121064 MW; 87F13A07E42B0AD1 CRC64;

Query Match 3.4%; Score 135.5; DB 1; Length 1117;  
Best Local Similarity 21.1%; Pred. No. 5.4;  
Matches 156; Conservative 94; Mismatches 255; Indels 233; Gaps 39;

QY 4 PARRARTKLFTHRSVSTSTTPTPTVYLG-----SKTPAS--IPGPSAASHL 51  
DB 206 PSYSSQETKIIP--SSLTNKTIVTISVRTNAATATGDSFIATSPASTLFPNSNQD 263  
QY 52 LIUFTLNTITNLYEN-----MWGSRKFNTERV-----LQGLLRPL 91  
DB 264 LVQ--TLASTTASPAYPNRQTILSPSVLSYSTPIYPSNITENGSSPSPSLSTVSPV 322  
QY 92 FKNTSGPLSGCLTLREKQGEAGVDAICTHRDPDTPGGLDRQLVLELS-QLTHS 150  
DB 323 YPSSTGNIL-----LSSLFTVDSSS-----PVSTLD--TIVVSSMQATIS 365  
QY 151 ITELPGYTLDRDSLYNGFTHRSVPPTSTGVVSEEPFTLNFTINLRYMADMGQGSGLK 210  
DB 366 SSSSRRTKTS-----SLSTSTSTATTENSST--TIVNLFNAVSTDEPPTV- 414  
QY 211 FNITDNVKKHLLSPLFORSLGARYTCRVIALRSVQNGAETRVLLCTYLQPLSGPLP 270  
DB 415 FDRSPNPM-----SLADGVSN-----DGP-IQ 435  
QY 271 IKQVFEHL-----SQOTHGIRLGPVSLDK-----DSLYLNGYNERGDEPP 312  
DB 436 TNKPYTNLIVGQESPAF--VYPYSLWKYTSSTSYGFAVQHTTVDQYSYGGYDSSGNAEYL 493  
QY 313 TTPKPATFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGATFNSTEGVL----- 368  
DB 494 VNP-----LGIAHVVSASNFPDSSMTQVDMETLSSTRVLSN 533  
QY 369 ---QHLLRPLFKSSMGPFYLGQQLISLRPEKGAATGVTTCYTHPDVPGGLDLOQLY 425  
DB 534 DSSNYLEIPLVQ--GMG-FATGIYHGSIN-AKIGSSVGFNTIVSESSNLAQGI-----LK 585  
QY 426 WELSQLTHGVTQLGFFVLDRLSLFINGYAPQNLISIRGEYQINFH-----IVNWLNSPD 479  
DB 586 YRIT-LINGVTWL--CYVIGPDDLTSTDF--SLEVSSEYBIKASASVDGIIQLAVA-PS 639  
QY 480 PTSSE-----YIT--LLRIDQDKVTLYK-----GSOL-----HDTFR 510  
DB 640 ETDYEVYDQAAGMYTNFKLGVSQDSTATYEFSTYTOGESASGSTMIFALPHHSSFS 699  
QY 511 FCLVTNLTMDSVLTVKALPSSNLDPSLVQVFLDKTLNASFHWLSTYQ----- 560  
DB 700 DIMQDYTGTLQASTTKGVNGLYTLTSLQ-----FSTSLNRQISWLPSSQLGNNLLEYSK 755  
QY 561 -----LVDIHVTMESVYQPTSSSTQHEVFLNFTINLEY-----SODKAQPGTTN 607  
DB 756 EQQLLAEVANSLEQVSISSISGLNT--YLGKVIDKYSYILLTVSEIITQDEASTKST- 812

QY 608 YQRNKENIEDALNQLFRN 625  
DB 813 ----LENIKSAPDILLQN 826

RESULT 12  
Q6BL88\_DEBHA ID Q6BL88\_DEBHA PRELIMINARY; PRT; 1526 AA.  
AC Q6BL88; (Created)  
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)  
DE Debaryomyces hansenii chromosome F of strain CBS767 of Debaryomyces hansenii.  
DE hansenii.  
GN OrderedLocusNames=DEHA0F16742g;  
OS Debaryomyces hansenii (Yeast) (Torulapora hansenii).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.  
OX NCBI\_TaxID=4959;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=ATCC 36239 / CBS 767;  
RX PubMed=15229592; DOI=10.1038/nature02579;  
RA Dujon B., Sherman D., Fischer G., Durand P., Casaregola S., Laifontaine I., de Montigny J., Marck C., Neveglise C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C., Boissame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jaumaux N., Joyet P., Kachouri R., Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A., Swennen D., Tekai F., Wesolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A., Boucher C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J., Wincker P., Souciet J.-L.;  
RT "Genome evolution in yeasts.";  
RL Nature 430:35-44 (2004).  
DR EMBL; CR382138; CAG89403.1; -; Genomic\_DNA.  
DR GO; GO:0005224; F-ATP binding; IEA.  
DR GO; GO:0004674; F-protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004688; P-protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000357; HEAT.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR022290; Ser\_thr\_pkinase.  
DR InterPro; IPR01680; WD40.  
DR Pfam; PF02985; HEAT; 2.  
DR Pfam; PF00400; WD40; 3.  
DR PRINTS; PR00320; GPROTEINRPT.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00320; WD40; 4.  
DR PROSITE; PS50077; HEAT\_REPEAT; 1.  
DR PROSITE; PS50111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; UNKNOWN\_1.  
DR PROSITE; PS50082; WD\_REPEATS\_2; 1.  
DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
KW Complete proteome.  
SQ SEQUENCE 1526 AA; 174291 MW; DF5CB86F03820D9C CRC64;

Query Match 3.4%; Score 134.5; DB 2; Length 1526;  
Best Local Similarity 19.4%; Pred. No. 10;  
Matches 159; Conservative 95; Mismatches 285; Indels 279; Gaps 34;

QY 115 GEATGVDAICTHRPDPDTGGLDRQLVLELSQLTHSITELGP----- 156  
DB 297 GDRPSVDITLNDYKDKCFPGFFVFLYDFMSLANNLDLFPDNDNLTPSLDKLEKIYK 356  
QY 157 -YTLDRDSLNVNGFTHRSVPPTSTGVVSEEPFTLN-----FTINLRYM 200



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Db 357 SYDKIADALQFNYSNDRSSLSQNSKFV---PLMLNLKGMKPNYVTKPTVTFMENN--YL 411
Qy 201 ADMGQPSGL-KFNTDNNMKHLLSLPQ----- 227
Db 412 ----QQGSLIILNIFLMSKFKQPLSKAKACELIVALSERVNDCKLDRCLPYLCNLLD 467
Qy 228 ----RSSLGARYTG---CRVIALRSVKNGAETRVLDLLCTVLOPLSGPL 269
Db 468 EYWDSSINYPQNFQNLSENFTSSSEVACIALTSI-----TTLMSCSYINPIN---- 518
Qy 270 PIQGVFHELQOOTHGIRLGFYSLDKSLYNGYNEPGDEPPTTPKPAATFLPPLSEAT 329
Db 519 -VLMFSVLLPKLHALISIPKNEKDLIKIT-----LAACLPLYLANVS 561
Qy 330 TAMGYHUKTL-----TINFYISNLQYSPDMGKGSATFNS-----TEGVLOHLL 372
Db 562 KKFWMMSKTPKNDVLDKLNLSLSPKLLDDKENVSDSYNSFSIRKEQLDSDFNLSKLL 621
Qy 373 ---RPLFKQSSMGPFYLGQCLISLRPEKGAATGVDTT-----CTYHPDP----- 414
Db 622 TDVNPWKVLSLVNIMPCLQFF-----GVDKTNDIILPHLYTILNDSYELRLA 670
Qy 415 -----VGPGLDIQQLYWELSQLTHGVTOLG-----FYVLDKSLFINGYA 454
Db 671 FLSSILGIGPVGV--LSFEQYILPLLIQTLGDLQEQFVILKVLRFIFYCFVRDL- INPKS 727
Qy 455 PQN-LSIRGEVQINFHVNNLSNPDPTSSEYITLLRD--IQDKVTLYK--GSQLDHDF 509
Db 728 EFNALSIYKELL-----TSSIKLALLPNEWIRQSVICLILALISDNLDDAD 772
Qy 510 RFCLAVTNLTWDSVLAVTKALFSSNLDPSLVEQV-----FLDKTNASFHWLGSTY 559
Db 773 KYCLYPIVIGFLVDYDNTNNTLYESITKPLSKQIYNLAIWSSNASKSLFWQKSP 832
Qy 560 QLVD-----IHTVEMESSVQPTSSSSTQHFYLNFTITNLPSQDKAQPTTNYQR 610
Db 833 SVFNDLKAAPTILPYSTNMKGSVIYPKSKNG---FSLNNTNSNIPLSPEKQ-----WVL 884
Qy 611 NKRNIEDALNQLFRNSSIKSVFSDQVSTFRSVNRHHTGVDSL-----CNFSPARRVD 665
Db 885 KLSVGLNDRDLWKIFILRDYIYHSSKS-----NTSPTAKDDFELPKDINITP--RNVF 936
Qy 666 RVAYIEFLMRNGTQLOQNTLDRSSVLDVGYSPNRPNEPLTGNASDIQHSGRSSLEGP 725
Db 937 FEVCYKSEPPSSGSKTAETNF-----ESV-----HTLSNKKDBDSTRGLNSLILP 982
Qy 726 RFEQKLIS-----EEDLNMTGHGHHH 747
Db 983 NFGVKVSLQTVQANVFGLDTSHDSSFNASSSHHHH 1020

RESULT 13
ID Q54E23 DICDI PRELIMINARY; PRT; 797 AA.
AC Q54E23
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein AAC1.
GN Name=AAC1; ORFNames=DD80201568;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.A.,
RA Sugang R., Beriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tungal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou P., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
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RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Wardner H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Loulroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Urushihara H., Hernandez J., Rabinowitz E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -i- CAUTION: The sequence shown here is derived from an
CC ENBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFI01000264; EAL61460.1; -; Genomic_DNA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007091; LRR_RNinh.
DR InterPro; IPR003590; LRR_RNinh_sub.
DR Pfam; PF00560; LRR_1; 2.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00368; LRR RI; 7.
KW Hypothetical protein; Leucine-rich repeat; Repeat.
SQ SEQUENCE 797 AA; 89497 MW; OCCB0676C5C581PF CRC64;

Query Match 3.4%; Score 132.5; DB 2; Length 797;
Best Local Similarity 19.2%; Pred. No. 5.2;
Matches 173; Conservative 118; Mismatches 311; Indels 299; Gaps 42;

Qy 6 RRARRTKLFTHRSVSTSTPGTPTVVLGASKTPASIFGPSAASHLLILFTLNFTINLR 65
Db 3 RTSNRNEATAKLSSTSTITTTTNNKYNNANAES-----SKSTTISNLI 48
Qy 66 YEENMPGSRKFNTERVQLGLRLPFPKNTSVGLYSGCKRLTLRPKGEA-----TGV 120
Db 49 PKYSLFNEPNNDT-----NSSTRP--NKQOKLLKSNESTTSTTTTTPI 92
Qy 121 DAICTHRPDPGTGLDR---EQLYLELSQLTHSITELGPTLDRDSLTVNGFTHRSSVPT 177
Db 93 TTTTITTTTTTTNLSKYNNYIEKQEKQNL---PTTETTTITPTLTITTTTTT 148
Qy 178 TSTGVVSE-----PFTL-----NFTINN 196
Db 149 TTTTITTKQONTTSTINHFLLIQKEIIFLLVELGSLNARKVKYKVKVCNGCVEN 208
Qy 197 LR-YMADMGQPSGLKFNITDNNMKHLLSPILFQSSLGARYTGCRVIALRSVKNGAETRV 255
Db 209 LNTYFTDIHLSASVK-HVSEVFKVLSNDFHLQSV-----SPINGAKNSIS 254
Qy 256 LLCTYLOPLSGP-----GLPIKQVPHLSQOOTHGITRLGPVSLDKDS 297
Db 255 YSEFYFNNVILPFIENVVRYNOTIENTFTIKFPPIRNNKSSQOL-----LPSKLVHST 309
Qy 298 LYLNGYNPEGPDDEPTTPKP-----ATFPLPPLSEATTAMGYHLKT----- 338
Db 310 SVSSSPPPPPPPPPPPQQTITAPTSTTAIVSSTTTTATGTLNANNNNNIPKGLNY 369
Qy 339 -LTINFTISNLQYSPDMGKGSAT-----FNSTEGVLQHLRLPLFKSGMGPYLCQLIS- 392
Db 370 YLTNNFKLKKINLK-NIGLSDRDKDFDFSSLSNVNNTLETLIICDNIQD--EGMQLLSV 426
Qy 393 -----LRPEKGAATGVDTTCTVHPDPVGPGLDIQQLYWELSQLTHGVTQLGF 440
Db 427 ILIKNLLKLVKRLLEQKN-----QFTNQSAYLNKV---LSCQEQLQLETNLSSN- 473
Qy 441 YVLDKSLFT--NGYAPQNLISIRGEYQINFHVNNLSNPDPTSSEYITLLRDIDQKVTT 498
Db 474 -RIDEQGLIMKDGFG-RNKSLEK-----EFIPSKNRLGNTDSV-----DFGKSITS 517
Qy 499 LYKGSQSLHDT-----FRFCVLNLTWDSVLVTVTKALFSSNLDPSLVEQVFLDKTL 548
Db 518 L-----DLHDSMWGSKQSIKGLSQVLFKFNESITSLNLSFNHIGSNEAIKSLSKSFAVNQTL 573
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Db 488 DSTISSTNYLSVLAQSSSTINCNCQNTQSTVLTNSQLSSGSGVANITGTNLYLS 547
Qy 598 QD-----KAQPTTNYQRKNIE-----DALNQLFNSSIKSVFSD 634
Db 548 GSSITGVTQNRMSWLSLNTQISSNVNMGVSTLSAGSTINSQNTQGSTI--YLSN 605
Qy 635 CQV-----STFRSVPNRHHTGV-----DSLGNFSPPLARRVDRVAIYEELFMRTRNG 680
Db 606 SQINGNVVPSSTKLYVTGSTISGVTQVSGSGFISLSSTSSSTVSDSLNATGST 665
Qy 681 TQLONFLDRSSVLVDGYS--PFRNEPLTNSADIQHS 716
Db 666 ITSTQNTQGSTLYISGTTVSNSKOTLTNTNAYISNS 703

RESULT 17
Q81FJ0_BACCR PRELIMINARY; PRT; 5017 AA.
AC Q81FJ0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cell surface protein.
GN OrderedLocustNames=BC1592;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kaparal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Coltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91 (2003).
DR EMBL; AB017003; NAP08571.1; -: Genomic_DNA.
DR GO; GO:0005727; C:extrachromosomal circular DNA; IEA.
DR InterPro; IPR001434; DUF11.
DR Pfam; PF01345; DUF11; 28.
DR TIGRFAMs; TIGR01451; B_ant_repeat; 35.
KW Complete proteome.
SQ SEQUENCE 5017 AA; 523460 MW; 599BEA8DA930224F CRC64;

Query Match 3.2%; Score 128; DB 2; Length 5017;
Best Local Similarity 18.6%; Pred. No. 1.7e+02;
Matches 152; Conservative 127; Mismatches 327; Indels 212; Gaps 39;

Qy 17 RSVSVSTSPGTTVVLGASKTPASIFGSAASHLLILFTL-----NFTITNLYEENW 70
Db 3658 QAQLAITKTSNPTVDIGGT-----ILYISEVKNGVDAININFDSI 3701
Qy 71 WPGSRKFNTERVQLGLRLPLF---KNTSVGLPSYSGRLTLL-----RPEKDGATG-V 120
Db 3702 -PAGTTFVDPDSVINGVLQGVNPGNGIPGTPPANSSKTLILQVQTNPPNETEIVNQS 3760

Qy 121 DAICTHRPDPGFLDR-----EQYLELSQL-----THSITELG 155
Db 3761 SATYQVSVIPTAPVNRANSNIVTTSLOQANIISVKSDVNFVSGIMITYNTLTQNIQ 3820

Qy 156 PYTL-----RDSLYNGFTHRSVP---TTSYGVSVSEPPFLNPI--N 195
Db 3821 TVPANNIVFDINPEDTIFEDSLAINNVQGNPNGVTLGTIQNETVTSFQVQLT 3880

Qy 196 NLRYMADMGPGSLKFNITDNVKKLL---SPFQRSSL--GARYTCGRVIALRSVK--NG 249
Db 3881 NI-----PEGNTVINISTSYEQIDPSPIQRRSLSNVNTVETVNTANVAIKSANR 3933

Qy 250 AETRVLLCTYLQPSGP--LPKIQVFHELSSQOQTHGTRILGPYSLDKDSLYLNGYNPGP 308

Db 3934 SITRIGQIITYVAVTNAGTIPITNTL--LLDAIASGTTTVPNSILVDGV-----PRP 3984
Qy 309 DBPPTTPKPAATFPLPLSEATTAMGYHLKTLTL-----NFTISNLOQSPDMGKG--SA 359
Db 3985 NENPITGINLDILP---NNTIIVFQSVSVIPPQNINNTAVIHYVRPDPSTPISE 4041
Qy 360 TFNSTEGVLQHLRLPLFQKSMGPPFYLGCOLISLRPEKDGAAATGVDTTCTTHPDPVGPGL 419
Db 4042 TTSNATNIQ-----FIDAILIATKSANTVLAT-IDETIETVTFIQNWGS 4085
Qy 420 DIQQLWELSQLTHGVTQLGFFVLDLDRDSLFIN-----GYAPONLSIRGEVQINF 468
Db 4086 ATTNSIFFTDTTADGT-----VFIPGSVIVNNTVLPADPNIGFSIPNVAAGOMATITP 4139
Qy 469 HIVNWNLS--NPDPTSSEYI-----TLLRDQDKVTTLTKGSQLHD---TFRFCILVTN 516
Db 4140 QVSVTNLPTVNTPTNTANIVDFINPDPFAPQKSTTSNTTFVQINDADIVLSKTVDLTS 4199
Qy 517 LTMDSVLTVTKALFSS--NLDPSELVEQVPLDKTLNASFHVLGTY-----QL-----VDIH 565
Db 4200 VTIGDILTVTTTLTNTGNTATAV--VFTDNI PDGTFIDGSLVNNIPQLNANPSVGIL 4257
Qy 566 VTEMSSVYQPTSSSTQHFYLNFTITNLPYSQDKAQPCTTNYQNRKNIEDALNQLFRN 625
Db 4258 VGTIAPNISIPVTF-----VTVALPASGHVQNSTSRY---TINVEQIST--SN 4304
Qy 626 SSIKSVFSDCOVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEFLRMTNRTG--QLQ 684
Db 4305 ITFTEVISANVIAT-KTTPIQ-----ADLQTIITPISITNNGNIQVE 4347
Qy 685 NF-----TLDRSSVLVDGYSFNRNEPLTNGSAD 712
Db 4348 NIIATDIIIPVNTSFIENSIVNGNARPNNDPLNGIQID 4385

RESULT 18
Q4UDD4_THEAN PRELIMINARY; PRT; 1166 AA.
AC Q4UDD4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=TA14175;
OS Theileria annulata;
OC Eukaryota; Alveolata; Apicomplexa; Piropasmdia; Theileridae;
OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9; Harris D.A., Quail M.A., Berriman M.,
RA Pain A., Renauld H., Murphy L.,
RA Hall N., Barrell B.G.;
RT "The chromosome 2 sequence of Theileria annulata."
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR940348; CAI74905.1; -: Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1166 AA; 135275 MW; 2023F80318A19591 CRC64;

Query Match 3.2%; Score 127; DB 2; Length 1166;
Best Local Similarity 20.6%; Pred. No. 22;
Matches 175; Conservative 120; Mismatches 297; Indels 258; Gaps 50;

Qy 16 HRSSVSTSTPCTPTVYLGASKTPASIFGSAASHLLILFTLNFITNL-----RYEEN 69
Db 47 NNSRLNSNVTPTTNNKGGT-----DFFDDP-----VTFVREFSSETLWPEFSKFN 96
Qy 70 MWPGSRKFNTERVQLGLRLPLFKNTSVGLPSYSGRLTLLRPEKDGATGVAICTHRPD 129
Db 97 VYK-SRYLNTQE--CFALLNAHYKMLMNN--YAPRVQTLVLTQSMITEFT-----KPK 143
Qy 130 PTGPGDLRQLYLEL--SOLT-HSITELGFYTLDR-----DSLYVNGFTHRSSVPTTSTGV 182
```

Db 144 ETG-----QYQYQYSEVTFEALNEMSLFTKDHMKSLVILVGNHNLNLEGLRT-- 195  
Qy 183 VSEPFLLTNNRLRYMADMGPGSLKFNITDNVMKHLSPF--QRSSLGARYTCRV 240  
Db 196 -----YVLN--VMRLLYRAVTGSK-----SNQVEKSRFLFTLTKNYNG-----RA 235  
Qy 241 IALRSVNGAETRVLLCTVLOPL--SGRGLPIKQVF-----HELSSQOOTHGIT 286  
Db 236 VLYML-----LLCTLEKLLWFSEPOLVDFFSFAFICSFVESATSKSTHQKD 286  
Qy 287 RLGPYSLDKSLYNGNEPGDEPPTTPKPAITFLPPLSEATTAMGYHLKTLTLNFTIS 346  
Db 287 LTNNYQKGSVL-----TDKPGTSRK--NDLIPAMASNTDMLVRHLSVUCF---LL 333  
Qy 347 NLQYSPMGKGSATFNTEGVLOHLLRPLFKQSMGPFYLGCLISLRPEKGAATGVD 406  
Db 334 KLKVT-----QNKSLLESVRFLRNALASIPNRKNLLLTWSIMIVLDPOEIPANT----- 386  
Qy 407 TCTVHPDPVGPGLDI--QOLYWELSQLTHGVTLGFGYVLDRLSLF-----INGYAPQNLISIR 461  
Db 387 -----FKIPRSLFIEVGEI--NDMTQLVHLVLCIDNCFRDLKFSNFVESINVS 433  
Qy 462 GEYQI-----NF--HI--VNMWLSNP----- 478  
Db 434 TFVQLFLENFWKWDALNEDLANEILLANSVLDSPNLYSVPAKYISQFTNSSESNTY 493  
Qy 479 ---DPTSEYITLRLDIQDK---VTT-----LYKGSQHLDTFRCLVNTLTMDSVLV 524  
Db 494 NALNPQHNQYNYREOEKKNQMTQEIKLSHRIQKSMELFNIAFGKSRQLQMAAVL 553  
Qy 525 TVKALFSSNDPSL-----VEQVFLDKTLNASFWHLGTYQLVDIHVTEMESVYQPT 577  
Db 554 ASKLMSSDVTTTLPRINKLYKSNMLD--LLNLS---LNNQYTVND---TDYE---YNTQ 603  
Qy 578 SSSSTOH--FYLNFTITNLPYSQDAQPGTNTYQNRKNTIEDALNQLFRNSSIKSYFSDC 635  
Db 604 YNNHTDVTDFYKONKLEPNQDKFVDLTL-----TLMSAFINHCWKEILSTL 654  
Qy 636 QVST-----FRSVNRHTG---VDSLGNFSPARRVDRVAIYEEFLRMTRNGTQLQNT 687  
Db 655 MSKTGPKLFEYQKNRPHNGFERVDS--GKLNAVEGYDRKDVYKNYNR-----E 703  
Qy 688 LDRSSVLVDGSPNREPLTNSADIQ-----HSGGRSSLE-----GPREFQK 730  
Db 704 IDR-----VDGV--DRESKIDG---DVQRVLVSRLSYLGSNATIDSLYSILFSGP--PPAK 753  
Qy 731 LISEEDLNMH 740  
Db 754 VLSYEALRAH 763

## RESULT 19

Q86AL8\_DICDI  
ID Q86AL8\_DICDI PRELIMINARY; PRT; 1364 AA.  
AC Q86AL8;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Similar to Dictyostelium discoideum (Slime mold). Hypothetical 127.0 kDa protein.  
DE Dictyostelium discoideum (Slime mold).  
OS Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
OC NCBI\_TaxID=44689;  
RN NCBI\_TaxID=44689;  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=AX4;  
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;  
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J.A., Bankier A.T., Dear P.H., Lehmann R., Baumgart C., Parra G., Abril J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;  
RA "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";  
RT

RL Nature 418:79-85 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=AX4;  
RA Baumgart C.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC116984; AAC051349.1; -; Genomic\_DNA.  
DR InterPro; IPR006209; EGF like.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN 1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN 1.  
KW Hypothetical protein.  
SQ SEQUENCE 1364 AA; 153737 MW; 3A194428A8D7DD8F CRC64;

Query Match 3.2%; Score 127; DB 2; Length 1364;

Best Local Similarity 21.1%; Pred. No. 28;

Matches 114; Conservative 65; Mismatches 190; Indels 172; Gaps 25;

Qy 181 GVSEBEPFLNTNNRLRYMADMGPGSLKFNITDNVMKHLSPFORSLSGA 233  
Db 107 GVQVFSRFSLSHINN-----SISLNFICQAIQIDYTKLDYKLMVNRFRKST--S 153

Qy 234 RYTCGRVIALRSVNGAETRVLLCTVLOHLLRPLFKQSMGPFYLGCLISLRPEKGAATGVD 290  
Db 154 NYGG-----YLOFTS--EYPLGQL--EYSNTSGVLSNTIENT 187

Qy 291 YSLDKDLSYNGNEPGDEPPTTPKPAITFLPPLSEATTAMGVHLKTLTLNFTISNLQY 350  
Db 188 ANLAGSGLMYN-----FRNLVSUNFVGLIYNNISYIEV----- 221

Qy 351 SPDMGKGSATFNTEGVLOHLLRPLFKQSMGPFYLGCLISLRPEKGAATGVDTTCT 409  
Db 222 -PSLYTNDVNSNSIVTMYPNQVQYNEFG--FGCPPLFTITNR-----TTDE 269

Qy 410 YHDPDPVGPGLDIQOLYWELSQLTHGVTLGFGYVLDRLSLFINGYAPQNLISIRGEYQINFH 469  
Db 270 YQP-----YFYV-----SLINGLGTGNIQIYPLYEINKM 298

Qy 470 IVNMWLSNPDPPTSEYITLRLDIQDKVTTYKGSQHLDTFRCLVNTLTMDSVLV 522  
Db 299 ATYIGHPDGAATPS--YTLFSDQSDNLSLTIYK-----VENLTVKLKQSFST 345

Qy 523 LVTVKALFSSNDPSLVEQVFLDKTLNASFWHLGTYQLVDIHVTEMESVYQPTSSSST 582  
Db 346 VVIATVILHGN-----ETLYNSSMTVISFN--SGILKQVDFPT-----VYRFQSSSS- 391

Qy 583 QHLYLNTITNLPYSQDAQPGTNTYQNRKNTIEDALNQLFRNSSIKSYFSDCQVSTFRS 642  
Db 392 -----VILNWPFGFSGQNFNFKSSH-----LQNLFSINSISSFTDKNISTVQ 438

Qy 643 VPMRHTGVDSLGNFSPARRVDRVAIYEEFLRMTRNGTQLQNF-----TLDR--SSVLVDG 697  
Db 439 SDIKTLGFSNLIYRYSIVEDNEVVVFETVDFPKN--YGLGNFYFDLSLRMKSYLVNN 497

Qy 698 Y 698  
Db 498 Y 498

## RESULT 20

Q54V40\_DICDI  
ID Q54V40\_DICDI PRELIMINARY; PRT; 885 AA.  
AC Q54V40;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=DDB0206085;  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
OX NCBI\_TaxID=44689;  
RN NCBI\_TaxID=44689;  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=AX4;



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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:30:27 ; Search time 39.8343 Seconds  
(without alignments)  
1552.466 Million cell updates/sec

Title: US-10-687-035-1

Perfect score: 3945

Sequence: 1 AAQPARRRARTKLFTHRSSV.....QKLISEEDLNMTHGHHHHH 748

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/iaa/5 COMB.pep.\*

2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*

3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*

4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*

5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*

6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3663	92.9	833	2	US-09-404-879A-389
2	3663	92.9	833	2	US-09-667-857-389
3	3663	92.9	833	2	US-10-198-053-389
4	3663	92.9	833	2	US-09-827-271-389
5	3663	92.9	914	2	US-09-404-879A-312
6	3663	92.9	914	2	US-09-338-933-312
7	3663	92.9	914	2	US-09-667-857-312
8	3663	92.9	914	2	US-10-198-053-312
9	3663	92.9	914	2	US-10-198-053-478
10	3663	92.9	914	2	US-09-827-271-312
11	3651	92.3	3451	2	US-10-198-053-595
12	3642	92.3	1148	2	US-10-198-053-458
13	3642	92.3	1148	2	US-10-198-053-479
14	3642	92.3	1148	2	US-09-827-271-458
15	3642	92.3	1156	2	US-10-198-053-459
16	3642	92.3	1156	2	US-09-827-271-459
17	3189	80.8	772	2	US-09-404-879A-388
18	3189	80.8	772	2	US-09-667-857-388
19	3189	80.8	772	2	US-10-198-053-388
20	3189	80.8	772	2	US-09-827-271-388
21	1996	50.6	438	2	US-10-198-053-483
22	1990	50.4	438	2	US-09-404-879A-390
23	1990	50.4	438	2	US-09-667-857-390
24	1990	50.4	438	2	US-10-198-053-390
25	1990	50.4	438	2	US-09-827-271-390
26	1436	36.4	304	2	US-10-198-053-486
27	1345	34.1	318	2	US-10-198-053-594

28	903	22.9	178	2	US-10-198-053-489	Sequence 489, App
29	903	22.9	233	2	US-10-198-053-488	Sequence 488, App
30	842.5	21.4	294	2	US-10-198-053-487	Sequence 487, App
31	814	20.6	313	2	US-10-198-053-461	Sequence 461, App
32	814	20.6	313	2	US-09-827-271-461	Sequence 461, App
33	809	20.5	155	2	US-10-198-053-591	Sequence 591, App
34	800	20.3	150	2	US-10-198-053-593	Sequence 593, App
35	697	17.7	134	2	US-10-198-053-592	Sequence 592, App
36	675.5	17.1	210	2	US-10-198-053-481	Sequence 481, App
37	662	16.8	230	2	US-10-198-053-480	Sequence 480, App
38	659.5	16.7	156	2	US-10-198-053-589	Sequence 589, App
39	651.5	16.5	156	2	US-10-198-053-596	Sequence 596, App
40	637.5	16.2	156	2	US-10-198-053-590	Sequence 590, App
41	611.5	15.5	268	2	US-10-198-053-485	Sequence 485, App
42	607.5	15.4	156	2	US-10-198-053-584	Sequence 584, App
43	600.5	15.2	156	2	US-10-198-053-587	Sequence 587, App
44	599.5	15.2	156	2	US-10-198-053-583	Sequence 583, App
45	598.5	15.2	156	2	US-10-198-053-586	Sequence 586, App
46	595.5	15.1	156	2	US-10-198-053-588	Sequence 588, App
47	592.5	15.0	156	2	US-10-198-053-580	Sequence 580, App
48	589.5	14.9	156	2	US-10-198-053-577	Sequence 577, App
49	585.5	14.8	156	2	US-10-198-053-574	Sequence 574, App
50	585.5	14.8	156	2	US-10-198-053-585	Sequence 585, App
51	583.5	14.8	156	2	US-10-198-053-582	Sequence 582, App
52	577.5	14.6	156	2	US-10-198-053-581	Sequence 581, App
53	572	14.5	130	2	US-10-198-053-573	Sequence 573, App
54	569	14.4	155	2	US-10-198-053-579	Sequence 579, App
55	568.5	14.4	158	2	US-10-198-053-575	Sequence 575, App
56	564	14.3	216	2	US-10-198-053-484	Sequence 484, App
57	485.5	12.3	122	2	US-10-198-053-576	Sequence 576, App
58	307	7.8	130	2	US-10-198-053-573	Sequence 573, App
59	161.5	4.1	635	2	US-09-545-814-32	Sequence 32, Appl
60	156	4.0	28	2	US-10-198-053-597	Sequence 597, App
61	146.5	3.7	466	2	US-09-604-107A-8	Sequence 8, Appl
62	144.5	3.7	50	2	US-09-360-237-53	Sequence 53, Appl
63	140	3.5	28	2	US-10-198-053-598	Sequence 598, App
64	138	3.5	666	2	US-09-213-888-27	Sequence 27, Appl
65	138	3.5	666	2	US-09-328-877D-27	Sequence 27, Appl
66	121.5	3.1	1475	2	US-09-538-092-1160	Sequence 1160, Ap
67	118.5	3.0	10182	2	US-09-134-001C-3159	Sequence 3159, Ap
68	118	3.0	28	2	US-10-198-053-599	Sequence 599, App
69	117.5	3.0	637	2	US-09-489-039A-9243	Sequence 9243, Ap
70	117.5	3.0	2446	1	US-08-551-356-2	Sequence 2, Appl
71	117.5	3.0	2446	4	PCT-US93-12687-2	Sequence 2, Appl
72	117	3.0	21	2	US-09-071-710-41	Sequence 41, Appl
73	117	3.0	21	2	US-08-912-276-25	Sequence 25, Appl
74	117	3.0	21	2	US-09-153-804-17	Sequence 17, Appl
75	117	3.0	21	2	US-08-944-483-76	Sequence 76, Appl
76	117	3.0	21	2	US-09-525-397-41	Sequence 41, Appl
77	117	3.0	21	2	US-09-566-876-16	Sequence 16, Appl
78	117	3.0	21	2	US-09-049-698-51	Sequence 51, Appl
79	117	3.0	21	2	US-09-065-383-33	Sequence 33, Appl
80	117	3.0	21	2	US-09-276-600-11	Sequence 11, Appl
81	117	3.0	21	2	US-09-193-884-29	Sequence 29, Appl
82	117	3.0	21	2	US-09-050-516-49	Sequence 49, Appl
83	117	3.0	21	2	US-10-278-547-49	Sequence 49, Appl
84	117	3.0	21	2	US-09-431-384B-31	Sequence 31, Appl
85	117	3.0	21	2	US-09-052-855A-30	Sequence 30, Appl
86	117	3.0	21	2	US-09-080-140-31	Sequence 31, Appl
87	117	3.0	21	2	US-09-092-297A-22	Sequence 22, Appl
88	116.5	3.0	910	2	US-09-270-767-42083	Sequence 42083, A
89	115.5	2.9	1377	2	US-09-949-016-6058	Sequence 6058, Ap
90	115.5	2.9	838	2	US-09-315-794-52	Sequence 52, Appl
91	112.5	2.9	838	2	US-09-389-341-52	Sequence 52, Appl
92	112.5	2.9	838	2	US-09-564-805-229	Sequence 229, App
93	112.5	2.9	862	2	US-09-328-352-4421	Sequence 4421, App
94	112	2.8	2327	6	5455158-1	Patent No. 5455158
95	111	2.8	1241	2	US-08-714-741-34	Sequence 34, Appl
96	111	2.8	2355	2	US-10-360-101-235	Sequence 235, App
97	111	2.8	2386	1	US-09-016-366A-12	Sequence 12, Appl
98	111	2.8	2386	2	US-09-961-403-1	Sequence 1, Appl
99	110.5	2.8	969	2	US-09-198-452A-501	Sequence 501, App
100	110.5	2.8	1155	2	US-09-949-016-9550	Sequence 9550, Ap

## ALIGNMENTS

## RESULT 1

US-09-404-879A-389  
; Sequence 389, Application US/09404879A  
; Patent No. 6468546  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Algate, Paul A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C2  
; CURRENT APPLICATION NUMBER: US/09/404, 879A  
; CURRENT FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 393  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 389  
; LENGTH: 833  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-404-879A-389

Query Match 92.9%; Score 3663; DB 2; Length 833;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	14	FTHRSSVSTTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLFTITNLRYEENWPG	73
Db	78	FTHRSSVSTTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLFTITNLRYEENWPG	137
Qy	74	SRKFNTERVQLGLRLPKNTSVGPLYSGCRLLTLRPEKDGATGVDALCTHRPDTGP	133
Db	138	SRKFNTERVQLGLRLPKNTSVGPLYSGCRLLTLRPEKDGATGVDALCTHRPDTGP	197
Qy	134	GLDREQLYLELSQTHSITELGPTTLDRDSLYNGFTHRSSVPTTSGVVSSEPTLNFT	193
Db	198	GLDREQLYLELSQTHSITELGPTTLDRDSLYNGFTHRSSVPTTSGVVSSEPTLNFT	257
Qy	194	INNLRVWADMGQPSGLKFNITDVMKHLSPFORSSIGARYTCRVIALRSVKNGAETR	253
Db	258	INNLRVWADMGQPSGLKFNITDVMKHLSPFORSSIGARYTCRVIALRSVKNGAETR	317
Qy	254	VDLLCTYLQPLSGPLPIKQVFHELSSQTHGTRGLGPSYLDKDSLYLNGYNEPDPDEPT	313
Db	318	VDLLCTYLQPLSGPLPIKQVFHELSSQTHGTRGLGPSYLDKDSLYLNGYNEPDPDEPT	377
Qy	314	TPKPATTFPLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKSATFNSSTEGVLQHLR	373
Db	378	TPKPATTFPLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKSATFNSSTEGVLQHLR	437
Qy	374	PLFOKSSMGPPYLGCLISLRPEKDGATGVDTTCTVHPDPVPGGLDIQQLYWELSOLTH	433
Db	438	PLFOKSSMGPPYLGCLISLRPEKDGATGVDTTCTVHPDPVPGGLDIQQLYWELSOLTH	497
Qy	434	GVTQLGFVLDRLDSLFINGVAPQNLISIRGEQINFHIVNWNLSNPDPTSSEYITLLRDIQ	493
Db	498	GVTQLGFVLDRLDSLFINGVAPQNLISIRGEQINFHIVNWNLSNPDPTSSEYITLLRDIQ	557
Qy	494	DKVTTLKYGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVQVFLDKTLNASFH	553
Db	558	DKVTTLKYGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVQVFLDKTLNASFH	617
Qy	554	WLGSTYQLVDLHVTEMSSVYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNQRKR	613
Db	618	WLGSTYQLVDLHVTEMSSVYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNQRKR	677
Qy	614	NIEDALNQLFNSSIKSYFSDCQVSTFRSVPNRHHTGVDLSLNCFSPLARRVDRVAIYEEF	673
Db	678	NIEDALNQLFNSSIKSYFSDCQVSTFRSVPNRHHTGVDLSLNCFSPLARRVDRVAIYEEF	737

Qy 674 LRMTRNGTQIQNFLLDRSSVLVDGYSFNRNEPLTGNS 710  
Db 738 LRMTRNGTQIQNFLLDRSSVLVDGYSFNRNEPLTGNS 774

## RESULT 2

US-09-667-857-389  
; Sequence 389, Application US/09667857  
; Patent No. 6695664  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Fling, Steven P.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary Richard  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C5  
; CURRENT APPLICATION NUMBER: US/09/667,857  
; CURRENT FILING DATE: 2000-09-20  
; NUMBER OF SEQ ID NOS: 455  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 389  
; LENGTH: 833  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-667-857-389

Query Match 92.9%; Score 3663; DB 2; Length 833;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	14	FTHRSSVSTTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLFTITNLRYEENWPG	73
Db	78	FTHRSSVSTTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLFTITNLRYEENWPG	137
Qy	74	SRKFNTERVQLGLRLPKNTSVGPLYSGCRLLTLRPEKDGATGVDALCTHRPDTGP	133
Db	138	SRKFNTERVQLGLRLPKNTSVGPLYSGCRLLTLRPEKDGATGVDALCTHRPDTGP	197
Qy	134	GLDREQLYLELSQTHSITELGPTTLDRDSLYNGFTHRSSVPTTSGVVSSEPTLNFT	193
Db	198	GLDREQLYLELSQTHSITELGPTTLDRDSLYNGFTHRSSVPTTSGVVSSEPTLNFT	257
Qy	194	INNLRVWADMGQPSGLKFNITDVMKHLSPFORSSIGARYTCRVIALRSVKNGAETR	253
Db	258	INNLRVWADMGQPSGLKFNITDVMKHLSPFORSSIGARYTCRVIALRSVKNGAETR	317
Qy	254	VDLLCTYLQPLSGPLPIKQVFHELSSQTHGTRGLGPSYLDKDSLYLNGYNEPDPDEPT	313
Db	318	VDLLCTYLQPLSGPLPIKQVFHELSSQTHGTRGLGPSYLDKDSLYLNGYNEPDPDEPT	377
Qy	314	TPKPATTFPLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKSATFNSSTEGVLQHLR	373
Db	378	TPKPATTFPLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKSATFNSSTEGVLQHLR	437
Qy	374	PLFOKSSMGPPYLGCLISLRPEKDGATGVDTTCTVHPDPVPGGLDIQQLYWELSOLTH	433
Db	438	PLFOKSSMGPPYLGCLISLRPEKDGATGVDTTCTVHPDPVPGGLDIQQLYWELSOLTH	497
Qy	434	GVTQLGFVLDRLDSLFINGVAPQNLISIRGEQINFHIVNWNLSNPDPTSSEYITLLRDIQ	493
Db	498	GVTQLGFVLDRLDSLFINGVAPQNLISIRGEQINFHIVNWNLSNPDPTSSEYITLLRDIQ	557
Qy	494	DKVTTLKYGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVQVFLDKTLNASFH	553
Db	558	DKVTTLKYGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVQVFLDKTLNASFH	617



QY 554 WLGSTYQVLDIHVTEMESSYQPTSSSTQHFYLNFTITNLPIYQDQAQPGTTNYQRNKR 613  
Db 618 WLGSTYQVLDIHVTEMESSYQPTSSSTQHFYLNFTITNLPIYQDQAQPGTTNYQRNKR 677  
QY 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLNCNFSPLARRVDRVAIYEFP 673  
Db 678 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLNCNFSPLARRVDRVAIYEFP 737  
QY 674 LRMRNGTQQLNFTLDRSSVLVDGYSNPRNEPLTGNS 710  
Db 738 LRMRNGTQQLNFTLDRSSVLVDGYSNPRNEPLTGNS 774

RESULT 3  
US-10-198-053-389  
; Sequence 389, Application US/10198053  
; Patent No. 6858710  
; GENERAL INFORMATION:  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Hill, Paul  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C9  
; CURRENT APPLICATION NUMBER: US/10/198.053  
; CURRENT FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 624  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 389  
; LENGTH: 833  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-198-053-389

Query Match 92.9%; Score 3663; DB 2; Length 833;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTNLFTITNLRYEENWPG 73  
Db 78 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTNLFTITNLRYEENWPG 137

QY 74 SRKFNTTERTVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDALCTHRPDTGP 133  
Db 138 SRKFNTTERTVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDALCTHRPDTGP 197

QY 134 GLDREQLYLELSQTHSITELGPTTLDRLDLSLVNGFTHRSSVPTTSTGVVSEBPFTLNFT 193  
Db 198 GLDREQLYLELSQTHSITELGPTTLDRLDLSLVNGFTHRSSVPTTSTGVVSEBPFTLNFT 257

QY 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNGAETR 253  
Db 258 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNGAETR 317

QY 254 VDLCTYLOPLSGPLPIKQVFHELSSQTHGTRIGLGPYSLDKDSLYLNGVNEPDPPEPT 313  
Db 318 VDLCTYLOPLSGPLPIKQVFHELSSQTHGTRIGLGPYSLDKDSLYLNGVNEPDPPEPT 377

QY 314 TPKPATTFPLPPLSEATTAMGYHLKTLTNTFTISNLOYSMDMGKGSATFNSTGVLOHLR 373  
Db 378 TPKPATTFPLPPLSEATTAMGYHLKTLTNTFTISNLOYSMDMGKGSATFNSTGVLOHLR 437

QY 374 PLFQKSSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDPVPGGLDIOQLYWELSOLTH 433  
Db 438 PLFQKSSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDPVPGGLDIOQLYWELSOLTH 497

QY 434 GVTQLGFYVLDRLDLSLFIINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSSEYITLLRDIO 493  
Db 498 GVTQLGFYVLDRLDLSLFIINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSSEYITLLRDIO 557

QY 494 DKVTTLYKGSQLDHTRFRCLVNTLMDSVLTVKALFSSNLDPSLVQVFLDKTLNASHF 553

Db 558 DKVTTLYKGSQLDHTRFRCLVNTLMDSVLTVKALFSSNLDPSLVQVFLDKTLNASHF 617  
QY 554 WLGSTYQVLDIHVTEMESSYQPTSSSTQHFYLNFTITNLPIYQDQAQPGTTNYQRNKR 613  
Db 618 WLGSTYQVLDIHVTEMESSYQPTSSSTQHFYLNFTITNLPIYQDQAQPGTTNYQRNKR 677  
QY 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLNCNFSPLARRVDRVAIYEFP 673  
Db 678 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLNCNFSPLARRVDRVAIYEFP 737  
QY 674 LRMRNGTQQLNFTLDRSSVLVDGYSNPRNEPLTGNS 710  
Db 738 LRMRNGTQQLNFTLDRSSVLVDGYSNPRNEPLTGNS 774

RESULT 4  
US-09-827-271-389  
; Sequence 389, Application US/09827271  
; Patent No. 6962980  
; GENERAL INFORMATION:  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.462C6  
; CURRENT APPLICATION NUMBER: US/09/827.271  
; CURRENT FILING DATE: 2001-04-04  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: Fast-Seq for Windows Version 3.0  
; SEQ ID NO 389  
; LENGTH: 833  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-827-271-389

Query Match 92.9%; Score 3663; DB 2; Length 833;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTNLFTITNLRYEENWPG 73  
Db 78 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTNLFTITNLRYEENWPG 137

QY 74 SRKFNTTERTVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDALCTHRPDTGP 133  
Db 138 SRKFNTTERTVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDALCTHRPDTGP 197

QY 134 GLDREQLYLELSQTHSITELGPTTLDRLDLSLVNGFTHRSSVPTTSTGVVSEBPFTLNFT 193  
Db 198 GLDREQLYLELSQTHSITELGPTTLDRLDLSLVNGFTHRSSVPTTSTGVVSEBPFTLNFT 257

QY 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNGAETR 253  
Db 258 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNGAETR 317

QY 254 VDLCTYLOPLSGPLPIKQVFHELSSQTHGTRIGLGPYSLDKDSLYLNGVNEPDPPEPT 313  
Db 318 VDLCTYLOPLSGPLPIKQVFHELSSQTHGTRIGLGPYSLDKDSLYLNGVNEPDPPEPT 377

QY 314 TPKPATTFPLPPLSEATTAMGYHLKTLTNTFTISNLOYSMDMGKGSATFNSTGVLOHLR 373  
Db 378 TPKPATTFPLPPLSEATTAMGYHLKTLTNTFTISNLOYSMDMGKGSATFNSTGVLOHLR 437

QY 374 PLFQKSSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDPVPGGLDIOQLYWELSOLTH 433  
Db 438 PLFQKSSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDPVPGGLDIOQLYWELSOLTH 497

QY 434 GVTQLGFYVLDRLDLSLFIINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSSEYITLLRDIO 493  
Db 498 GVTQLGFYVLDRLDLSLFIINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSSEYITLLRDIO 557

QY 494 DKVTTLYKGSQLDHTRFRCLVNTLMDSVLTVKALFSSNLDPSLVQVFLDKTLNASHF 553

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Db 558 DKVTTYKGSQSLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 617
QY 554 WLGSYQLVDIHVTEMESVYQPTSSSTQHLYNFTTNLPSQDKAQPGTTNQRKR 613
Db 618 WLGSYQLVDIHVTEMESVYQPTSSSTQHLYNFTTNLPSQDKAQPGTTNQRKR 677
QY 614 NIEDALNQLFRNSSIKSYSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673
Db 678 NIEDALNQLFRNSSIKSYSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 737
QY 674 LRMTRNGTQLONFLLDRSSVLVDGYSPNRNEPLTGN 710
Db 738 LRMTRNGTQLONFLLDRSSVLVDGYSPNRNEPLTGN 774

RESULT 5
US-09-404-879A-312
; Sequence 312, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404, 879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-404-879A-312

Query Match 92.9%; Score 3663; DB 2; Length 914;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 73
Db 159 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218
QY 74 SRKENTERVLOGLLRPLFKNTSVGLYSGCRLLTLLRPEKDGATGVDAICTHRPDP TGP 133
Db 219 SRKENTERVLOGLLRPLFKNTSVGLYSGCRLLTLLRPEKDGATGVDAICTHRPDP TGP 278
QY 134 GLDREQLYLELSQTHSITELGPVTLDRDLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPVTLDRDLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
QY 194 INNLRYMADMGQPSGLKFNITDNVMKLLSPLFORSSILGARYTCRVIALRSVKNGAETR 253
Db 339 INNLRYMADMGQPSGLKFNITDNVMKLLSPLFORSSILGARYTCRVIALRSVKNGAETR 398
QY 254 VDLCTYLOPLSGPLPKQVFEHLSQTHGTRIGPYSLDKSLYNGYNEPGDEPPT 313
Db 399 VDLCTYLOPLSGPLPKQVFEHLSQTHGTRIGPYSLDKSLYNGYNEPGDEPPT 458
QY 314 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSFTEGVLOHLLR 373
Db 459 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSFTEGVLOHLLR 518
QY 374 PLFQKSSMGPPYLGCOLISLRPEKDGATGVDDTCTTHPDPVGPGLDIQQLYWELSOLTH 433
Db 519 PLFQKSSMGPPYLGCOLISLRPEKDGATGVDDTCTTHPDPVGPGLDIQQLYWELSOLTH 578
QY 434 GVTOLGFVYLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ 493
Db 579 GVTOLGFVYLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ 638
QY 494 DKVTTYKGSQSLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553

Db 639 DKVTTYKGSQSLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 698
QY 554 WLGSYQLVDIHVTEMESVYQPTSSSTQHLYNFTTNLPSQDKAQPGTTNQRKR 613
Db 699 WLGSYQLVDIHVTEMESVYQPTSSSTQHLYNFTTNLPSQDKAQPGTTNQRKR 758
QY 614 NIEDALNQLFRNSSIKSYSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSSIKSYSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 818
QY 674 LRMTRNGTQLONFLLDRSSVLVDGYSPNRNEPLTGN 710
Db 819 LRMTRNGTQLONFLLDRSSVLVDGYSPNRNEPLTGN 855

RESULT 6
US-09-338-933-312
; Sequence 312, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; FILE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338, 933
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-338-933-312

Query Match 92.9%; Score 3663; DB 2; Length 914;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 73
Db 159 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218
QY 74 SRKENTERVLOGLLRPLFKNTSVGLYSGCRLLTLLRPEKDGATGVDAICTHRPDP TGP 133
Db 219 SRKENTERVLOGLLRPLFKNTSVGLYSGCRLLTLLRPEKDGATGVDAICTHRPDP TGP 278
QY 134 GLDREQLYLELSQTHSITELGPVTLDRDLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPVTLDRDLSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
QY 194 INNLRYMADMGQPSGLKFNITDNVMKLLSPLFORSSILGARYTCRVIALRSVKNGAETR 253
Db 339 INNLRYMADMGQPSGLKFNITDNVMKLLSPLFORSSILGARYTCRVIALRSVKNGAETR 398
QY 254 VDLCTYLOPLSGPLPKQVFEHLSQTHGTRIGPYSLDKSLYNGYNEPGDEPPT 313
Db 399 VDLCTYLOPLSGPLPKQVFEHLSQTHGTRIGPYSLDKSLYNGYNEPGDEPPT 458
QY 314 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSFTEGVLOHLLR 373
Db 459 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSFTEGVLOHLLR 518
QY 374 PLFQKSSMGPPYLGCOLISLRPEKDGATGVDDTCTTHPDPVGPGLDIQQLYWELSOLTH 433
Db 519 PLFQKSSMGPPYLGCOLISLRPEKDGATGVDDTCTTHPDPVGPGLDIQQLYWELSOLTH 578
QY 434 GVTOLGFVYLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ 493
Db 579 GVTOLGFVYLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ 638
QY 494 DKVTTYKGSQSLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553
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Db 639 DKVTLYKGSQQLHDTFRCLVNTLMDSVLVTVKALFSSNLDPSLVQVFLDKTLNASFH 698  
Qy 554 WLGSTYQLVDIHVTEMSSVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQNRK 613  
Db 699 WLGSTYQLVDIHVTEMSSVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQNRK 758  
Qy 614 NIEDALNQLFRNSIKSYFSDCVSTFRSPVNRHHTGVDSLCNFSPILARRVDRVAIYEEF 673  
Db 759 NIEDALNQLFRNSIKSYFSDCVSTFRSPVNRHHTGVDSLCNFSPILARRVDRVAIYEEF 818  
Qy 674 LRMRNGTQLQNFLLDRSSVLVDGYSNREPLTNS 710  
Db 819 LRMRNGTQLQNFLLDRSSVLVDGYSNREPLTNS 855  
RESULT 7  
US-09-667-857-312  
; Sequence 312, Application US/09667857  
; Patent No. 6699664  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Gordon E.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Fling, Steven P.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary Richard  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C5  
; CURRENT APPLICATION NUMBER: US/09/667,857  
; CURRENT FILING DATE: 2000-09-20  
; NUMBER OF SEQ ID NOS: 455  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 312  
; LENGTH: 914  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-667-857-312

Query Match 92.9%; Score 3663; DB 2; Length 914;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 14 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSPAASHLLILFTLNFTITNLRYEENWPG 73  
Db 159 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSPAASHLLILFTLNFTITNLRYEENWPG 218  
Qy 74 SRKFNTTERTVQLLRPLFNTSVGPLYSGCRLLTLRPEKGEATGVDAICTHRPDTGP 133  
Db 219 SRKFNTTERTVQLLRPLFNTSVGPLYSGCRLLTLRPEKGEATGVDAICTHRPDTGP 278  
Qy 134 GLDREQLYLELSQTHSITELGPYTLDRSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193  
Db 279 GLDREQLYLELSQTHSITELGPYTLDRSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 338  
Qy 194 INNLRYMADMGQPSLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNCAETR 253  
Db 339 INNLRYMADMGQPSLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNCAETR 398  
Qy 254 VDLCTYQLPSGPGLPKQVPHLSQOQTHGTRGLPYSLDKSLYNGYNEPDPPT 313  
Db 399 VDLCTYQLPSGPGLPKQVPHLSQOQTHGTRGLPYSLDKSLYNGYNEPDPPT 458  
Qy 314 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373  
Db 459 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518  
Qy 374 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTTCTTYHPDPVGPGLDIOQLYWELSQLTH 433

Db 519 PLFOKSMGPFYLGCOLISLRPEKGAATGVDTTCTTYHPDPVGPGLDIOQLYWELSQLTH 578  
Qy 434 GVTOLGPFVLDROSLFRINGVAPQNLISIRGEVQNFHIVNNLSNPDPTSSSEYITLARDIQ 493  
Db 579 GVTOLGPFVLDROSLFRINGVAPQNLISIRGEVQNFHIVNNLSNPDPTSSSEYITLARDIQ 638  
Qy 494 DKVTLYKGSQQLHDTFRCLVNTLMDSVLVTVKALFSSNLDPSLVQVFLDKTLNASFH 553  
Db 639 DKVTLYKGSQQLHDTFRCLVNTLMDSVLVTVKALFSSNLDPSLVQVFLDKTLNASFH 698  
Qy 554 WLGSTYQLVDIHVTEMSSVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQNRK 613  
Db 699 WLGSTYQLVDIHVTEMSSVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQNRK 758  
Qy 614 NIEDALNQLFRNSIKSYFSDCVSTFRSPVNRHHTGVDSLCNFSPILARRVDRVAIYEEF 673  
Db 759 NIEDALNQLFRNSIKSYFSDCVSTFRSPVNRHHTGVDSLCNFSPILARRVDRVAIYEEF 818  
Qy 674 LRMRNGTQLQNFLLDRSSVLVDGYSNREPLTNS 710  
Db 819 LRMRNGTQLQNFLLDRSSVLVDGYSNREPLTNS 855  
RESULT 8  
US-10-198-053-312  
; Sequence 312, Application US/10198053  
; Patent No. 6858710  
; GENERAL INFORMATION:  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Hill, Paul  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C9  
; CURRENT APPLICATION NUMBER: US/10/198,053  
; CURRENT FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 624  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 312  
; LENGTH: 914  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-198-053-312

Query Match 92.9%; Score 3663; DB 2; Length 914;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 14 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSPAASHLLILFTLNFTITNLRYEENWPG 73  
Db 159 FTHRSSVSTSTPGTPTVYLKASKTPASIFGSPAASHLLILFTLNFTITNLRYEENWPG 218  
Qy 74 SRKFNTTERTVQLLRPLFNTSVGPLYSGCRLLTLRPEKGEATGVDAICTHRPDTGP 133  
Db 219 SRKFNTTERTVQLLRPLFNTSVGPLYSGCRLLTLRPEKGEATGVDAICTHRPDTGP 278  
Qy 134 GLDREQLYLELSQTHSITELGPYTLDRSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193  
Db 279 GLDREQLYLELSQTHSITELGPYTLDRSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 338  
Qy 194 INNLRYMADMGQPSLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNCAETR 253  
Db 339 INNLRYMADMGQPSLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNCAETR 398  
Qy 254 VDLCTYQLPSGPGLPKQVPHLSQOQTHGTRGLPYSLDKSLYNGYNEPDPPT 313  
Db 399 VDLCTYQLPSGPGLPKQVPHLSQOQTHGTRGLPYSLDKSLYNGYNEPDPPT 458  
Qy 314 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373  
Db 459 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518

Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSSTEGVLQHLLR 518  
 QY 374 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTTHPDPVGPGLDIQQLYWELSQLTH 433  
 Db 519 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTTHPDPVGPGLDIQQLYWELSQLTH 578  
 QY 434 GVTQLGFFVLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ 493  
 Db 579 GVTQLGFFVLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ 638  
 QY 494 DKVTTLYKGSQQLHDTFRFCLVTLNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASPH 553  
 Db 639 DKVTTLYKGSQQLHDTFRFCLVTLNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASPH 698  
 QY 554 WLGSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTIITNLPYSQDKAOPGTTNYQRNKR 613  
 Db 699 WLGSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTIITNLPYSQDKAOPGTTNYQRNKR 758  
 QY 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDLNCNFSPLARRVDRVAIYEEF 673  
 Db 759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDLNCNFSPLARRVDRVAIYEEF 818  
 QY 674 LRMTRNGTQLQNFILDRSSVLVDGYSPNRNEPLTGNS 710  
 Db 819 LRMTRNGTQLQNFILDRSSVLVDGYSPNRNEPLTGNS 855

RESULT 10  
 US-09-827-271-312  
 ; Sequence 312, Application US/09827271  
 ; Patent No. 6962980  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Retter, Marc W.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.462C6  
 ; CURRENT APPLICATION NUMBER: US/09/827,271  
 ; CURRENT FILING DATE: 2001-04-04  
 ; NUMBER OF SEQ ID NOS: 461  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 312  
 ; LENGTH: 914  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 ; US-09-827-271-312

Query Match 92.9%; Score 3663; DB 2; Length 914;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSPSAASHLLILFTLNTITNLYEENMWP 73  
 Db 159 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSPSAASHLLILFTLNTITNLYEENMWP 218  
 QY 74 SRKFNTERVLOGLRLPLFKNTSVGPLYSGCRLTLRPEKGEATGVDICTHRDPDPTGP 133  
 Db 219 SRKFNTERVLOGLRLPLFKNTSVGPLYSGCRLTLRPEKGEATGVDICTHRDPDPTGP 278  
 QY 134 GLDREQLYLELSQTHSITELGPTLDRDLSLVNGFTTHRSSVPTTSTGVVSEEPFLNFT 193  
 Db 279 GLDREQLYLELSQTHSITELGPTLDRDLSLVNGFTTHRSSVPTTSTGVVSEEPFLNFT 338  
 QY 194 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSLGARYTCRVIARLVKNGAETR 253  
 Db 339 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSLGARYTCRVIARLVKNGAETR 398  
 QY 254 VDLCTYQLPSGGLPIKQVPHLSQOOTHGITELGPTSLDKDLSLVNGYNEPGDEPPT 313  
 Db 399 VDLCTYQLPSGGLPIKQVPHLSQOOTHGITELGPTSLDKDLSLVNGYNEPGDEPPT 458  
 QY 314 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSSTEGVLQHLLR 373

QY 374 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTTHPDPVGPGLDIQQLYWELSQLTH 433  
 Db 519 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTTHPDPVGPGLDIQQLYWELSQLTH 578  
 QY 434 GVTQLGFFVLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ 493  
 Db 579 GVTQLGFFVLDRLDSLFINGYAPQNLISIRGEYQINFIHVNWNLSPDPPTSSEYITLLRDIQ 638  
 QY 494 DKVTTLYKGSQQLHDTFRFCLVTLNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASPH 553  
 Db 639 DKVTTLYKGSQQLHDTFRFCLVTLNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASPH 698  
 QY 554 WLGSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTIITNLPYSQDKAOPGTTNYQRNKR 613  
 Db 699 WLGSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTIITNLPYSQDKAOPGTTNYQRNKR 758  
 QY 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDLNCNFSPLARRVDRVAIYEEF 673  
 Db 759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDLNCNFSPLARRVDRVAIYEEF 818  
 QY 674 LRMTRNGTQLQNFILDRSSVLVDGYSPNRNEPLTGNS 710  
 Db 819 LRMTRNGTQLQNFILDRSSVLVDGYSPNRNEPLTGNS 855

RESULT 9  
 US-10-198-053-478  
 ; Sequence 478, Application US/10198053  
 ; Patent No. 6858710  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bangur, Chaitanya S.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Hill, Paul  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121.462C9  
 ; CURRENT APPLICATION NUMBER: US/10/198,053  
 ; CURRENT FILING DATE: 2002-07-17  
 ; NUMBER OF SEQ ID NOS: 624  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 478  
 ; LENGTH: 914  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-198-053-478

Query Match 92.9%; Score 3663; DB 2; Length 914;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSPSAASHLLILFTLNTITNLYEENMWP 73  
 Db 159 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGSPSAASHLLILFTLNTITNLYEENMWP 218  
 QY 74 SRKFNTERVLOGLRLPLFKNTSVGPLYSGCRLTLRPEKGEATGVDICTHRDPDPTGP 133  
 Db 219 SRKFNTERVLOGLRLPLFKNTSVGPLYSGCRLTLRPEKGEATGVDICTHRDPDPTGP 278  
 QY 134 GLDREQLYLELSQTHSITELGPTLDRDLSLVNGFTTHRSSVPTTSTGVVSEEPFLNFT 193  
 Db 279 GLDREQLYLELSQTHSITELGPTLDRDLSLVNGFTTHRSSVPTTSTGVVSEEPFLNFT 338  
 QY 194 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSLGARYTCRVIARLVKNGAETR 253  
 Db 339 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSLGARYTCRVIARLVKNGAETR 398  
 QY 254 VDLCTYQLPSGGLPIKQVPHLSQOOTHGITELGPTSLDKDLSLVNGYNEPGDEPPT 313  
 Db 399 VDLCTYQLPSGGLPIKQVPHLSQOOTHGITELGPTSLDKDLSLVNGYNEPGDEPPT 458  
 QY 314 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSSTEGVLQHLLR 373

Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQVSPDMGKGSATFNSTEGVLOHLR 518  
Qy 374 PLFKQSMGPFYLGCCQLISLRPEKGAATGVDTTCTYHPDPVGPGLDIOQLYWELSLTH 433  
Db 519 PLFKQSMGPFYLGCCQLISLRPEKGAATGVDTTCTYHPDPVGPGLDIOQLYWELSLTH 578  
Qy 434 GVTQLGPFYLDRLDLSFLNGVAPQNLISIRGEYQINPHIVNMNLSNPDPPTSEYITLLRDIQ 493  
Db 579 GVTQLGPFYLDRLDLSFLNGVAPQNLISIRGEYQINPHIVNMNLSNPDPPTSEYITLLRDIQ 638  
Qy 494 DKVTLLYKGSQSLDHTFRCLVTLNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASEH 553  
Db 639 DKVTLLYKGSQSLDHTFRCLVTLNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASEH 698  
Qy 554 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPCTTNYQRNKR 613  
Db 699 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPCTTNYQRNKR 758  
Qy 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLCNFSPLARRVDRVAIYEEF 673  
Db 759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLCNFSPLARRVDRVAIYEEF 818  
Qy 674 LRMTNGTQLQNFTRDSSVLDGYSNRPNEPLTGS 710  
Db 819 LRMTNGTQLQNFTRDSSVLDGYSNRPNEPLTGS 855

RESULT 11  
US-10-198-053-595  
; Sequence 595, Application US/10198053  
; Patent No. 6858710  
; GENERAL INFORMATION:  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Hill, Paul  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C9  
; CURRENT APPLICATION NUMBER: US/10/198,053  
; CURRENT FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 624  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 595  
; TYPE: PRP  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: 177, 335, 523, 618, 663, 875, 961, 1001, 1441, 1555, 1560,  
; LOCATION: 1563, 1574, 1585, 2065, 2070, 2683, 2990, 3269, 3381, 3401  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-10-198-053-595

Query Match 92.5%; Score 3651; DB 2; Length 3451;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTGPTPVYLGASKTPASIFGSAASHLLILFTLNTITNLRYEENWPG 73  
Db 2696 FTHRSSVSTSTGPTPVYLGASKTPASIFGSAASHLLILFTLNTITNLRYEENWPG 2755  
Qy 74 SRKFNTTREVLOGLLRPLKNTSVGLYSGRITLLRPEKDGATGVDAICTHRPPTGP 133  
Db 2756 SRKFNTTREVLOGLLRPLKNTSVGLYSGRITLLRPEKDGATGVDAICTHRPPTGP 2815  
Qy 134 GLDREQLYLSQTHSITELGPTVTLDRSLYNGFTHRSSVPTTSTGVVSEBPFLLNFT 193  
Db 2816 GLDREQLYLSQTHSITELGPTVTLDRSLYNGFTHRSSVPTTSTGVVSEBPFLLNFT 2875  
Qy 194 INNLRYMADMGQPSLKFNTIDNMKHLSPFORSSLGARYTGCRIALRSYKGAETR 253  
Db 2876 INNLRYMADMGQPSLKFNTIDNMKHLSPFORSSLGARYTGCRIALRSYKGAETR 2935

Qy 254 VDLCTYLQPLSGPLPIKQVPHLSQOHTGIRLGPYSLDKOSLYLNGYNEPDEPPT 313  
Db 2936 VDLCTYLQPLSGPLPIKQVPHLSQOHTGIRLGPYSLDKOSLYLNGYNEPDEPPT 2995  
Qy 314 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQVSPDMGKGSATFNSTEGVLOHLR 373  
Db 2996 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQVSPDMGKGSATFNSTEGVLOHLR 3055  
Qy 374 PLFKQSMGPFYLGCCQLISLRPEKGAATGVDTTCTYHPDPVGPGLDIOQLYWELSLTH 433  
Db 3056 PLFKQSMGPFYLGCCQLISLRPEKGAATGVDTTCTYHPDPVGPGLDIOQLYWELSLTH 3115  
Qy 434 GVTQLGPFYLDRLDLSFLNGVAPQNLISIRGEYQINPHIVNMNLSNPDPPTSEYITLLRDIQ 493  
Db 3116 GVTQLGPFYLDRLDLSFLNGVAPQNLISIRGEYQINPHIVNMNLSNPDPPTSEYITLLRDIQ 3175  
Qy 494 DKVTLLYKGSQSLDHTFRCLVTLNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASEH 553  
Db 3176 DKVTLLYKGSQSLDHTFRCLVTLNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASEH 3235  
Qy 554 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPCTTNYQRNKR 613  
Db 3236 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPCTTNYQRNKR 3295  
Qy 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLCNFSPLARRVDRVAIYEEF 673  
Db 3296 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLCNFSPLARRVDRVAIYEEF 3355  
Qy 674 LRMTNGTQLQNFTRDSSVLDGYSNRPNEPLTGS 710  
Db 3356 LRMTNGTQLQNFTRDSSVLDGYSNRPNEPLTGS 3392

RESULT 12  
US-10-198-053-458  
; Sequence 458, Application US/10198053  
; Patent No. 6858710  
; GENERAL INFORMATION:  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Hill, Paul  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C9  
; CURRENT APPLICATION NUMBER: US/10/198,053  
; CURRENT FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 624  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 458  
; LENGTH: 1148  
; TYPE: PRP  
; ORGANISM: Homo sapiens  
US-10-198-053-458

Query Match 92.3%; Score 3642; DB 2; Length 1148;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTGPTPVYLGASKTPASIFGSAASHLLILFTLNTITNLRYEENWPG 73  
Db 393 FTHRSSVSTSTGPTPVYLGASKTPASIFGSAASHLLILFTLNTITNLRYEENWPG 452  
Qy 74 SRKFNTTREVLOGLLRPLKNTSVGLYSGRITLLRPEKDGATGVDAICTHRPPTGP 133  
Db 453 SRKFNTTREVLOGLLRPLKNTSVGLYSGRITLLRPEKDGATGVDAICTHRPPTGP 512  
Qy 134 GLDREQLYLSQTHSITELGPTVTLDRSLYNGFTHRSSVPTTSTGVVSEBPFLLNFT 193  
Db 513 GLDREQLYLSQTHSITELGPTVTLDRSLYNGFTHRSSVPTTSTGVVSEBPFLLNFT 572  
Qy 194 INNLRYMADMGQPSLKFNTIDNMKHLSPFORSSLGARYTGCRIALRSYKGAETR 253

Db 573 INNLRYADMGQSGSLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNGAETR 632  
Qy 254 VDLCTYLQPLSGPLPIKOVFHELSSQTHGIRLGPYSLDKSLYNGNPGDEPPT 313  
Db 633 VDLCTYLQPLSGPLPIKOVFHELSSQTHGIRLGPYSLDKSLYNGNPGDEPPT 692  
Qy 314 TPXPATTFPLPPLSEATTAMGYHLKTLTFLNFTISNLOYSPDMGKGSATFNSSTEGVLOHLLR 373  
Db 693 TPXPATTFPLPPLSEATTAMGYHLKTLTFLNFTISNLOYSPDMGKGSATFNSSTEGVLOHLLR 752  
Qy 374 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDITCTYHPDPVGPGLDIQOLYWELSOLTH 433  
Db 753 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDITCTYHPDPVGPGLDIQOLYWELSOLTH 812  
Qy 434 GVTOLGFYVLDRLDSLFNGVAPQNLISIRGEYQINFIHIVNNLSNPDPSTSEYITLLRDIQ 493  
Db 813 GVTOLGFYVLDRLDSLFNGVAPQNLISIRGEYQINFIHIVNNLSNPDPSTSEYITLLRDIQ 872  
Qy 494 DKVTLLYKGSQQLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553  
Db 873 DKVTLLYKGSQQLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 932  
Qy 554 WLGSYQQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 613  
Db 933 WLGSYQQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 992  
Qy 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLNFSPPLARRVDRVAIYEEF 673  
Db 993 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLNFSPPLARRVDRVAIYEEF 1052  
Qy 674 LRMTNGTQLONFTRDRSSVLVDGYSNRPNEPLTGNS 710  
Db 1053 LRMTNGTQLONFTRDRSSVLVDGYSNRPNEPLTGNS 1089

## RESULT 13

US-10-198-053-479

; Sequence 479, Application US/10198053

; Patent No. 6858710

; GENERAL INFORMATION:

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Hill, Paul

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 210121.462C9

; CURRENT APPLICATION NUMBER: US/10/198,053

; CURRENT FILING DATE: 2002-07-17

; NUMBER OF SEQ ID NOS: 624

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 479

; LENGTH: 1148

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-198-053-479

Query Match 92.3%; Score 3642; DB 2; Length 1148;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 73  
Db 393 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 452  
Qy 74 SRKFNTERVQLGLLRPLFKNTSVGPLYSGRLTLRLPEKDGATGVDAICTHRPDPDTPG 133  
Db 453 SRKFNTERVQLGLLRPLFKNTSVGPLYSGRLTLRLPEKDGATGVDAICTHRPDPDTPG 512  
Qy 134 GLDREQLYLELSQTHSITELGPYTLDRDLSLYNNGFTHRSSVPTTSTGVSEEPFTLNFT 193  
Db 513 GLDREQLYLELSQTHSITELGPYTLDRDLSLYNNGFTHRSSVPTTSTGVSEEPFTLNFT 572

Qy 194 INNLRYADMGQSGSLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNGAETR 253  
Db 573 INNLRYADMGQSGSLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNGAETR 632  
Qy 254 VDLCTYLQPLSGPLPIKOVFHELSSQTHGIRLGPYSLDKSLYNGNPGDEPPT 313  
Db 633 VDLCTYLQPLSGPLPIKOVFHELSSQTHGIRLGPYSLDKSLYNGNPGDEPPT 692  
Qy 314 TPXPATTFPLPPLSEATTAMGYHLKTLTFLNFTISNLOYSPDMGKGSATFNSSTEGVLOHLLR 373  
Db 693 TPXPATTFPLPPLSEATTAMGYHLKTLTFLNFTISNLOYSPDMGKGSATFNSSTEGVLOHLLR 752  
Qy 374 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDITCTYHPDPVGPGLDIQOLYWELSOLTH 433  
Db 753 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDITCTYHPDPVGPGLDIQOLYWELSOLTH 812  
Qy 434 GVTOLGFYVLDRLDSLFNGVAPQNLISIRGEYQINFIHIVNNLSNPDPSTSEYITLLRDIQ 493  
Db 813 GVTOLGFYVLDRLDSLFNGVAPQNLISIRGEYQINFIHIVNNLSNPDPSTSEYITLLRDIQ 872  
Qy 494 DKVTLLYKGSQQLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553  
Db 873 DKVTLLYKGSQQLHDTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 932  
Qy 554 WLGSYQQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 613  
Db 933 WLGSYQQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 992  
Qy 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLNFSPPLARRVDRVAIYEEF 673  
Db 993 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLNFSPPLARRVDRVAIYEEF 1052  
Qy 674 LRMTNGTQLONFTRDRSSVLVDGYSNRPNEPLTGNS 710  
Db 1053 LRMTNGTQLONFTRDRSSVLVDGYSNRPNEPLTGNS 1089

## RESULT 14

US-09-827-271-458

; Sequence 458, Application US/09827271

; Patent No. 6962980

; GENERAL INFORMATION:

; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 210121.462C6

; CURRENT APPLICATION NUMBER: US/09/827,271

; CURRENT FILING DATE: 2001-04-04

; NUMBER OF SEQ ID NOS: 461

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 458

; LENGTH: 1148

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-827-271-458

Query Match 92.3%; Score 3642; DB 2; Length 1148;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 73  
Db 393 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 452  
Qy 74 SRKFNTERVQLGLLRPLFKNTSVGPLYSGRLTLRLPEKDGATGVDAICTHRPDPDTPG 133  
Db 453 SRKFNTERVQLGLLRPLFKNTSVGPLYSGRLTLRLPEKDGATGVDAICTHRPDPDTPG 512  
Qy 134 GLDREQLYLELSQTHSITELGPYTLDRDLSLYNNGFTHRSSVPTTSTGVSEEPFTLNFT 193  
Db 513 GLDREQLYLELSQTHSITELGPYTLDRDLSLYNNGFTHRSSVPTTSTGVSEEPFTLNFT 572

194 INNLRYMADMGQSGSLKFNITDNVWKHLLSPLFORSSLGARYTGCRRVIALRSVKNAGETR 253  
573 INNLRYMADMGQSGSLKFNITDNVWKHLLSPLFORSSLGARYTGCRRVIALRSVKNAGETR 632  
254 VDLCTYLQPLSGPGLPIKOVFHELSQOOTHGIRLGPYSLDKDLSLYLNGYNEPDPPT 313  
633 VDLCTYLQPLSGPGLPIKOVFHELSQOOTHGIRLGPYSLDKDLSLYLNGYNEPDPPT 692  
314 TPKPATTFPLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKGSATFNSSTEGVLOHLR 373  
693 TPKPATTFPLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKGSATFNSSTEGVLOHLR 752  
374 PLFQKSSMGPFYLGCOLISLRPEKOGAATGVDTTCYTHPDPVGPGLDIQOLYWELSLTH 433  
753 PLFQKSSMGPFYLGCOLISLRPEKOGAATGVDTTCYTHPDPVGPGLDIQOLYWELSLTH 812  
434 GVTOLGFYVLDRLSFLNGYAPQNLISIRGEYQINPHI VNMNLSNPDPPTSSEYITLLRDIQ 493  
813 GVTOLGFYVLDRLSFLNGYAPQNLISIRGEYQINPHI VNMNLSNPDPPTSSEYITLLRDIQ 872  
494 DKVTLYKGSQSLHDTFRFCVLTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553  
873 DKVTLYKGSQSLHDTFRFCVLTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 932  
554 WLGSTYQVLDIHVTEMESVYQPTSSSTQHFYLPNFTITNLPYSQDKAOPGTTNYQRNKR 613  
933 WLGSTYQVLDIHVTEMESVYQPTSSSTQHFYLPNFTITNLPYSQDKAOPGTTNYQRNKR 992  
614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673  
993 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 1052  
674 LRMTNGTQLOQNTFLDRSSVLVDGYSNRPNEPLTGNS 710  
1053 LRMTNGTQLOQNTFLDRSSVLVDGYSNRPNEPLTGNS 1089

## RESULT 15

US-10-198-053-459  
; Sequence 459, Application US/10198053  
; Patent No. 6858710  
; GENERAL INFORMATION:  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Hill, Paul  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C9  
; CURRENT APPLICATION NUMBER: US/10/198,053  
; CURRENT FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 624  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 459  
; LENGTH: 1156  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-198-053-459

Query Match 92.3%; Score 3642; DB 2; Length 1156;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

14 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 73  
401 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 460  
74 SRKFNTTERRVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKOGAATGVDAICTHRPDPPTGP 133  
461 SRKFNTTERRVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKOGAATGVDAICTHRPDPPTGP 520  
134 GLDREQLYLELSQTHSITELGPTITLDRSLYNGFTHRSSVPTTSTGVVSEBPTLNFT 193

521 GLDREQLYLELSQTHSITELGPTITLDRSLYNGFTHRSSVPTTSTGVVSEBPTLNFT 580  
194 INNLRYMADMGQSGSLKFNITDNVWKHLLSPLFORSSLGARYTGCRRVIALRSVKNAGETR 253  
581 INNLRYMADMGQSGSLKFNITDNVWKHLLSPLFORSSLGARYTGCRRVIALRSVKNAGETR 640  
254 VDLCTYLQPLSGPGLPIKOVFHELSQOOTHGIRLGPYSLDKDLSLYLNGYNEPDPPT 313  
641 VDLCTYLQPLSGPGLPIKOVFHELSQOOTHGIRLGPYSLDKDLSLYLNGYNEPDPPT 700  
314 TPKPATTFPLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKGSATFNSSTEGVLOHLR 373  
701 TPKPATTFPLPPLSEATTAMGYHLKTLTINFTISNLQYSPDMGKGSATFNSSTEGVLOHLR 760  
374 PLFQKSSMGPFYLGCOLISLRPEKOGAATGVDTTCYTHPDPVGPGLDIQOLYWELSLTH 433  
761 PLFQKSSMGPFYLGCOLISLRPEKOGAATGVDTTCYTHPDPVGPGLDIQOLYWELSLTH 820  
434 GVTOLGFYVLDRLSFLNGYAPQNLISIRGEYQINPHI VNMNLSNPDPPTSSEYITLLRDIQ 493  
821 GVTOLGFYVLDRLSFLNGYAPQNLISIRGEYQINPHI VNMNLSNPDPPTSSEYITLLRDIQ 880  
494 DKVTLYKGSQSLHDTFRFCVLTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553  
881 DKVTLYKGSQSLHDTFRFCVLTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 940  
554 WLGSTYQVLDIHVTEMESVYQPTSSSTQHFYLPNFTITNLPYSQDKAOPGTTNYQRNKR 613  
941 WLGSTYQVLDIHVTEMESVYQPTSSSTQHFYLPNFTITNLPYSQDKAOPGTTNYQRNKR 1000  
614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 673  
1001 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 1060  
674 LRMTNGTQLOQNTFLDRSSVLVDGYSNRPNEPLTGNS 710  
1061 LRMTNGTQLOQNTFLDRSSVLVDGYSNRPNEPLTGNS 1097

## RESULT 16

US-09-827-271-459  
; Sequence 459, Application US/09827271  
; Patent No. 6962980  
; GENERAL INFORMATION:  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C6  
; CURRENT APPLICATION NUMBER: US/09/827,271  
; CURRENT FILING DATE: 2001-04-04  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 459  
; LENGTH: 1156  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-827-271-459

Query Match 92.3%; Score 3642; DB 2; Length 1156;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 694; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

14 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 73  
401 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 460  
74 SRKFNTTERRVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKOGAATGVDAICTHRPDPPTGP 133  
461 SRKFNTTERRVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKOGAATGVDAICTHRPDPPTGP 520  
134 GLDREQLYLELSQTHSITELGPTITLDRSLYNGFTHRSSVPTTSTGVVSEBPTLNFT 193



Db 521 GLDREQLYLELSQTHSITELGPTTLDRDLSYNGFTHRSSVPTTSTGVVSEBFFTLNFT 580  
Qy 194 INNLRYMADMGQPGSLKFNTDNNMKHLLSPLFORSSLGARYTTCRVIALRSVKNAGETR 253  
Db 581 INNLRYMADMGQPGSLKFNTDNNMKHLLSPLFORSSLGARYTTCRVIALRSVKNAGETR 640  
Qy 254 VDLCTYQLPSGPGPLIKOVFHELSSQTHGITRLGYSLDKSLYNGYNEPDPBPPT 313  
Db 641 VDLCTYQLPSGPGPLIKOVFHELSSQTHGITRLGYSLDKSLYNGYNEPDPBPPT 700  
Qy 314 TPXPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 373  
Db 701 TPXPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 760  
Qy 374 PLFKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 433  
Db 761 PLFKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 820  
Qy 434 GVTOLGFYVLDRLSLFNGYAPQNLISIRGEYQINFHIVNNLSNPDPTSSEYITLLRDIO 493  
Db 821 GVTOLGFYVLDRLSLFNGYAPQNLISIRGEYQINFHIVNNLSNPDPTSSEYITLLRDIO 880  
Qy 494 DKVTTLKGSQSLDHTFRFCLVTLNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 553  
Db 881 DKVTTLKGSQSLDHTFRFCLVTLNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 940  
Qy 554 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 613  
Db 941 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 1000  
Qy 614 NIEDALNQLFRNSSIKYFSDCQVSTFRSPNRRHTGVDLSLCPSPARRVDRVAIYEEF 673  
Db 1001 NIEDALNQLFRNSSIKYFSDCQVSTFRSPNRRHTGVDLSLCPSPARRVDRVAIYEEF 1060  
Qy 674 LRMTNRGTQLQNFLLDRSSVLVDGYSNRRNEPLTGN 710  
Db 1061 LRMTNRGTQLQNFLLDRSSVLVDGYSNRRNEPLTGN 1097

## RESULT 17

US-09-404-879A-388

; Sequence 388, Application US/09404879A

; Patent No. 6468546

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: King, Gordon E.

; APPLICANT: Algate, Paul A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.462C2

; CURRENT APPLICATION NUMBER: US/09/404,879A

; CURRENT FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 393

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 388

; LENGTH: 772

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-404-879A-388

Query Match 80.8%; Score 3189; DB 2; Length 772;  
Best Local Similarity 100.0%; Pred. No. 1.8e-282;  
Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTHRSSVTTSTPGTPTVYLGASKTPASIFGPSAASHLLIILFTLNFTITNLRYENMMWPG 73  
Db 159 FTHRSSVTTSTPGTPTVYLGASKTPASIFGPSAASHLLIILFTLNFTITNLRYENMMWPG 218  
Qy 74 SRKFNTERVQLGLLRPLFKNTSVGLYSGCRLTLRLPEKDGATGVDAICTHRPDPTGP 133  
Db 219 SRKFNTERVQLGLLRPLFKNTSVGLYSGCRLTLRLPEKDGATGVDAICTHRPDPTGP 278

Qy 134 GLDREQLYLELSQTHSITELGPTTLDRDLSYNGFTHRSSVPTTSTGVVSEBFFTLNFT 193  
Db 279 GLDREQLYLELSQTHSITELGPTTLDRDLSYNGFTHRSSVPTTSTGVVSEBFFTLNFT 338  
Qy 194 INNLRYMADMGQPGSLKFNTDNNMKHLLSPLFORSSLGARYTTCRVIALRSVKNAGETR 253  
Db 339 INNLRYMADMGQPGSLKFNTDNNMKHLLSPLFORSSLGARYTTCRVIALRSVKNAGETR 398  
Qy 254 VDLCTYQLPSGPGPLIKOVFHELSSQTHGITRLGYSLDKSLYNGYNEPDPBPPT 313  
Db 399 VDLCTYQLPSGPGPLIKOVFHELSSQTHGITRLGYSLDKSLYNGYNEPDPBPPT 458  
Qy 314 TPXPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 373  
Db 459 TPXPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 518  
Qy 374 PLFKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 433  
Db 519 PLFKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 578  
Qy 434 GVTOLGFYVLDRLSLFNGYAPQNLISIRGEYQINFHIVNNLSNPDPTSSEYITLLRDIO 493  
Db 579 GVTOLGFYVLDRLSLFNGYAPQNLISIRGEYQINFHIVNNLSNPDPTSSEYITLLRDIO 638  
Qy 494 DKVTTLKGSQSLDHTFRFCLVTLNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 553  
Db 639 DKVTTLKGSQSLDHTFRFCLVTLNLTMDSVLVTKALFSSNLDPSLVEQVFLDKTLNASFH 698  
Qy 554 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 613  
Db 699 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSYQDKAQPGTTNYQRNKR 758  
Qy 614 NIEDA 618  
Db 759 NIEDA 763

## RESULT 18

US-09-667-857-388

; Sequence 388, Application US/09667857

; Patent No. 6699664

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: King, Gordon E.

; APPLICANT: Algate, Paul A.

; APPLICANT: Fling, Steven P.

; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary Richard

; APPLICANT: Reed, Steven G.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.462C5

; CURRENT APPLICATION NUMBER: US/09/667,857

; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 455

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 388

; LENGTH: 772

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-667-857-388

Query Match 80.8%; Score 3189; DB 2; Length 772;  
Best Local Similarity 100.0%; Pred. No. 1.8e-282;  
Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTHRSSVTTSTPGTPTVYLGASKTPASIFGPSAASHLLIILFTLNFTITNLRYENMMWPG 73  
Db 159 FTHRSSVTTSTPGTPTVYLGASKTPASIFGPSAASHLLIILFTLNFTITNLRYENMMWPG 218  
Qy 74 SRKFNTERVQLGLLRPLFKNTSVGLYSGCRLTLRLPEKDGATGVDAICTHRPDPTGP 133



Db 219 SRKFNTERVQLGLRPLFKNTSVGLYSGCRLLTLRPEKOGATGVDALCTHRPDTGP 278  
Qy 134 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSTGVVSEBPTLNFT 193  
Db 279 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSTGVVSEBPTLNFT 338  
Qy 194 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSIGARYTCRCVIALRSVKNAGETR 253  
Db 339 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSIGARYTCRCVIALRSVKNAGETR 398  
Qy 254 VDLCTVLPGLSGPLPIKOVFHELSCQTHGITRLGYSKLDKSLYLNGYNEPGDPPT 313  
Db 399 VDLCTVLPGLSGPLPIKOVFHELSCQTHGITRLGYSKLDKSLYLNGYNEPGDPPT 458  
Qy 314 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373  
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518  
Qy 374 PLFOKSMGPFYLGCOLISLRPEKOGAATGVDTTCTYHPDPVGPGLDIQOLYWELSOLTH 433  
Db 519 PLFOKSMGPFYLGCOLISLRPEKOGAATGVDTTCTYHPDPVGPGLDIQOLYWELSOLTH 578  
Qy 434 GVTOLGFVLDRLSLFINGYAPQNLSIRGEYQINFHIVNNLSNPDPTSEYITLLRDIQ 493  
Db 579 GVTOLGFVLDRLSLFINGYAPQNLSIRGEYQINFHIVNNLSNPDPTSEYITLLRDIQ 638  
Qy 494 DKVTLLYKGSQQLHDTFRFCVLTNLTMDSVLVTVKALFSSNLDPSLVQVFLDKTLNASPH 553  
Db 639 DKVTLLYKGSQQLHDTFRFCVLTNLTMDSVLVTVKALFSSNLDPSLVQVFLDKTLNASPH 698  
Qy 554 WLGSSTYQLVDIHVTEMESSYVQPTSSSTQHFYLNFTITNLPSQDKAQPQTNYQRNKR 613  
Db 699 WLGSSTYQLVDIHVTEMESSYVQPTSSSTQHFYLNFTITNLPSQDKAQPQTNYQRNKR 758  
Qy 614 NIEDA 618  
Db 759 NIEDA 763

## RESULT 19

US-10-198-053-388

; Sequence 388, Application US/10198053

; Patent No. 6858710

; GENERAL INFORMATION:

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Bangur, Marc W.

; APPLICANT: Panger, Gary R.

; APPLICANT: Hill, Paul

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.462C9

; CURRENT APPLICATION NUMBER: US/10/198,053

; CURRENT FILING DATE: 2002-07-17

; NUMBER OF SEQ ID NOS: 624

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 388

; LENGTH: 772

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-198-053-388

Query Match 80.8%; Score 3189; DB 2; Length 772;  
Best Local Similarity 100.0%; Pred. No. 1.8e-282;  
Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 73  
Db 159 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 218  
Qy 74 SRKFNTERVQLGLRPLFKNTSVGLYSGCRLLTLRPEKOGATGVDALCTHRPDTGP 133  
Db 219 SRKFNTERVQLGLRPLFKNTSVGLYSGCRLLTLRPEKOGATGVDALCTHRPDTGP 278

Qy 134 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSTGVVSEBPTLNFT 193  
Db 279 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSTGVVSEBPTLNFT 338  
Qy 194 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSIGARYTCRCVIALRSVKNAGETR 253  
Db 339 INNLRYMADMGQPGSLKFNITDNVMKHLSPFORSSIGARYTCRCVIALRSVKNAGETR 398  
Qy 254 VDLCTVLPGLSGPLPIKOVFHELSCQTHGITRLGYSKLDKSLYLNGYNEPGDPPT 313  
Db 399 VDLCTVLPGLSGPLPIKOVFHELSCQTHGITRLGYSKLDKSLYLNGYNEPGDPPT 458  
Qy 314 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373  
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518  
Qy 374 PLFOKSMGPFYLGCOLISLRPEKOGAATGVDTTCTYHPDPVGPGLDIQOLYWELSOLTH 433  
Db 519 PLFOKSMGPFYLGCOLISLRPEKOGAATGVDTTCTYHPDPVGPGLDIQOLYWELSOLTH 578  
Qy 434 GVTOLGFVLDRLSLFINGYAPQNLSIRGEYQINFHIVNNLSNPDPTSEYITLLRDIQ 493  
Db 579 GVTOLGFVLDRLSLFINGYAPQNLSIRGEYQINFHIVNNLSNPDPTSEYITLLRDIQ 638  
Qy 494 DKVTLLYKGSQQLHDTFRFCVLTNLTMDSVLVTVKALFSSNLDPSLVQVFLDKTLNASPH 553  
Db 639 DKVTLLYKGSQQLHDTFRFCVLTNLTMDSVLVTVKALFSSNLDPSLVQVFLDKTLNASPH 698  
Qy 554 WLGSSTYQLVDIHVTEMESSYVQPTSSSTQHFYLNFTITNLPSQDKAQPQTNYQRNKR 613  
Db 699 WLGSSTYQLVDIHVTEMESSYVQPTSSSTQHFYLNFTITNLPSQDKAQPQTNYQRNKR 758  
Qy 614 NIEDA 618  
Db 759 NIEDA 763

## RESULT 20

US-09-827-271-388

; Sequence 388, Application US/09827271

; Patent No. 6962980

; GENERAL INFORMATION:

; APPLICANT: Retter, Marc W.

; APPLICANT: Panger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 210121.462C6

; CURRENT APPLICATION NUMBER: US/09/827,271

; NUMBER OF SEQ ID NOS: 461

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 388

; LENGTH: 772

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-827-271-388

Query Match 80.8%; Score 3189; DB 2; Length 772;  
Best Local Similarity 100.0%; Pred. No. 1.8e-282;  
Matches 605; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 73  
Db 159 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 218  
Qy 74 SRKFNTERVQLGLRPLFKNTSVGLYSGCRLLTLRPEKOGATGVDALCTHRPDTGP 133  
Db 219 SRKFNTERVQLGLRPLFKNTSVGLYSGCRLLTLRPEKOGATGVDALCTHRPDTGP 278  
Qy 134 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSTGVVSEBPTLNFT 193  
Db 279 GLDREQLYLELSQTHSITELGPTTLDRLDSLYVNGFTHRSSVPTTSTGVVSEBPTLNFT 338

Mon Mar 20 08:49:44 2006

QY	194	INNLRVWADMGQPSLKFNITDNNMKHLLSPFORSSLGARYTGCVRVIALRSVKNGAETR	253
Db	339	INNLRVWADMGQPSLKFNITDNNMKHLLSPFORSSLGARYTGCVRVIALRSVKNGAETR	398
QY	254	VDLLCTYLOPLSGPLPIKQVHEHLSQOQTHGIIIRLGPYSLDKDSLYLNGYNEPGDEPPT	313
Db	399	VDLLCTYLOPLSGPLPIKQVHEHLSQOQTHGIIIRLGPYSLDKDSLYLNGYNEPGDEPPT	458
QY	314	TPKPATTFPLPPLSEATTAMGYHUKTUTLNFPTISNLQYSPDMGKGSATFNSTEGVLOHLLR	373
Db	459	TPKPATTFPLPPLSEATTAMGYHUKTUTLNFPTISNLQYSPDMGKGSATFNSTEGVLOHLLR	518
QY	374	PLFKQSSMGPFYLGCOLISLRPEKGAATGVDITCTVHPDPVGPGLDIOQLYWELSQLTH	433
Db	519	PLFKQSSMGPFYLGCOLISLRPEKGAATGVDITCTVHPDPVGPGLDIOQLYWELSQLTH	578
QY	434	GVTLQGFYVLDRLDSLFINGYAPQNLISIRGEYQINFHIVNNLNSNPDPPTSSEYITLLRDIQ	493
Db	579	GVTLQGFYVLDRLDSLFINGYAPQNLISIRGEYQINFHIVNNLNSNPDPPTSSEYITLLRDIQ	638
QY	494	DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH	553
Db	639	DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH	698
QY	554	WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSODKAQPGTTNYQRNKR	613
Db	699	WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSODKAQPGTTNYQRNKR	758
QY	614	NIEDA 618	
Db	759	NIEDA 763	

Search completed: March 20, 2006, 07:31:33  
Job time : 43.8343 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:29:34 ; Search time 27.2939 Seconds  
(without alignments)  
2636.859 Million cell updates/sec

Title: US-10-687-035-1  
Perfect score: 3945  
Sequence: 1 AAQPARARRTKLFTHRSSV.....QKLISEEDLNMTHGHHHHH 748

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96215763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	144.5	3.7	1408	2 H69068	cell surface glyco
2	135.5	3.4	1117	2 S63399	probable membrane
3	123.5	3.1	2477	2 S14428	fibronectin precur
4	122	3.1	631	2 I52257	episialin - mouse
5	121.5	3.1	1475	2 S42718	nuclear pore compl
6	121.5	3.1	2471	2 T42977	large tegument pro
7	121.5	3.1	5005	2 P82884	hypothetical prote
8	121	3.1	1131	2 T41144	hypothetical serin
9	118	3.0	532	2 T34235	hypothetical prote
10	117.5	3.0	1377	2 A38926	DNA-binding protei
11	116	2.9	1848	2 A41140	cellulose-binding
12	115.5	2.9	1474	2 F69009	probable membrane
13	115	2.9	888	2 A54280	cell differentiat
14	114.5	2.9	709	2 A35364	carcinoembryoni
15	113.5	2.9	855	2 T07015	Cf-4A protein - to
16	113.5	2.9	1004	2 B25039	outer cell wall pr
17	113.5	2.9	1369	2 T17504	hypothetical prote
18	113.5	2.9	3344	2 JQ1899	genome polyprotein
19	113.5	2.9	5762	2 A41819	proline-rich pepti
20	112.5	2.9	838	2 S38156	hypothetical prote
21	112.5	2.9	948	2 T11678	hypothetical prote
22	112.5	2.9	1348	2 AH1115	cell surface prote
23	112.5	2.9	4936	2 A28515	hypothetical prote
24	112	2.8	643	2 S55593	membrane protein S
25	112	2.8	3587	2 T31075	tyrocidine synthet
26	111.5	2.8	919	2 S45889	probable regulator
27	111.5	2.8	1622	2 AB1717	probable cell surf
28	111	2.8	1777	2 T34369	hypothetical prote
29	111	2.8	2386	1 FNHU	fibronectin precur

30	110.5	2.8	530	2 A39344	tumor-associated m
31	110.5	2.8	1778	2 JT0382	apolipoprotein B -
32	110.5	2.8	2508	2 S61441	surface-associated
33	110	2.8	628	1 A39262	transcription fact
34	110	2.8	1128	2 A49960	bud emergence prot
35	110	2.8	1349	2 A11476	cell surface prote
36	110	2.8	3131	2 T39553	vacuolar protein a
37	109.5	2.8	1268	1 A39640	neural cell adhesi
38	109	2.8	989	2 I56333	apolipoprotein B -
39	109	2.8	998	2 C75489	conserved hypothet
40	108.5	2.8	500	2 D97302	hypothetical prote
41	108.5	2.8	504	2 T33485	hypothetical prote
42	108.5	2.8	537	2 A35400	surface protein T6
43	108.5	2.8	776	2 A82787	tonB-dependent rec
44	108.5	2.8	1040	2 D88568	protein ZK757.3 [1
45	108.5	2.8	1113	2 H84105	hypothetical prote
46	108.5	2.8	1642	2 T19130	hypothetical prote
47	108	2.7	609	2 T25120	hypothetical prote
48	108	2.7	628	1 A33333	transcription fact
49	108	2.7	630	1 A46149	transcription fact
50	108	2.7	709	2 T28712	hypothetical prote
51	108	2.7	1035	2 T23165	hypothetical prote
52	108	2.7	1037	2 S37879	nuclear pore prote
53	108	2.7	1084	2 B64088	hemoglobin-binding
54	108	2.7	3603	1 D69681	peptide synthetase
55	107.5	2.7	661	2 S21221	hemocyanin chain c
56	107.5	2.7	934	2 G86548	polymorphic outer
57	107.5	2.7	934	2 A72075	polymorphic membra
58	107.5	2.7	952	2 D81593	ascitesialoglyco
59	107.5	2.7	1630	2 A53577	probable cell-adhe
60	107.5	2.7	2140	2 T18543	hypothetical prote
61	107	2.7	611	2 B71220	hypothetical prote
62	107	2.7	664	2 C70584	probable serine-th
63	107	2.7	771	2 T34376	hypothetical prote
64	107	2.7	1118	1 A49724	protein-tyrosine-p
65	107	2.7	1609	2 S25345	probable membrane
66	106.5	2.7	967	2 S66852	hypothetical prote
67	106.5	2.7	1301	2 S18118	apoptosis signal-r
68	106.5	2.7	1379	2 JCS778	tenascin precursor
69	106.5	2.7	1810	1 A32230	probable exported
70	106	2.7	777	2 AE0462	hypothetical prote
71	106	2.7	821	2 T41364	hypothetical prote
72	106	2.7	1298	2 A64157	probable membrane
73	106	2.7	1636	2 S60403	probable membrane
74	105.5	2.7	853	2 T17461	disease resistance
75	105.5	2.7	916	2 F97053	penicillin-binding
76	105.5	2.7	1163	2 I56126	lymphocyte functi
77	105.5	2.7	1250	2 B84339	probable restricti
78	105.5	2.7	1679	2 T30271	surface protein -
79	105.5	2.7	1695	2 A56921	kinasin family pro
80	105.5	2.7	1962	2 A32634	lactocepin (EC 3.4
81	105	2.7	1770	2 S56221	hypothetical prote
82	104.5	2.6	872	2 T50369	probable serine/th
83	104.5	2.6	2629	2 I48569	apolipoprotein B -
84	104.5	2.6	2710	2 A37052	toxin A - Clostrid
85	104	2.6	446	2 A27424	tubulin beta chain
86	104	2.6	562	2 AD0074	probable hemolysin
87	104	2.6	621	2 S73155	hypothetical prote
88	104	2.6	624	2 S44938	nitrogen permease
89	104	2.6	701	2 A11501	internalin protein
90	104	2.6	845	2 T07039	Hcr-0 protein - t
91	104	2.6	952	2 T50451	hypothetical coile
92	104	2.6	1093	2 B86748	hypothetical prote
93	104	2.6	1522	2 T39371	transcription regu
94	104	2.6	1824	2 S68553	surface layer prot
95	104	2.6	3124	2 A40020	collagen alpha 1(X
96	103.5	2.6	449	1 UBCKBA	tubulin beta chain
97	103.5	2.6	555	2 T00778	probable tRNA aden
98	103.5	2.6	792	2 S03232	hypothetical prote
99	103.5	2.6	952	2 JC7227	ent-kaurene syntha
100	103.5	2.6	977	2 T16232	hypothetical prote

## ALIGNMENTS

## RESULT 1

H69068  
cell surface glycoprotein (s-layer protein) related protein - Methanobacterium thermoautotrophicum  
C;Species: Methanobacterium thermoautotrophicum  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: H69068  
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiawani, N.; Ji, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funch  
A;Reference number: A69000; MUID: 98037514; PMID: 9371463  
A;Accession: H69068  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-1408 <MTH>  
A;Cross-references: UNIPROT:O27557; UNIPARC:UPI0000066761; GB:AE000911; GB:AE000666; NID  
A;Experimental source: strain Delta H  
C;Genetics:  
A;Gene: MTH1513  
A;Start codon: TTG

Query Match 3.7%; Score 144.5; DB 2; Length 1408;  
Best Local Similarity 20.1%; Pred. No. 0.19; Mismatches 258; Indels 269; Gaps 40;  
Matches 157; Conservative 99;  
QY 58 NFTITNLRYBENMWPGRKFNNT---ERVQLGLRLPLFKNTSVGPLYSGCRLTLRLPEKD 114  
DB 444 NFTVT-----PDACKNNLGLSDGLTRFPFIISNLSVPL----- 480  
QY 115 GEATGVDAICTHRPDTPGGLDRQLYLEL-SOLTHSITELGPVTLDRDLYNGFTHRS 173  
DB 481 -----NGTGP-----LTVLRGNITCGDGTGWYRLD---LYNGY--RT 515  
QY 174 SVPTSTGVVSEEPFLNFII-----NNLRVMDMGQ 205  
DB 516 AGKWEVGSLETFEPEFEYELTRNSRAYSVGNPPATRVFVGLPIIPENLRVTPSGGQ 575  
QY 206 PGSLEKFNITDNMVKHLLSPLFORSLGARVTGCRVIALRSVKGAEATRV----- 254  
DB 576 E-PLKVNVTADLVNNGDLPDSYRAEL---YIDGVLLDSRVNVTNASSRTTVSNRLLAAG 631  
QY 255 --DLLCTYLP-----LSGCLPLIKQVHELSSQTHG-----ITRL--GPYSLDK 295  
DB 632 LYEITINDLEPELVVMEGKFIYEN--FTLTPOSGAAPLTVTVSAMITNIDNSPRSYTA 689  
QY 296 DSLYLNG-----YNEPGDEPPTPKPATTELPPLSEATTAMGYH---LKTLT-LNF 343  
DB 690 -TIYVNGVPDHTKVLNTPGES---TVPFSTIILPDRGLYTISLNNVSGTVRVLSANF 745  
QY 344 TISNLQVSPDMGKGSATFNSTEGVQLHLLRPLFOKSSMGPPFLGCQLISLRPEKDGAAIG 403  
DB 746 TLSNVTVPVEGKSPLVNVTVAIV-----RNGDLAAG 777  
QY 404 VDTTCTYHPDPVPGGLDIQQLYBELSOLTHGVTLQGVFVLDRLDLSFNGYAPQNLSTIRGE 463  
DB 778 -DPAVTLVLDVA-----WETRTVS-----VPGKSSVLVS--FKKELAPFGE 816  
QY 464 YQINFHI---VNNWLSNPDPTSSSYIILLRDIQDKVTLTKGSQLHDTFRCL-VTN--- 516  
DB 817 YRLNSGTDVTHRVLPDPDPTITGF-----NVTPEVTGPAFL--SVRASLVNTPHD 865  
QY 517 -----LTMDSVLVTVKALFNSNLDPSLVEQVFLDKLTNAPSHWLG----- 556  
DB 866 LVIGFTARLMDVGVVQENIV---SLSPGETREIATMGTLTTPGNHTVINEFSKIVRVL 922  
QY 557 -STYQLVDIHTVMESSYQ-----TSSSSTQHLYNFT-----INLPYSQDKAQPGT 605  
DB 923 PASITLSDLRVT--PSSGFSPLTITATATARTGEVDGNTAVLYINGLAVDKKNVTGVA 980

QY 606 TNYQRNKRNIEDALNQLFRNSSI-----KSYFSDCQCVSTFRSVP-----NRHHT 649  
DB 981 -----GRSVQVAFNHTIENAGIYLAGISLTPLDVRVLSEPAISNLSATPLTGVSPHRI 1034  
QY 650 GVDSLCNFS-----PLARRVDRVAIYEEFLRMTRNGTOLQNTTLDRS-----SVLVDG 697  
DB 1035 IVTALVSTTBEGSGNTAGIYDGVNVQNRVTRVTPGPGSVLVSTADISEFGHEQVTVNS 1094  
QY 698 YSP 700  
DB 1095 LSP 1097  
RESULT 2  
S63399  
Probable membrane protein YNR067c - yeast (Saccharomyces cerevisiae)  
N;Alternate names: Hypothetical protein N3547  
C;Species: Saccharomyces cerevisiae  
C;Date: 27-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 09-Jul-2004  
C;Accession: S63399  
R;Duesterhoeft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.  
submitted to the Protein Sequence Database, April 1996  
A;Reference number: S62944  
A;Accession: S63399  
A;Molecule type: DNA  
A;Residues: 1-1117 <DUE>  
A;Cross-references: UNIPROT:P53753; UNIPARC:UPI000013BACB; EMBL:Z71682; NID:gl302597; P1  
A;Experimental source: strain S288C  
C;Genetics:  
A;Gene: MIPS:YNR067c  
A;Cross-references: SGD:S0005350  
A;Map position: 14R  
C;Keywords: transmembrane protein  
F;6-22/Domain: transmembrane #status predicted <TMM>  
Query Match 3.4%; Score 135.5; DB 2; Length 1117;  
Best Local Similarity 21.1%; Pred. No. 0.56;  
Matches 156; Conservative 94; Mismatches 255; Indels 233; Gaps 39;  
QY 4 PARRARTKLFTHRSSVSTSTPGTPTVYLG-----SKTPAS--IFGPSAASHL 51  
DB 206 PSYSSQETKIIP--SSLTSNKTIYTSVRTNAATATGDSFIATSPASTFLFPSNSTQD 263  
QY 52 LILFTLNTLTNLRYBEN---MWPGRKFNFTERV-----LQGLRLPL 91  
DB 264 LVQ-TLASTAGAPAYSNRTOITLSVSVLSYTSPTIPSPNITENGSSPSLSSTVSPV 322  
QY 92 FKNTSVGLYSGCRLTLRLPEKDEATGVDAICTHRPDTPGGLDRQLYLELS-QUTHS 150  
DB 323 YPSSSTGNIL---LSSLFSTVDSSSS-----PVSSTLD--TIYVSSSQATIS 365  
QY 151 ITELGPVTLDRDLSLYNGFTHRSVPTSTGVVSEEPFLTNFTINNLRYMADMGPGLSLK 210  
DB 366 SSSSSRQTKTSS-----SLSTSTSTATTENSSTT--TIVNLFNAVSTDEPPTV- 414  
QY 211 FNITDNMVKHLLSPLFORSLGARVTGCRVIALRSVKGAEATRVDLLCTYLPGLSGPLP 270  
DB 415 FDRSPNPM-----SLADGVSN-----DGP-IQ 435  
QY 271 IKQVFHEL---SQOTHGITRLGPYSLDK-----DSLYNGYNEPGPDEPP 312  
DB 436 TNKFTYTNLI VGSQESPAF--VYPVSLWKYTSSTSYGPAVQHTTVDOYSGVGYDDSGNAYL 493  
QY 313 TTPKPAFTFPLPPLSEATTAMGYHLKTLTNFTISNLOYSMDMGKGSATFNSTEGVL----- 368  
DB 494 VNP-----LGIHVVFSAFNSPDSMTMQVDEMTLSSTRVVLSESN 533  
QY 369 ---QHLLRPLFOKSSMGPPFLGCQLISLRPEKDGAAIGVDTTCTYHPDPVPGGLDIQQLY 425  
DB 534 DSSNLYEIPLIQ--GMC-FATGIYHGLN-AKIGSSVGFNTIVSESSNLAQGI-----LK 585  
QY 426 WELSQTLGHVGTQGLFFYVLDRLDLSFNGYAPQNLISIRGEYQINFH-----IVNNLSNPD 479



Db 843 -VYSPSEGSSTELNLPETANSV-----TSLDL-----QPG-VQYNITIVAVE 893  
QY 220 --HLLSPLF-QRSSLG-----ARYTGRVIALRSVKNAGET--RVLLCT 259  
Db 884 ENQESTPVFIQOETGTGPRSDVPAPKDLQFVEVTDVKVTIMWTPPNSAVTGYRVDVLPV 943  
QY 260 YLQPLSGPLPI-KQVFHELSSQOHTGIT---RLGPYSLDKDSLNGYNEPQDEP--- 311  
Db 944 NLGEHGORLVNRNTPFAEVTGLSPGYTYLFKVFANVHOGRESKPLTAQOITKLDAPNLQ 1003  
QY 312 ---PTTPKPATFLPP-----LSEATTAMG-----YHLKTLTLNFTISNLQVSPDMG- 355  
Db 1004 FVNETDRTVLVWTPPRARIAGYRLTVGLTGGQPKQYVGNPMAKYPLRNLPGSEYTV 1063  
QY 356 ----KGSATFNSTEGVLQHLLRPLFOKSSMGFP-----YLGCOLISL 393  
Db 1064 TLMVAVGNQOSPKATGVFT-TLOPL---RSIPPYNTVEVTTIVITWTPAPRIGPKL-GV 1118  
QY 394 RPEKDGAAATGVDTCTVYHPPVGVPLDILQOLYXWELSQLTHGVTLQGPYVL-----DRD 446  
Db 1119 RPSGGAPREVTS-----DGSIV--VSLTFCGVEY--YTIQVLRDQGERD 1162  
QY 447 SLFINGYA-----PQNLISIRGEYQINPHIVNWLNS-NPD-----PTSSSYITILLR 491  
Db 1163 APIVNRVVTPPLSPPTNLHLEANPDTGVLTVSWERSTTPDITGYRIITTTPTNGQOQTALRE 1222  
QY 492 IQDKVTLLYKGSQLDHTRFCLVTN-----LTMSVLVTVK-----ALFSSNL---DPSLV 539  
Db 1223 V-----VHADQSSCTFENRPNPGLYVSVYTVKDKESAPISDTVPIPEVQLT 1270  
QY 540 EQVFLDKT-LNASPHW--LGSTQVLDIHTVEMESS---VYOPTSSSSSTQHFLYNFTIT 592  
Db 1271 DLSFVDITDSIGLURWPLNSS-TIIGYRITVNAAGEGIPFEDFVDSVGY-----YTVT 1325  
QY 593 NLPYSQDKAOPGTNYQRNKRNI-----EDALNQLFRNSSI-----KSYFSDCQVSTF 640  
Db 1326 GL-----EPG-IDYDISVITLLINGGESAPTTLTQCTAVPPPTDLRFTNIGPDMRVTW 1377  
QY 641 RSVNRIHTGVDSLCNFSPLARRVDRVAIYEEFLRMTRNGTQLON-----FTLDRSSVL 694  
Db 1378 APPPSIELTNL--LVRYSPVKNEED--VAELSISPSDNAVLTNLLPGTEYLVSVSV- 1431  
QY 695 VDGYSFNRNPLTQNSADIQHSGRSSIEGPR-PEQKLISEDLNMH-----TGH-- 743  
Db 1432 ---YEQHESIPLRGQ-----KTGLDSTGDFSDSDVANSFTVHWVAPRATIGYII 1480  
QY 744 -HHHH 748  
Db 1481 RHAEH 1486  
RESULT 4  
I52257  
A:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I52257; I65210  
R:Vos, H.L.; De Vries, Y.; Hilkens, J.  
Biochem. Biophys. Res. Commun. 181, 121-130, 1991  
A:Title: The mouse epistatin (Mucl) gene and its promoter. Rapid evolution of the repeti  
A:Reference number: I52257; MUID:92068178; PMID:1958179  
A:Accession: I52257  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-631 <RES>  
A:CROSS-references: UNIPROT:Q02496; UNIPARC:UPI000002A11B; GB:M77226; NID:g199835; PIDN:  
A:Accession: I65210  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-631 <RES2>  
A:CROSS-references: UNIPARC:UPI000002A11B; GB:M84683; NID:g199842; PIDN:AAA39756.1; PID:  
C:Genetics:  
A:Gene: Mucl

A;Introns: 20/1; 454/3; 472/2; 517/1; 557/3; 607/3  
Query Match 3.1%; Score 122; DB 2; Length 631;  
Best Local Similarity 21.4%; Pred. No. 1.9;  
Matches 122; Conservative 55; Mismatches 207; Indels 186; Gaps 26;  
QY 89 RPLFKNITGVPLSGCRLTLRPEKDGATGVDAICTHRPDPPTGPGDLRQLYLELSQLT 148  
Db 58 RPPGDSTS-SPVQSSSTSPATRAPEDSTSTAV-LSGTSSPATAP-----VNSASSPVA 109  
QY 149 HSTELGPLYTLDRD---SLYVNGFTHRSSVPTTSTGVSEEPFLTNLTNNLYMADMGQ 205  
Db 110 HGTSTSPATSLKSDNSSPVHSGT--SSAPATTAPVDS---TSSPVHGGTSSPATSP 163  
QY 206 PGSCLKENITDNWVKHLLSPLFORSSILGARVTCGRVIALRSVKNAGETRVLLCTYLQPLS 265  
Db 164 PGD-----STSSPDHSSSTSPATRAPEDSTSTAV-----LS 194  
QY 266 GPGLP--IKQVFHELSSQOHTGITRLGPIYSLDKDSLNGYNEP---GPDEPPTPKPAT 319  
Db 195 GTSSPATAPVDSTSPVAHDDTSSPATSLSEDSA-----SSPVAHGGTSSPATSPLRDS 249  
QY 320 TFLPPLSEATTAMGYHLKT-----LTNFTISNLQYSPDMKGSATFNSTE 365  
Db 250 TSSPVHSSASI---QNIKTSLDASTPDHNGTSVTTTSSALGATSATPDHSGTSTTTNSSE 306  
QY 366 GVLQHLRLPLFOKSSMGPPVILGQLISLRPEKGAATGVDTCTYHPPDPVPGP-LDIQQL 424  
Db 307 SVL--ATTPVY--SSM-PF-----STTKVTSGLAIPDHNGSSVLPTSSV 346  
QY 425 YWELSQLTHGVTLQGFVFLDRDSLFLINGYAPQNLISIRGEYQINPHIVNWLNSNPDPTSSSE 484  
Db 347 LGSATSLVNTSAIATTPVS-----NGTQP--SVPSQYPV-----SPTMATTS 388  
QY 485 YITLDRDIQDKVTLLYKGSQLDHTRFCLVTNLTMSVLTVKALPSSNLDPSLVEQVFL 544  
Db 389 HSTI-----ASSSYSTVFP-----STFSSSPQL----- 414  
QY 545 DKTINASFWLGSYQLVDIHTVEMESSVYQPTSSSTQHFLYNFTITNLPYSQDKAQP 604  
Db 415 --SVGVSF-----FFLSYIQNHFFNSSLSDPS 440  
QY 605 TTNVQRNKRNIEDALNQLFRN-----SSIK 629  
Db 441 SNYQELKRNIISGLFQIFNGDFLGISIK 470  
RESULT 5  
S42718  
nuclear pore complex protein nup153 - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S42718; S37477  
R:McMorrow, I.; Bastos, R.; Horton, H.; Burke, B.  
Biochim. Biophys. Acta 1217, 219-223, 1994  
A:Title: Sequence analysis of a cDNA encoding a human nuclear pore complex protein, hnup  
A:Reference number: S42718; MUID:94154002; PMID:8110839  
A:Accession: S42718  
A:Molecule type: mRNA  
A:Residues: 1-1475 <MCM>  
A:CROSS-references: UNIPROT:P49790; UNIPARC:UPI000012FC15; EMBL:Z25535; NID:g406224; PID:  
Query Match 3.1%; Score 121.5; DB 2; Length 1475;  
Best Local Similarity 19.4%; Pred. No. 8.1;  
Matches 86; Conservative 57; Mismatches 162; Indels 139; Gaps 17;  
QY 7 RARTRKLFTHRSSVSTSTP-----GTPVTYLGASKTPASIFGFSAAHLLILFTLNFT 60  
Db 351 QAKREKVDQYPPVQRLMTPKPVSIAIATNSVYFPKSLTPSG-----EFR 394  
QY 61 ITNLR-----YEENWPGSRKFNTERVLOGLRPLPKNTSVGPLYSGRLTLRPE 112  
Db 395 KTNQRIDNKCSTGYEKNMTPQNR-----EQRESGFSYPNFS-----LPA 434

Query Match	3.1%;	Score	121.5;	DB	2;	Length	2471;
Best Local Similarity	18.1%;	Pred. No.	19;				
Matches	139;	Conservative	123;	Mismatches	279;	Indels	229;
						Gaps	34;
QY	1	AAQARRARRTKLFTHRSSVSTSTPGTPTVYLGA	SKTPASIFGPSAASHLLILFTLNFT	60			
DB	291	SSKPAKAQKPKQSKNPSSKNTLTLPKHTTI	-----EEHL-----QBFS	329			
QY	61	ITNLRBYENWMPGSRKFNTERVLQGLLRPLFK	MTSVGPLYSGCRLTLLRPEKDGATG	119			
DB	330	QSEANKQEHTPFS--HPTER-----KTPG	TDSLISGINSKRRKREDDLESNGN	376			
QY	120	-----VDAICT-HRPDPTGCLDRBQILYELS	QLTSHITELGPTTLDRLSYV	166			
DB	377	VSSKLKEDBDGWIDDIPTLVNSDTEATNSDQ	ETIYMGIDENIHDMWSYVDDOT--DRTL	434			
QY	167	NGFTHRSSVPTSTGVVSESPFTLNFINNLR	YMDMGQPSGLKFNITDNVMKH--LLSP	224			
DB	435	N-PVOLDKVITSLQNIPINNFTPIIDKPSNR	HIKEGKALHAIDRIILTIIEHGLTSP	493			
QY	225	LFQRSSLGARVTGCRVIALRSVKNGAET	-----RVDLLCTYLQPLSGCPLPIKQVF	277			
DB	494	---PNSWSKCKSLQFVVLWSEKUSIPTKDL	TKLTKNLNLTETAKVASTKL-TNNIF--	547			
QY	278	LSQOQTGITRLGYPYSLDKDSLNGVNEP	GGPDEPPTPKPATTELPPLSEATTAMGYHLK	337			
DB	548	---KNNIITKLNK-CMBKIKL-----ETGD	N-----YKOLLALISHKSTTIQVATT	589			
QY	338	TLTLNFITISLQYSPMDMGKSATFNSTEG	-----VLQHLRLPLF---QKSSMGPFY	388			

## RESULT 7

Db 932 -----NSDDNHVLDSQKT-----PGFSTPKASFDLVSVTASDVVDVANVKNNSVHIVI 979  
Qy 444 DRDLFLFINGYAPQNLSSIRGYSQI-----NFHIVNNLNSPD----- 479  
Db 980 NNDGTSLLNCKAKIVYNDGHELDVNNFVNLVNGVNEYDFNLDDLKHNRYSFKKLIYTE 1039  
Qy 480 PTSSEY-ITLRLDIQKVTLTKYKSQLHDTFRCLVTLNLTWDSVLVTVKALFNSNL----- 534  
Db 1040 PNQNDYKFSFLNN--KQITNTFKTASVNE-----QLTIDTKLVRKP---DSNLNKNIN 1086  
Qy 535 -----DP-----SLVEQVFLDKTLNAGFHWLG-----STVQLVDIHHVTEWESSVYQ 575  
Db 1087 LKQINDPNDFLEQDSILEITFHEKDKTTHNVIGKINDVANNKNTLEFSEVENTNFKIQ 1146  
Qy 576 PTSSSTQHLYLNTFNLPY-SODKAQPGTT-NYQNKKNIEDALNQLFRNSIKSYFS 633  
Db 1147 P-----NHKYI---VDNINVTAKTKIOPANAISNNNSKNISYDASS---NPSKILSFTN 1194  
Qy 634 DCQVSTER-SVNPHEHTGVDSLCLNFSPLAR-----RVDRAIYEEFELEMTRENGTQLOQNT 687  
Db 1195 ELFVNNINVAQPN-----TNLNPASIDVELKSSQNLKDDQYLALYIDNNHOKIW 1245  
Qy 688 LDRSSVLVDGVSPPNRNPLTGNSSADIOH 715  
Db 1246 SDYASV-----NNVDLAH 1258

RESULT 8  
T41144  
hypothetical serine rich protein - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T41144; T41591  
R;Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, October 1998  
A;Reference number: Z21973  
A;Accession: T41144  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1131 <HIL>  
A;Cross-references: UNIPARC:UPI000006A713; EMBL:AL031907; NID:g3766362;  
A;Experimental source: strain 972h-; cosmid c18  
R;Murphy, L.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, September 1998  
A;Reference number: Z21968  
A;Accession: T41591  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 44-1131 <MUR>  
A;Cross-references: UNIPARC:UPI0000161F34; EMBL:AL031543; NID:g4239667; PIDN:CAA20837.1;  
A;Experimental source: strain 972h-; cosmid c74  
C;Comment: For a possible alternative initiator product, see PIR:T42367.  
C;Genetics:  
A;Gene: SPCC74.07C; SPDB:SPCC18.01C  
A;Map position: 3  
C;Keywords: alternative initiators

Query Match 3.1%; Score 121; DB 2; Length 1131;  
Best Local Similarity 18.6%; Pred. No. 5.7;  
Matches 161; Conservative 130; Mismatches 353; Indels 222; Gaps 30;

Qy 2 AQPARRARTKLFTHRSVSTSTPGTPVYLGAKTPASIFGFSASHLILFTLFTI 61  
Db 341 ASSSSSSASATATSAESSIAT--SPITSSNNVSVSISTSSMDSSAVSSVYVQSSLASII 398  
Qy 62 TNLAYENMWPGRKENTERVLOGLRLPLFKNTSVGLYSGCLTLRLRPEKDEATGVD 121  
Db 399 S-----NAYTATSKSLGNSGVSTLLASPTSSSTFTVTSL-----LRRSIDGSASSS 445

Qy 122 ---AICTRHPDPTGFLDREQLYLELSQLTHSITELGPLYTLDRSLVYNGFTHRSSVPTT 178  
Db 446 ASLAVPTVSSSTTG-----SLHYK-TTTTVMTEVFTRYLGDDSTPVS-----SSIFST 494

Qy 179 ST-----GVVSEEPFTLNFTINNRLYMADMGPQSLKFNITDNVMKHLSPFOR 228  
Db 495 ATBATSTVQTSATYDSSSTSNIQSSSVYASSTGALSNSLSSSTSSVSTSYINASS 554  
Qy 229 SSLGARYTCGRVIALRSVRNGAETRVDLLCTLYQLPLSGFGLPIKQVHFELSQOHTGIRL 288  
Db 555 SVYASSTEALSSNLSSSTSSAST-----SYIPSASSSVYEVASNSDDYVQTVSSITAS 608  
Qy 289 GPVSLDKSL-----YLNG-----YNEPGDEPPTTPKPAATFLPPLSEATAMG 333  
Db 609 GTTSTSEIVSTPASNSNTGSLNGTSSFNVNSVGPSSSQTTPTTSSSITGSQLKETSPP 668  
Qy 334 YHLKTLTLNFTISNLQVSPDMGKSATFNS-----TEGVLOH 370  
Db 669 AYVS--TVSTSSVD-----SSSTYNSTGSSSDSQSFSTTYSDPTTITSEVSSI 720  
Qy 371 LRLPLFKSMGPFYLCQLISLRPEKGAATGVDTTCTYHPDPVGPGLDIOQLYELSQL 430  
Db 721 LSSPTSMQSSVS-----RQSSGDASGNT-----IFTISIQ 752  
Qy 431 LTHGVTLQGFVLDRLSFLINGYAPQNLSTIRGEYQINFHIV-----NNLNSP 478  
Db 753 SSDGET--SGYTISSNSQNSASEPQTAFPTSSSSATPTITQSSISTSVSSQSSMSSYS 810  
Qy 479 DPTSSEVITLRLDIQDKV-----TTLYKGSQHLDTFRCLV 514  
Db 811 SPISNSVTSSTSISSIASSTYSPISSTSIASSFFDASGFTSYNGTKAGSSSFALA 870  
Qy 515 TNLTMDSVLTVKALFSSNLDPQLVQVFLDKTLN-----ASFHWLGSTYQLVDI 564  
Db 871 SNESGA-----SDVLSSTIAKPTPKFSTNSGTSYSIPSSSRNEGTTSSYNNI 921  
Qy 565 HVTEWESSVYQ--TSSSSTQHLYLNTFNLPYSDKAQPGTNNYQNKKNIEDALNQL 622  
Db 922 TVT---SSTLKPSTSVSTASSYIASSSNTLS---TEPKTFS---SSSTLSESISI 972  
Qy 623 FRN-----SSIKSVFSDCQVSTFRSPVN--RHHTGVDSLCLNFSPLARR----- 663  
Db 973 NTNSLTVPESLSSSTTSGLTSSSTIPSTSESENSEASSTSSASKRSSSTSLVQSN 1032  
Qy 664 -VDRVAIYEBF-----LRMTRNGTQLOQNTFLDRSSVLVDGYSPNRNEPTUGNS----- 710  
Db 1033 PVKTVVSLSEYKFTTSKISLVKNPKTYTVDVETNVVQTHVTSVYEHSTSYTWVHTTL 1092  
Qy 711 ---ADQHSGRSLSLEGPRFEQKLIS 733  
Db 1093 YEYADVEASTKSTSEPSAKSRNAVS 1118

RESULT 9  
T34235  
hypothetical protein F22A3.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T34235  
R;Hallsworth, K.  
submitted to the EMBL Data Library, November 1995  
A;Description: The sequence of C. elegans cosmid F22A3.  
A;Reference number: Z21492  
A;Accession: T34235  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-532 <HAL>  
A;Cross-references: UNIPROT:Q19695; UNIPARC:UPI000017B91C; EMBL:U41547; PIDN:AAA83194.1;  
C;Genetics:  
A;Gene: CESP:F22A3.1  
A;Introns: 55/1; 99/1; 148/3; 176/3; 190/1; 239/1; 303/1; 331/3; 357/1; 391/1; 511/1;  
P;446-527/Domain: ets DNA-binding domain homology <ETS>

Query Match 3.0%; Score 118; DB 2; Length 532;  
Best Local Similarity 20.5%; Pred. No. 2.7;  
Matches 101; Conservative 59; Mismatches 171; Indels 162; Gaps 25;







Query Match 2.9%; Score 115; DB 2; Length 888;  
Best Local Similarity 19.6%; Pred. No. 10;  
Matches 157; Conservative 109; Mismatches 235; Indels 298; Gaps 47;

QY 110 RPEKGE--ATG-----VDAICTHRP-----DPT-----GPGLD 136  
DB 130 KPTSGEDIVITSYLRLFGPNFLINSIDVNRPFVVKGNFSDPDCNNITVTFPPGSG 189  
QY 137 REQLYELSLQTHSITELG--PYTLD-----RDSLXYNG--FTHRSSVPT 177  
DB 190 KFLYYD-----ETGNPVPFYSPISSVSDSKQIITINGDNFFTDKDLVKV 240  
QY 178 TSGVSWSEBPTLNFTI-----NNLRVMDMGQPSLKFNTI----- 214  
DB 241 SPDGI--DQD--NFIISSVNHKIQVNNYRV--DPGPMVNIITVEVSIENKVIHCP 291  
QY 215 -----DNVWKHL-----LSPILFORSLSGARVTGCRVIALRSVKNQ 249  
DB 292 PAIITSISSVSNHLDGIVTIKGBKSLSTLYLTPSI--TIGDKY-----VLIKSTTTE 343  
QY 250 AETRVLLCTYLQPLSGPLPIKQVPH-----ELSQOHTGI----- 285  
DB 344 LECKLD-----ANELGKGLPVNNVFGGCDSTPNGVSTFYNIPTLSRGSYSNGIVTLIG 398  
QY 286 TRLGYSYLDKDSIYLANG-----YNEPGDEPPTPKPATFLPPLSEAT-----TAM 332  
DB 399 TNLGTNNESSIQLYGDIGKNTNISQFNVSSDE-----KSVTFELPHLCRSFNINFTRS 453  
QY 333 GYHLKTLTLNFTIS--NLOVSPDMKGSATFNSTEGVQLHLLRPLFOKSGMPYLCQLI 391  
DB 454 GITAKTLSIASLVNVRPTV-----SNGIL-----NIEIYMDCTIS 493  
QY 392 SLRPE-----KOGAATGVDTTCTVHPDPVPGPLDIQQLYWELSLQTHGVTO 437  
DB 494 SSAPSTVGDSSASPCSPSSNSSTYETC-----PTPYGTGIN--KQIFKINSET----- 544  
QY 438 LGFYVLDRLDSLFINGYAP--QNLISIRGE--YQINPHIVNNNLS-----NPDPTSSBY 485  
DB 545 -----VSDQFS-----YAPPEVENRTISDDGTNIELAGNFGNSTSLIKVYNGSDISSE- 594  
QY 486 IYLLRDIQD-----KVTLYK-----GSLQHDHTFRPL-----VTNLTMDSV----- 522  
DB 595 ---IOLEPHQTLIKILDSYENGPIINITVDGNTMDSLFLYTLPPVIYRITNKDKNTLACG 651  
QY 523 -LVTVKALFSSNLDPSLVQVFLDKTLNASFWLGSYQLVDIHVTEMESVYQPT----- 577  
DB 652 GLITVS---GKNLLTSDKBKFNKVNKNNTTVFAQDEKILIVRDSRESSLFTVTFIGV 708  
QY 578 -SSSTQHPLYLNFITNLPSYQDKAQPGTNTYQNRKNIEDALNQLFRNSSIKSYFS--- 633  
DB 709 RSGPSTLYIKPMISEIPTIENKIEGILAIIRG--YSTDILNASLTVSSETVPLSCNL 767  
QY 634 DCQVS-----TFRVPRNHHHTGVDSL--CNFSPPLARRVDRVAIYEEFLMRTRNGTQLO- 684  
DB 768 ECLSPNEILDSDSSETNITNSNTDCLSCHSGSSVKNTSGV-----LYLLFNSTSFQY 821  
QY 685 NFTLDRSSVLVDGYSNPN 703  
DB 822 NVTIEEIKL-----SPSPN 835

RESULT 14  
A35364  
carcinoembryonic antigen-related protein (clone mCGM1) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 17-Aug-1990 #sequence\_revision 17-Aug-1990 #text\_change 09-Jul-2004  
C:Accession: A35364  
R:Rebatock, S.; Lucas, K.; Thompson, J.A.; Zimmermann, W.  
J. Biol. Chem. 265, 7872-7879, 1990  
A:Title: cDNA and gene analyses imply a novel structure for a rat carcinoembryonic antigen  
A:Reference number: A35364; MUID:90243655; PMID:2335509  
A:Accession: A35364

A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-709 <REB>  
A:Cross-references: UNIPROT:Q63111; UNIPARC:UPI000008B1AF; GB:M32474; NID:G203430; PIDN:/P;  
C:Superfamily: carcinoembryonic antigen precursor amino-terminal homology <CEA1>  
F;1-137/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA1>  
F;168-217/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA2>  
F;242-378/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA3>  
F;480-612/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA3>  
F;633-690/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA3>

Query Match 2.9%; Score 114.5; DB 2; Length 709;  
Best Local Similarity 20.0%; Pred. No. 7.6;  
Matches 136; Conservative 80; Mismatches 263; Indels 201; Gaps 30;

QY 134 GLDREQLYLELSQTHSITELGTYLDRSLYNGFTHRSSVPTTSGVSEBPTLNFT 193  
DB 70 GLTNMISGVALYSLTYNVTVTGPHSGRETLYNSGLSMIQNTQKDTGTFY----- 120  
QY 194 INNLRYMDMGQPSLKFNTITONVMKHLSPILFORSLSGARVTGCRVIALRSVKNQGAETR 253  
DB 121 ---LRTISNHB-----IVSNTSLH--LHVYESTLTCGPAATSAQ--LSIESVPTSISKG 168  
QY 254 VDLCTYLOPLSGPLP--IKQVPH-----ELSQOHTGITRL--GPYSLDKDSLY 299  
DB 169 ESAL-----LLAHLNLPENLRAIFWKGAIVFKDLEVARVYICTNSVPGPAHSGRETMY 222  
QY 300 LAG-----YNEPGDEPPTPKPATFLPPLSEATTAMGY--HLKTLTLNFTISNLOYSMD 354  
DB 223 SNGSLLLQVNTNDAGFYTLKTLST-----DLKTEIAYVQLQVDTCFMSYAGPPTSQAOL 276  
QY 355 GKGSATFNSTEG---VLQHLRPP-----LFQKSSMGPFVLCQLISLAPKD 398  
DB 277 TVESAPTSVAEGASVLLLVNLPENLRAIFWKGVILFKDLEVARVYICTNSVPGPAHS 336  
QY 399 GAATGVDTTCTVHPDPVPGPLDIQQLYWELSLQTHGVTO--LGFYVLDRLDSLFINGYAPQ 456  
DB 337 GRET-----MYSNGSLLLQVNTNDAGFYTLRTLTSLDLCARV-- 373  
QY 457 NLSIRGEYQINPHIVNNNLSNPDPTSSSEYITLLRDIQDKVTT--LYKGSOLHDTFRCLVT 515  
DB 374 ---VHVLQVNV-----TSSCCDPLTPALLTI-----DPVPRHAKG----- 406  
QY 516 NLTMDSVLTVKALFSSNLDPSLVQVFLDKTLNASFWLGSYQLVDIHVTEMESV--- 572  
DB 407 ---ESVLLQVR-----NLPEDL-----RMFIFKSVYTSQIKIAYSRAINY 446  
QY 573 VYQPTSSSTQHPLYLNFITNLPSYQDKAQPGTNTYQNRKNIEDALNQLFRNSSIKSYF 632  
DB 447 VFRGPAHSGRETVYTGNSL---LLQDATEKDTGLY-----TLQIYRNFKIETAH 493  
QY 633 SDCQVST-----FRSVPRNHHHTGVDSL--CNFSPPLARRVDRVAIYEEFLMRTRNGT 681  
DB 494 VQVSVHTCVHPSTTQQLVIESVPPNVVEGVDL-----LLVHNMP 534  
QY 682 QLQNFPLDRSSVLVDGYSNPNRNEPLTGNADT--OHSGGSSSLEGPFEQKLISEEDLNM 739  
DB 535 NLOQSPWYKGVAVINRHEISRN--ITASNRSTLGPASHSGRETIYNSGSLLLHNATEEDNGL 593  
QY 740 HT-----GHHHHHH 748  
DB 594 YTLWTVNRHSETQGIHVH 613

RESULT 15  
T07015  
Cf-4A protein - tomato  
C:Species: Lycopersicon esculentum (tomato)  
C>Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T07015  
R:Takken, F.B.; Schipper, D.; Nijkamp, H.J.; Hill, J.  
Plant J. 14, 401-411, 1998  
A:Title: Identification and De-tagged isolation of a new gene at the Cf-4 locus of tomato









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Result No.	Query			Description		
	Score	Match	Length	ID		
1	3658	92.7	1890	7	US-11-033-039-314	Sequence 314, Appl
2	166.5	4.2	308	7	US-11-046-456-6	Sequence 6, Appl
3	166.5	4.2	308	7	US-11-046-644-6	Sequence 6, Appl
4	134.5	3.4	98	6	US-10-952-535A-15	Sequence 15, Appl
5	134.5	3.4	123	6	US-10-952-535A-16	Sequence 16, Appl
6	134.5	3.4	155	6	US-10-952-535A-17	Sequence 17, Appl
7	130	3.3	401	6	US-10-949-720-419	Sequence 419, App
8	126.5	3.2	614	6	US-10-517-696-128	Sequence 128, App
9	119	3.0	957	7	US-11-108-172-1065	Sequence 1065, Ap
10	118.5	3.0	2223	7	US-11-193-561-2	Sequence 2, Appli
11	118.5	3.0	2223	7	US-11-193-771-2	Sequence 2, Appli
12	118.5	3.0	2223	7	US-11-193-789-2	Sequence 2, Appli
13	118.5	3.0	2223	7	US-11-193-806-2	Sequence 2, Appli
14	118.5	3.0	2223	7	US-11-193-857-2	Sequence 2, Appli
15	118.5	3.0	2421	7	US-11-193-561-17	Sequence 17, Appl
16	118.5	3.0	2421	7	US-11-193-771-17	Sequence 17, Appl
17	118.5	3.0	2421	7	US-11-193-789-17	Sequence 17, Appl
18	118.5	3.0	2421	7	US-11-193-806-17	Sequence 17, Appl
19	118.5	3.0	2427	7	US-11-193-857-17	Sequence 17, Appl
20	118.5	3.0	2477	7	US-11-193-561-15	Sequence 15, Appl
21	118.5	3.0	2477	7	US-11-193-771-15	Sequence 15, Appl
22	118.5	3.0	2477	7	US-11-193-789-15	Sequence 15, Appl
23	118.5	3.0	2477	7	US-11-193-806-15	Sequence 15, Appl
24	118.5	3.0	2477	7	US-11-193-857-15	Sequence 15, Appl
25	117	3.0	21	7	US-11-185-111-41	Sequence 41, Appl

99	104	2.6	1234	6	US-10-995-561-870	Sequence 870, App
100	104	2.6	1366	6	US-10-995-561-868	Sequence 868, App
ALIGNMENTS						
RESULT 1						
US-11-033-039-314						
; Sequence 314, Application US/11033039						
; Publication No. US20060002947A1						
; GENERAL INFORMATION:						
; APPLICANT: HUMPHREYS, ROBERT						
; APPLICANT: XU, MINZHEN						
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES						
; FILE REFERENCE: REH-2017US01						
; CURRENT APPLICATION NUMBER: US/11/033,039						
; CURRENT FILING DATE: 2005-01-11						
; PRIOR APPLICATION NUMBER: 10/245,871						
; PRIOR FILING DATE: 2002-09-17						
; PRIOR APPLICATION NUMBER: 10/197,000						
; PRIOR FILING DATE: 2002-07-17						
; PRIOR APPLICATION NUMBER: 09/396,813						
; PRIOR FILING DATE: 1999-09-14						
; NUMBER OF SEQ ID NOS: 1452						
; SOFTWARE: PatentIn version 3.3						
; SEQ ID NO 314						
; LENGTH: 1890						
; TYPE: PRT						
; ORGANISM: Homo sapiens						
US-11-033-039-314						
Query Match 92.7%; Score 3658; DB 7; Length 1890;						
Best Local Similarity 99.7%; Pred. No. 1.2e-287;						
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;						
QY	14	FTHRSSVSTTSGTPTVYLGASKTPASIFGSAASHLLILFTLNFTLNRYEENWMPG	73			
DB	1135	FTHRSSVSTTSGTPTVYLGASKTPASIFGSAASHLLILFTLNFTLNRYEENWMPG	1194			
QY	74	SRKFNTERVLOGLRLPLPKNTSVGLYSGCKLTLLRPEKGEATGVDAICTHRPDPDTPG	133			
DB	1195	SRKFNTERVLOGLRLPLPKNTSVGLYSGCKLTLLRPEKGEATGVDAICTHRPDPDTPG	1254			
QY	134	GLDREQLYLELSQTHSITELGPTLDRDLSLVNGFTHRSSVPTTSTGVWSEEPDPTLNFT	193			
DB	1255	GLDREQLYLELSQTHSITELGPTLDRDLSLVNGFTHRSSVPTTSTGVWSEEPDPTLNFT	1314			
QY	194	INNLRYMADMGPGSKFNITDNMKHLLSPLPQSSIGARTGCRVIALSVKNGAETR	253			
DB	1315	INNLRYMADMGPGSKFNITDNMKHLLSPLPQSSIGARTGCRVIALSVKNGAETR	1374			
QY	254	VDLLCTVLOPLSPGPIKQVPHLSQQTHGTLRLGYPYSLDKDLSLYLNGYNEPGDDEPPT	313			
DB	1375	VDLLCTVLOPLSPGPIKQVPHLSQQTHGTLRLGYPYSLDKDLSLYLNGYNEPGDDEPPT	1434			
QY	314	TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTLSNLQYSPDMGKGSATFNSTEGVLQHLR	373			
DB	1435	TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTLSNLQYSPDMGKGSATFNSTEGVLQHLR	1494			
QY	374	PLFKQSMGPFYLGQCLISLRPEKGAATGVDTCTTCTHPDVPGLDIOQLYWEISQLTH	433			
DB	1495	PLFKQSMGPFYLGQCLISLRPEKGAATGVDTCTTCTHPDVPGLDIOQLYWEISQLTH	1554			
QY	434	GVTLGFWLDRDLSLFNGVAPQNLSTRGYQNFHIVNNLSNPDPTSEYITLLRDIQ	493			
DB	1555	GVTLGFWLDRDLSLFNGVAPQNLSTRGYQNFHIVNNLSNPDPTSEYITLLRDIQ	1614			
QY	494	DKVTLLYKGSQLDHDTFRFCLVTNLTDMSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH	553			
DB	1615	DKVTLLYKGSQLDHDTFRFCLVTNLTDMSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH	1674			

; PRIOR APPLICATION NUMBER: US 60/539,605  
; PRIOR FILING DATE: 2004-01-27  
; PRIOR APPLICATION NUMBER: US 60/619,241  
; PRIOR FILING DATE: 2004-10-15  
; NUMBER OF SEQ ID NOS: 178  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 308  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: GIPF VSHis tag  
US-11-046-644-6

Query Match 4.2%; Score 166.5; DB 7; Length 308;  
Best Local Similarity 70.2%; Pred. No. 7.3e-06;  
Matches 33; Conservative 1; Mismatches 10; Indels 3; Gaps 1;

QY 705 PLTGSADIQHSGRSSLEGPRPEQKLISEEDLNM---HTGHHHHH 748  
Db 262 PAKGNSADIQHSGRSSLEGPRPEGPPIPNLLGLDSTRTGHHHHH 308

## RESULT 4

US-10-952-535A-15  
; Sequence 15, Application US/10952535A  
; Publication No. US20050255113A1  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Messer, Anne  
; APPLICANT: Lecerf, Jean-Michel  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE  
; FILE REFERENCE: INR-004CP  
; CURRENT APPLICATION NUMBER: US/10/952,535A  
; PRIOR APPLICATION NUMBER: 2004-09-27  
; PRIOR FILING DATE: 2004-09-27  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Construct  
US-10-952-535A-15

Query Match 3.4%; Score 134.5; DB 6; Length 98;  
Best Local Similarity 78.1%; Pred. No. 0.0005;  
Matches 25; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 717 GGRSSLEGPRPEQKLISEEDLNMHTGHHHHH 748  
Db 68 GGSTMSRGP-PEQKLISEEDLNMHTGHHHHH 98

## RESULT 5

US-10-952-535A-16  
; Sequence 16, Application US/10952535A  
; Publication No. US20050255113A1  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Messer, Anne  
; APPLICANT: Lecerf, Jean-Michel  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE  
; FILE REFERENCE: INR-004CP  
; CURRENT APPLICATION NUMBER: US/10/952,535A  
; PRIOR APPLICATION NUMBER: 2004-09-27  
; PRIOR FILING DATE: 1999-07-27

; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Construct  
US-10-952-535A-16

Query Match 3.4%; Score 134.5; DB 6; Length 123;  
Best Local Similarity 78.1%; Pred. No. 0.00071;  
Matches 25; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 717 GGRSSLEGPRPEQKLISEEDLNMHTGHHHHH 748  
Db 93 GGSTMSRGP-PEQKLISEEDLNMHTGHHHHH 123

## RESULT 6

US-10-952-535A-17  
; Sequence 17, Application US/10952535A  
; Publication No. US20050255113A1  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Messer, Anne  
; APPLICANT: Lecerf, Jean-Michel  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE  
; FILE REFERENCE: INR-004CP  
; CURRENT APPLICATION NUMBER: US/10/952,535A  
; PRIOR APPLICATION NUMBER: 2004-09-27  
; PRIOR FILING DATE: 1999-07-27  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 155  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Construct  
US-10-952-535A-17

Query Match 3.4%; Score 134.5; DB 6; Length 155;  
Best Local Similarity 78.1%; Pred. No. 0.001;  
Matches 25; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 717 GGRSSLEGPRPEQKLISEEDLNMHTGHHHHH 748  
Db 125 GGSTMSRGP-PEQKLISEEDLNMHTGHHHHH 155

## RESULT 7

US-10-949-720-419  
; Sequence 419, Application US/10949720  
; Publication No. US20050249736A1  
; GENERAL INFORMATION:  
; APPLICANT: Kraenoperov, Valery  
; APPLICANT: Zozulya, Sergey  
; APPLICANT: Kertesz, Nathalie  
; APPLICANT: Reddy, Ramachandra  
; APPLICANT: Gill, Parkash  
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING  
; FILE REFERENCE: VASG-P02-002  
; CURRENT APPLICATION NUMBER: US/10/949,720  
; PRIOR APPLICATION NUMBER: 2004-09-23  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 60/454,432  
; PRIOR APPLICATION NUMBER: US 60/454,300

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; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 419
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-949-720-419

Query Match          3.3%; Score 130; DB 6; Length 401;
Best Local Similarity 32.7%; Pred. NO. 0.01;
Matches 50; Conservative 12; Mismatches 53; Indels 38; Gaps 8;

632 FSDCQVSTFRSVP-----NRHHTGVDSLGNFSPLARR---VDRVAIYEE----- 672
251 FEPVNVTTDREVPVAVSDIRVTRSPFSLSLAWAVPRAPSGAWLDEVKHEKGAEGPSS 310
673 --FLMRTRNGTQONFTLDR--SSVLVD-----CYSP-----NRNEPLTGNASADIOHSGG 718
311 VRFLLKTSNRAELRG--LKRGSYLVQVRRASEAGYPGQGHHSQTQLDSEGWREQQG 368
719 RSSLEGPRFEQKLISEEDLNM---HTGHHHHHH 748
369 RSSLEGPRFEQKPIPNPLGLDSTRTGHHHHHH 401

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DB 369 RSLGPRFGKPIPNPLGLDSTRGHHHH 401

RESULT 8

US-10-517-696-128

Sequence 128, Application US/10517696

Publication No. US20060051759A1

GENERAL INFORMATION:

APPLICANT: diaDexus, Inc.

APPLICANT: Salceda, Susana

APPLICANT: Macina, Roberto A.

APPLICANT: Turner, Leah R.

APPLICANT: Sun, Yongming

APPLICANT: Liu, Chenghua

TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and

FILE REFERENCE: DEX-0432

CURRENT APPLICATION NUMBER: US/10/517,696

CURRENT FILING DATE: 2004-12-13

PRIOR APPLICATION NUMBER: US 60/389,327

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 171

SOFTWARE: PatentIn version 3.1

SEQ ID NO 128

LENGTH: 614

TYPE: PRT

ORGANISM: Homo sapien

US-10-517-696-128

Query Match 3.2%; Score 126.5; DB 6; Length 614;

Best Local Similarity 19.5%; Pred. No. 0.037;

Matches 110; Conservative 63; Mismatches 223; Indels 169; Gaps 19;

QY 151 ITELGPYTLDRDSLXYNGFTHRSSVP-----TTSTGVVSEPPFFLNFNTINNLRYMADMGQ 205

DB 15 LTVLTATTAPKPAVTVTSQGHASSTPGGKETSATQSRSSVPSSTEKNAVSMSTSSVLSSHS 74

QY 206 PGSGLFNITDNVMKHLSPFLFORSSILGARYTCRVIALRSVKNGAETRVDLLCTYLOPLS 265

DB 75 PGS--GSSTQGDVTLAPATEPAGSAAATWQDVTSV-----PVT 113

QY 266 GPGCLPIKQVHELSSQOHTGITLGPYSLDKSLYNGYNEGP-----DEPPTT 314

DB 114 RPAL-----GSTTPAHVDVTSAPD-----NKPAPGSTAPPAGHGVTSAPDTR 154

QY 315 PKPATFTLPLPSAATAMGHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLRP 374

DB 155 PARGST-APPAGHGVTSAPDNRNRPALGSTAPPVHVNTVSAGSAGSASTLVHNGTSARATTT 213

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1065
; LENGTH: 957
; TYPE: PRG
; ORGANISM: Homo sapiens
US-11-108-172-1065

Query Match      3.0%; Score 119; DB 7; Length 957;
Best Local Similarity 19.0%; Pred. No. 0.29;
Matches 146; Conservative 81; Mismatches 269; Indels 280; Gaps 31;

QY 17 RSSVSTSTGCTPTVYLGASTPASIFGSAASHLLILFTLNFTITNLRNENWPGSRK 76
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 20 QESTASHSSPGSTDTLSPGSTASSLGPESTTF-----HSGPGSTE 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 77 F-----NTTERRVQLGLRLPFLKNTSVGLYSGCRLTLRP-----EKDGEATGVDALCTHR 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 TTLPLDNTTASGLLEASTVHSSST-----GSPHTTSLPAGSTTRQGESSTTQSS-WPNS 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 128 PDPTGPGLOREQLYLELSQTHSITELGPTVTLDRDSLTVNG-----FTHRSSVPT--- 177
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 KDTTPAPPTTTSAPVELSTTSHGSPSSTPTTHFSASSTTLGRSEESTTVHSSPVATATP 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 178 -----TSTGVVSEPPFTLNFTINNLRNRYMADMGQPSLKFNITNV-----MK 219
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 174 SPARSTTSLGVBE-----STYHSSPGSTQTMHFPESDTTSGRGEESTTSHSST 223
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 220 HLLS-----PLFORSSIGAR-----YTGCRVI 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 224 HTISSAPSTTSALVEETSTHSSPGSTATTTHFPDSSTTSGRSEESTASHNQATGIVL 283
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 242 ALRSVRN---GAETRVLLCTYLQPSGGPLIKQVPHLSQOQTHGITRLGPIYSLDKDSL 298
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 284 PARSTTVLLGEESTTSPISGSMETALPG-----STTTPGLS-----EKSST 326
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 299 YLNGYNEPGDEPTTPKPAATFLPPLS-EATTAMGYHLKTLTLNFTISNLQVSPDMGKG 357
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 327 F-----HSSPRSPATLSPASTTSSGVSEESTTSHSRPGSTHTTAPDSTT--TPGLSRH 379
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 358 SATFNSTEGVQLHLLRPLFKSMGPPYLGCLISLRPKDGAATGVDCTTVHDPD--- 414
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 380 STTSHSPGSDTTLPLASTTTS-GP-----SQBSTTSHSPGST 418
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 415 ---VGPGLDIQOLYWELSQLTHGVTQLGFGYVLDRLDLSLFIINGYAPONLSIRGEYQINFHIV 471
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 419 DTALSPG-----STTALSF-----QBSTTTFH-- 440
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 472 NWNLSPDPTSSSYIILLRIQKVYLYKGSQHLHDTFRCLVTNLMTDSVLVTVKALFS 531
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 441 ---SSP---GSTHTTLFPDSTTSSGIVEASTRVHS-----STGSPRTTSLSP--A 481
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 532 SNLDPSLVEQVFLDKTLNASFHMLGSLTYQLVDIHTVTEMESVYQPTSSSTQHPYLNFT- 590
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 482 SSTSPGLQGESTAFQTHPASTHTTPTSPATAPVEE-STYTHRSPESTTTHFPASST 540
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 591 -----ITNLPYSQKQAPG- 604
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 541 SCHSEKSTIHFHSPDASGTTSPSAHSTTSGRGEESTTSRISPGSTEITTLPGS--TTTPGL 598
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 605 ---TTNYQRNKRNIEDALNQLFRNSSIKSYFSDCQVSTFRSVNRHHTGTVDLSLCNFS 659
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 599 SEASTTYPSPRSPPTTLSP-----ASMTSLGVGEESTTSRSPQSGSTHSTVSPASTTTP 652

RESULT 10
US-11-193-561-2
; Sequence 2, Application US/11193561
; Publication No. US20060024757A1
; GENERAL INFORMATION:
; APPLICANT: Husea, Robert
; APPLICANT: Shorter, Simon
; TITLE OF INVENTION: Detection of Oncofetal Fibronectin for Selection of Concepti
; FILE REFERENCE: 17101-080001/831
```

```
Db 1070 ---YTVTGL-----EPG-IDYDISVITLNGESAPTTLTQCTAVPPPTDLRFTNIGP 1118
Qy 638 STFRS--VPMRHTGVDSLCNFSPLARRVDRVAIYEFELMRNGTOLQ-----FTLD 689
Db 1119 DTRVVTWAPPSPIDLTNLFVRYSPVKNED---VAELSISSPDNAVVLTLNLPCTEYVVS 1175
Qy 690 RSSVLVDGYSFNRNEPLTGNADIQHSGRSSLEGGPFEQKLISEEDLNH-----T 741
Db 1176 VSSV---YQHESTPLRG-----RQKTGLDSTGIDFSD--ITANSFTVHWIAPRATIT 1224
Qy 742 GHHHHH 748
Db 1225 GYRIRHH 1231

RESULT 11
US-11-193-771-2
; Sequence 2, Application US/11193771
; Publication No. US20060024722A1
; GENERAL INFORMATION:
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: Hickok, Durlin
; APPLICANT: LaPointe, Jerome P.
; TITLE OF INVENTION: Samples for Detection of Oncofetal Fibronectin and uses thereof
; FILE REFERENCE: 17101-027001/828
; CURRENT APPLICATION NUMBER: US/11/193,771
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2223
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-193-771-2

Query Match 3.0%; Score 118.5; DB 7; Length 2223;
Best Local Similarity 18.9%; Pred. No. 1.2;
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

Qy 19 SVSTSTPGTPTVVLGAS-----KTPASIFGSPASASHLLILFTLNTLRYE---- 67
Db 445 TTTSTPTVNTVTGETTPSPPLVATSESVTEITASSFVVSWSASDVTSGFRVYELS 504
Qy 68 -----ENMPGSKFKNTTERRVLQGLLRPLFKNTSVGLPYSGCKRLT 107
Db 505 BEGDEPQVLDLPSTATSVNIPDLPLGRKYIVNVVQISEDGQSHLSTS----- 553
Qy 108 LLRPEKDEAGTVDAICTRPDTPGDLRQLYLELSQLTHSITELGPYTLDRDSLY-- 165
Db 554 -----QTTPADA---PPDPTVDQDDTSIVVRWSRQPAPIT---GYRI---VYSP 594
Qy 166 -VNGFTRSSVPTTSTGVVSEPTFLNFTINNLRYMADMGPGLSKFNITDNVM---KHL 221
Db 595 SVEGSSTELNLPETANSV-----TSLSDL-----QPG-VQVNIITVAYEENQES 636
Qy 222 LSPLFORSILG-----ARYTCRVIALRSVKNGAET--RVDLLCTYLOPL 264
Db 637 TPVVIQETTGTTPSDTVPSPRDQFVEVTVKVTIMTTPPESAVTGYRVDVIPNLPGE 696
Qy 265 SGPGLP1-KQVFHELSSQTHGIT---RLGPYSLDKOSLYLNGYNEPGDEP-----PT 313
Db 697 HGQRLPISRNTFAEVTGLSPGVTVYFKVFAVSHGRESKPLTAQQTTLKLDAPTNLQFVNET 756
```

```
Qy 314 TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSPDMGKGSATFNSTEGVLQHLR 373
Db 757 DSTVIVRWTPPRAQIT--GYRL-TVGLRFGQPROY-----NVGPSVSKYPLR 801
Qy 374 PLPQSKSMGPFYLGCOLISLRPEKOG-AATGVDTTCTYHPDPVGPGLDIOQLXWELSQLT 432
Db 802 NLQPASE---YTVSLVAIKGQESPKATGVFTT-----LQPGSSIPPYNTEVTETT 849
Qy 433 HGVY---QLGF-----YVL-----DR 445
Db 850 IVITWTPAPRIGFKLGVRSQGGAPREVTSDSGSIVVSGLTGFEVXYVTIQVLRDQGR 909
Qy 446 DSLFINGYA-----PONLSIRGEYQINFHIVNNWLSNPDPSTSEYITLLRDIQDKVVTLY 500
Db 910 DAFIVKVVTPLSPTNLHLEANPDGTGLTVSWERSTTPTDITGYRIT-----TTPT 960
Qy 501 KGSQ-----LHDTFRFCVLVNTLT-----MDSVLVTVKALFSS 532
Db 961 NGQGGNSLEBWHADQSSCTFDNLSPGLEYNVSVYTVKDKESVPISDTIPEV----- 1014
Qy 533 NLDPSLVEQVFLDKT-LNASFWH--LGSTYQLVDYDIHVTEMES-----VYQPTSSSSQHF 585
Db 1015 ---PQLTDLFSVDITDSSIGLRWTLPLNS--TIIGYRITVVAAGEGIPFSDFDVSSVGY- 1069
Qy 586 YLNFITINLPYSQDKAQPGTNTYQNRKNI-----EDALNQLFRNSSIKS---YFSDCQV 637
Db 1070 ---YTVTGL-----EPG-IDYDISVITLNGESAPTTLTQCTAVPPPTDLRFTNIGP 1118
Qy 638 STFRS--VPMRHTGVDSLCNFSPLARRVDRVAIYEFELMRNGTOLQ-----FTLD 689
Db 1119 DTRVVTWAPPSPIDLTNLFVRYSPVKNED---VAELSISSPDNAVVLTLNLPCTEYVVS 1175
Qy 690 RSSVLVDGYSFNRNEPLTGNADIQHSGRSSLEGGPFEQKLISEEDLNH-----T 741
Db 1176 VSSV---YQHESTPLRG-----RQKTGLDSTGIDFSD--ITANSFTVHWIAPRATIT 1224
Qy 742 GHHHHH 748
Db 1225 GYRIRHH 1231

RESULT 12
US-11-193-789-2
; Sequence 2, Application US/11193789
; Publication No. US20060024723A1
; GENERAL INFORMATION:
; APPLICANT: Husea, Robert
; APPLICANT: Fisher-Colbrie, Mark
; APPLICANT: LaPointe, Jerome
; APPLICANT: Senyei, Andrew
; APPLICANT: Shorter, Simon
; TITLE OF INVENTION: Methods for detecting Oncofetal Fibronectin
; FILE REFERENCE: 17101-029001/830
; CURRENT APPLICATION NUMBER: US/11/193,789
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2223
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-193-789-2
```

Query Match 3.0%; Score 118.5; DB 7; Length 2223;  
Best Local Similarity 18.9%; Pred. No. 1.2;  
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

QY 19 SVSTTSPGPTVYLGAS-----KTPASIFGPSAASHLLILFTLNFTTNLYE----- 67  
DB 445 TTTSTSTPVTNTVTGETTFFPLVATSEVTEITASSFVSVWSASDVTSGRVEVELS 504  
QY 68 -----ENMPPGSRKENTTERTVLQGLLRPLFKNTSVGPLYSGRLT 107  
DB 505 BEGDEPOYLDLPSTATSVNIPDLPGKYVNVYQISEDEQSILSTS----- 533  
QY 108 LLRPEKDGATGDAICTHRPDTPGGLDREQLYLELSQLTHSITELGPTVTLDRDLSY-- 165  
DB 554 -----QTAPDA-----PPDPTVDQDDTISVWRMSRPOAPIT---GYRI---VYSP 594  
QY 166 -VNGFTHRSSVPTTSTGVVSEEPFTLNFTLNRLYMADMGQPSLKFNITDNVM---KHL 221  
DB 595 SVESGSTEMLNLPETANSV-----TLSDL-----OPG-VQYNITIYAVEENQES 636  
QY 222 LSPFLQRSSLG-----ARYTGCRVIALRSVKNGAET--RVDLLCTVYLQPL 264  
DB 637 TPVVIQOETTGTPRSPTVPSRDLQFVEVTDVKVTIMWTPPEASAVTGYRVDVIPNLPG 696  
QY 265 SGPGLPV-KQVFHELSSQOHTGIT---RLGYSILDKDSLVLNGYNEPGDPEP-----PT 313  
DB 697 HGQRLPISRNTFAEVTGLSPGVTYFKVAVSHGRESKPLTAQOQTKLDAPTNLQFVNET 756  
QY 314 TPKPATFPLPSEATAMGYHLKTLTNFTLNRLYMADMGQPSLKFNITDNVM---KHL 221  
DB 757 DSTVLVRWTPPRAQIT---GYRL-TVGLTRGQPROY-----NVGPSVSKYPLR 801  
QY 374 PLFQKSMGPFYLGCOLISLRPEKDG-AATGVDITCTYHPDPVPGGLDIQQLWELLSOLT 432  
DB 802 NLQASE-----YTVSLVAIKGNQESPKATGVFTT-----LQPGSSIPPYNTEVETT 849  
QY 433 HGVY-----QLGF-----YVL-----DR 445  
DB 850 IVITWTPAPRIGFKLGVRSQGGAPREVTSDSGSIIVSVGLTPGVEVYVYTIQVLRDQER 909  
QY 446 DSLFINGYA-----PONLSIRGEYQINFIHVNWNLNPDPTSEYITLLARDIQDKVTLLY 500  
DB 910 DAPIVNVKVTPLSPPTNLHLEANPDGVLTVSWERSTTPTDITGYRIT-----TTPT 960  
QY 501 KGSQ-----LHDTFRFCLVNLNLT-----MDSVLVTVKALFSS 532  
DB 961 NQOQNSLEEVVHADQSSCTFDNLSPGLEYNVSVYTVKDKESVPISDTIIPV----- 1014  
QY 533 NLDPQLVEQVFLDKT-LNASFWH--LGSTYQVLDIIVHTEMSS-----VYQPTSSSTQHF 585  
DB 1015 ---POLTDLDFVDITDSSIGLWTPNLSS-TIIGYRITVVAAGEGIPEDFVDSVGY- 1069  
QY 586 YLNPFTINLPYSQDKAQPGTNTYQNKENT-----EDALNQLFRNSSIKS-----YFSDCQV 637  
DB 1070 ---YTVTGL-----EPG-IDYDISVITLINGESAPTTLTQQTAVPPPTDLRFTNIGP 1118  
QY 638 STFRS--VPRNHTGVDSLNCNFSGLARRVDRVAIYEFBLMTNGTQLOH-----FTLD 689  
DB 1119 DTRVTVWAPPSPSDLTNLFVRYSPVKNED---VAELISIPSDNNAVVLMLLPGTEYVVS 1175  
QY 690 RSSVLVDGYSFNRNEPTNGSADIQHSGRSSLEGPRFEQKLISEEDLNH-----T 741  
DB 1176 VSSV---YEQHESSTPLRG-----RQKTGLDSTPGIDFSD--ITANSFTVHMTAPRATIT 1224  
QY 742 CHHHHH 748  
DB 1225 GYRIHH 1231

RESULT 13

US-11-193-806-2

; Sequence 2, Application US/11193806

Publication No. US20060024724A1  
GENERAL INFORMATION:  
APPLICANT: Hussa, Robert  
APPLICANT: Fisher-Colbrie, Mark  
APPLICANT: Lapointe, Jerome  
APPLICANT: Shorter, Simon  
TITLE OF INVENTION: Oncofetal Fibronectin as a Marker for Health and Disease  
FILE REFERENCES: 17101-028001/829  
CURRENT APPLICATION NUMBER: US/11/193,806  
CURRENT FILING DATE: 2005-07-29  
PRIOR APPLICATION NUMBER: 60/592,823  
PRIOR FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: 60/592,803  
PRIOR FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: 60/592,825  
PRIOR FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: 60/592,804  
PRIOR FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: 60/592,824  
PRIOR FILING DATE: 2004-07-30  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 2223  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-11-193-806-2

Query Match 3.0%; Score 118.5; DB 7; Length 2223;  
Best Local Similarity 18.9%; Pred. No. 1.2;  
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

QY 19 SVSTTSPGPTVYLGAS-----KTPASIFGPSAASHLLILFTLNFTTNLYE----- 67  
DB 445 TTTSTSTPVTNTVTGETTFFPLVATSEVTEITASSFVSVWSASDVTSGRVEVELS 504  
QY 68 -----ENMPPGSRKENTTERTVLQGLLRPLFKNTSVGPLYSGRLT 107  
DB 505 BEGDEPOYLDLPSTATSVNIPDLPGKYVNVYQISEDEQSILSTS----- 553  
QY 108 LLRPEKDGATGDAICTHRPDTPGGLDREQLYLELSQLTHSITELGPTVTLDRDLSY-- 165  
DB 554 -----QTAPDA-----PPDPTVDQDDTISVWRMSRPOAPIT---GYRI---VYSP 594  
QY 166 -VNGFTHRSSVPTTSTGVVSEEPFTLNFTLNRLYMADMGQPSLKFNITDNVM---KHL 221  
DB 595 SVESGSTEMLNLPETANSV-----TLSDL-----OPG-VQYNITIYAVEENQES 636  
QY 222 LSPFLQRSSLG-----ARYTGCRVIALRSVKNGAET--RVDLLCTVYLQPL 264  
DB 637 TPVVIQOETTGTPRSPTVPSRDLQFVEVTDVKVTIMWTPPEASAVTGYRVDVIPNLPG 696  
QY 265 SGPGLPV-KQVFHELSSQOHTGIT---RLGYSILDKDSLVLNGYNEPGDPEP-----PT 313  
DB 697 HGQRLPISRNTFAEVTGLSPGVTYFKVAVSHGRESKPLTAQOQTKLDAPTNLQFVNET 756  
QY 314 TPKPATFPLPSEATAMGYHLKTLTNFTLNRLYMADMGQPSLKFNITDNVM---KHL 221  
DB 757 DSTVLVRWTPPRAQIT---GYRL-TVGLTRGQPROY-----NVGPSVSKYPLR 801  
QY 374 PLFQKSMGPFYLGCOLISLRPEKDG-AATGVDITCTYHPDPVPGGLDIQQLWELLSOLT 432  
DB 802 NLQASE-----YTVSLVAIKGNQESPKATGVFTT-----LQPGSSIPPYNTEVETT 849  
QY 433 HGVY-----QLGF-----YVL-----DR 445  
DB 850 IVITWTPAPRIGFKLGVRSQGGAPREVTSDSGSIIVSVGLTPGVEVYVYTIQVLRDQER 909  
QY 446 DSLFINGYA-----PONLSIRGEYQINFIHVNWNLNPDPTSEYITLLARDIQDKVTLLY 500  
DB 910 DAPIVNVKVTPLSPPTNLHLEANPDGVLTVSWERSTTPTDITGYRIT-----TTPT 960  
QY 501 KGSQ-----LHDTFRFCLVNLNLT-----MDSVLVTVKALFSS 532







Db 1055 NLQASE-----YTVSLVAIKGNQSPKATGVFTT-----LQPGSSIPPYNTEVTETT 1102  
Qy 433 HGVT-----OLGF-----YVL-----DR 445  
Db 1103 IVITWTPAPRIGFKLGVPRSGGGEAPREVTSDSGSIIVVSGLTGVEVYVYTIQVLRDQGER 1162  
Qy 446 DSLFINGYA-----PQNLISIRGEVQINFHIVNNLSNPDPTSSEYITLLARDIQDKVTTLY 500  
Db 1163 DAPIVNVKVTPLSPPTNLHLEANDPTGVLTVSWERSTTDPITGYRIT-----TTPT 1213  
Qy 501 KGSQ-----LHDTFRFCIVTNLT-----MDSVLVTVKALFSS 532  
Db 1214 NGQGNLSLEEVHADQSSCTFDNLSPGLEYNVSVYTVKDKESVPISDTIPEV-----1267  
Qy 533 NLDPQLVEQVFLDKT-INASFHW--LGSTYQVLDIHTVEMESS-----VYQPTSSSSQHF 585  
Db 1268 ---PQLTDLFSVDITDSSIGLWTPNLSS--TIIGYRITVVAAGGEGIFEDFVDSVGVY- 1322  
Qy 586 YLNFITINLPYSQDKAQPGTNYQNRKNI-----EDALNOLFNRSSIKS-----YFSDQV 637  
Db 1323 ---YTVTGL-----EPG-IDYDISVITLINGSAPTTLTQQTAVPPPTDLRFTNIGP 1371  
Qy 638 STFRS--VPRNHRHTGVDSLNCNFSPLARRVDRVAIYEEFLMRNRTGLOLN-----FTLD 689  
Db 1372 DTRVWTPAPPSIDLTVLRYSPVKNEED---VAELSISSDNNAVLTNLLPCTEYVVS 1428  
Qy 690 RSSVLVDGYSPPNRNEPLTGNADIOHSGGRSSLEGPRFEOKLISEEDLNH-----T 741  
Db 1429 VSSV---YEQHESSTPLRG-----RQKTGLDSTPTGIDFSD--ITANSFTVHWIAPRATIT 1477  
Qy 742 GHHHHH 748  
Db 1478 GYRIRHH 1484

## RESULT 17

US-11-193-789-17  
; Sequence 17, Application US/11193789  
; Publication No. US20060024723A1  
; GENERAL INFORMATION:  
; APPLICANT: Husse, Robert  
; APPLICANT: Fisher-Colbrie, Mark  
; APPLICANT: Lapointe, Jerome  
; APPLICANT: Seney, Andrew  
; APPLICANT: Shorter, Simon  
; TITLE OF INVENTION: Methods for detecting Oncofetal Fibronectin  
; FILE REFERENCE: 17101-029001/830  
; CURRENT APPLICATION NUMBER: US/11/193,789  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: 60/592,823  
; PRIOR FILING DATE: 2004-07-30  
; PRIOR APPLICATION NUMBER: 60/592,803  
; PRIOR FILING DATE: 2004-07-30  
; PRIOR APPLICATION NUMBER: 60/592,825  
; PRIOR FILING DATE: 2004-07-30  
; PRIOR APPLICATION NUMBER: 60/592,804  
; PRIOR FILING DATE: 2004-07-30  
; PRIOR APPLICATION NUMBER: 60/592,824  
; PRIOR FILING DATE: 2004-07-30  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 2421  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank NM 212475  
; DATABASE ENTRY DATE: 2005-06-10  
US-11-193-789-17

Query Match 3.0%; Score 118.5; DB 7; Length 2421;  
Best Local Similarity 18.9%; Pred. No. 1.3;  
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

Qy 19 SVSTTTSTPGTPTVVLGAS-----KTPASIPGSAASHLLILFTLNFITNRYE----- 67  
Db 698 TTTTSTPTVNTVTGETTFFSPSLVAITSVTEITASSFVSVWSASDVTSGFRVEVELS 757  
Qy 68 -----ENMWPGRSRKFNFTTVERVLQGLLRFLKXNTSVGLYSGRLT 107  
Db 758 BEGDEPOYLDLPSTATSVNIPDLLPGRKYIVNVQISEDGEQSLILSTS----- 806  
Qy 108 LLPEKDEGATGVDAICTHRDPDTPGLDREQLYLELSQLTHSITELGPTLDRDSLY-- 165  
Db 807 -----QTTAPDA-----PPDPTVDQDDTSIVVWRSPQAPIT--GYRI--VYSP 847  
Qy 166 -VNGFTHRSVPSTSTGVWSEEPFTLNFITNLRMYADMGPGLSKFNKFNIDNMV--KHL 221  
Db 848 SVESSTELMLPETANSV-----TUSDL-----OPG-VQNIITIIYAVEENQES 889  
Qy 222 LSLFORSSLG-----ARYTGCRIALRSVKNGAET--RVDLLCTYLQPL 264  
Db 890 TPVVIQOETTGTPRSDDTVPSPRDLQFVEVTDVKVTIMWTPPESAVTGYRVDVIPVNLPG 949  
Qy 265 SGPLPT-KQVFHELQOQTHGIT--RLGYSYLDKDSLYLNGYNEPGPDEP-----PT 313  
Db 950 HGQRLPISRNTFAEVTGLSPGVTYYPKFAVSHGRESKPLTAQQTTKLDAPTNLQFVNET 1009  
Qy 314 TPXPATTFPLPPLSEATTAMGYHLKTLNFTINLQYSPDMGKGSATFNSTEGVLOHLR 373  
Db 1010 DSTVLVWTPPRAQIT--GYRL--TVGLTRGQPRQY-----NVGPSVSKYPLR 1054  
Qy 374 PLFQKSGMGPFFYLGCOLISLRPEKOG--AATGVDTTCTYHPDPVPGPLDIQOLYWELSQLT 432  
Db 1055 NLQASE-----YTVSLVAIKGNQSPKATGVFTT-----LQPGSSIPPYNTEVTETT 1102  
Qy 433 HGVT-----OLGF-----YVL-----DR 445  
Db 1103 IVITWTPAPRIGFKLGVPRSGGGEAPREVTSDSGSIIVVSGLTGVEVYVYTIQVLRDQGER 1162  
Qy 446 DSLFINGYA-----PQNLISIRGEVQINFHIVNNLSNPDPTSSEYITLLARDIQDKVTTLY 500  
Db 1163 DAPIVNVKVTPLSPPTNLHLEANDPTGVLTVSWERSTTDPITGYRIT-----TTPT 1213  
Qy 501 KGSQ-----LHDTFRFCIVTNLT-----MDSVLVTVKALFSS 532  
Db 1214 NGQGNLSLEEVHADQSSCTFDNLSPGLEYNVSVYTVKDKESVPISDTIPEV-----1267  
Qy 533 NLDPQLVEQVFLDKT-INASFHW--LGSTYQVLDIHTVEMESS-----VYQPTSSSSQHF 585  
Db 1268 ---PQLTDLFSVDITDSSIGLWTPNLSS--TIIGYRITVVAAGGEGIFEDFVDSVGVY- 1322  
Qy 586 YLNFITINLPYSQDKAQPGTNYQNRKNI-----EDALNOLFNRSSIKS-----YFSDQV 637  
Db 1323 ---YTVTGL-----EPG-IDYDISVITLINGSAPTTLTQQTAVPPPTDLRFTNIGP 1371  
Qy 638 STFRS--VPRNHRHTGVDSLNCNFSPLARRVDRVAIYEEFLMRNRTGLOLN-----FTLD 689  
Db 1372 DTRVWTPAPPSIDLTVLRYSPVKNEED---VAELSISSDNNAVLTNLLPCTEYVVS 1428  
Qy 690 RSSVLVDGYSPPNRNEPLTGNADIOHSGGRSSLEGPRFEOKLISEEDLNH-----T 741  
Db 1429 VSSV---YEQHESSTPLRG-----RQKTGLDSTPTGIDFSD--ITANSFTVHWIAPRATIT 1477  
Qy 742 GHHHHH 748  
Db 1478 GYRIRHH 1484

## RESULT 18

US-11-193-806-17  
; Sequence 17, Application US/11193806  
; Publication No. US20060024724A1  
; GENERAL INFORMATION:  
; APPLICANT: Husse, Robert  
; APPLICANT: Fisher-Colbrie, Mark

APPLICANT: LaPointe, Jerome  
APPLICANT: Shorter, Simon  
TITLE OF INVENTION: Oncofetal Fibronectin as a Marker for Health and Disease  
FILE REFERENCE: 17101-028001/829  
CURRENT APPLICATION NUMBER: US/11/193,806  
CURRENT FILING DATE: 2005-07-29  
PRIOR APPLICATION NUMBER: 60/592,823  
PRIOR FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: 60/592,803  
PRIOR FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: 60/592,825  
PRIOR FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: 60/592,804  
PRIOR FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: 60/592,824  
PRIOR FILING DATE: 2004-07-30  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17  
LENGTH: 2421  
TYPE: PRT  
ORGANISM: Homo Sapiens  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: GenBank NM 212475  
DATABASE ENTRY DATE: 2005-06-10  
US-11-193-806-17

Query Match 3.0%; Score 118.5; DB 7; Length 2421;  
Best Local Similarity 18.9%; Pred. No. 1.3;  
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

19 SVSTTSTPGTPTVYLGAAS-----KTPASIFGPSAASHLLILFTLNFTITNLYE--- 67  
698 TTTTSTPTVNTVTGETTTPSPPLVATSEVTETASSFVSVWSASDITVSGFRVELS 757  
68 -----ENMFGSRKFNTERVQLGLRLPLFKNTSVGPLYSGRLT 107  
758 EGDPEQYLDLPSTATSVNIPDLLPGKRYVNVYQISEDEQSLILSTS----- 806  
108 LLRPEKDGATGVAICTHRPDPTGCLDREQLYLELSQLTHSITELGPVTLDRDSLX-- 165  
807 -----QTTAPDA-----PPDPTQVDDTTSIVVWRSRQAPIT---GYRI---VYSP 847  
166 -VNGFTHRSSVPTTSGVSEEPFTLNFTINNLYRMADMGPGLSKFNITDNVW----KHL 221  
848 SVEGSSTELNLPETANSV-----TSLDL-----QPG-VQYNTIYAVENQES 889  
222 LSPFORSLG-----ARYTGCRVIALRSVNGAET--RVDLLCTYLQPL 264  
890 TPVVIQQTGTGPRSDTPSPRLQFVEVTDVKVTIMWTTPESAVTGYRVDVIPNLPGE 949  
265 SGPLPI-KQVHLSQOHTGII--RLGYPYSLDKDSLYINGNEPGDPEP-----PT 313  
950 HGQRLPISNTFAEVTGLSPGVYTPKVFVAVSHGRESKPLTAQOYTKLDAPTNLQVFNET 1009  
314 TPKPATTFPLPSEATATAGYHLKTLTINFTISNLQVSPDMGKSATFNSTEGVLQHLR 373  
1010 DSTVLVRWTPPRAQIT---GYRL-TVGLTRGPRQY-----NVGPSVKYPLR 1054  
374 PLFQKSGMGPFYLGCOLISLRPEKOG-AANGVDVTTCTYHPDPVPGGLDIOQLWELSQLT 432  
1055 NLQPASE-----YTVSLVAIKNGQESPKATGVFTT-----LQPGSSIPPVNTVETTT 1102  
433 HGVY-----QLGR-----YVL-----DR 445  
1103 IVITWTAPRIPKGLGVRSQGEAREVTSDSGSIVWSGLTPGVYVYVITQVLRDQGR 1162  
446 DSLFINGYA-----PONLSIRGEYQINFIHVNWNLSNPDPSTSEYITLLARDIQDKVTILY 500  
1163 DAPIVKNVVTPLSPPTNLHLEANPDGVLTVSWERSTTPTDITGYRIT-----TTT 1213  
501 KGSQ-----LHDTFRFCVLVNTLT-----MDSVLVTVKALFSS 532

Db 1214 NGQOGNSLEEVNADQSSCTFDNLSPGLEYNVSVYTKDDKSPISDTIPEV----- 1267  
QY 533 NLDPSLVEQVFLDKT-LNASFWH--LGSTVOLVDIHWTESS-----VYOPTSSSTQHF 585  
Db 1268 ---PQLTDLISFVDITDSSIGLRTPLNSS-TIIGYRITVVAAGEGIPFDVDFVDSVGY- 1322  
QY 586 YLNFITNLFPYSQDKAQPCTNYQRKNRI-----EDALNQLFRNSSIKS-----YFSDCQV 637  
Db 1323 ---YTVTGL-----EPG-IDYDISVITLINGSAPTTLTQCTAVPPPTDLRFTNIGP 1371  
QY 638 STERS--VPRHHTGVDSLNCNFSPLARRVDRVAIYSEFLMRNGTQLON-----FTLD 689  
Db 1372 DTRMTVWAPPPSIDLTFNLVRYSPVKNED---VABLSISPSDNAVVLTLPLGTEYVWS. 1428  
QY 690 RSSVLVDGYSPNRNEPLTGNASADIOHSGGRSSLEGRFEOKLISEEDLNMH-----T 741  
Db 1429 VSSV-----YEOHSTPLRG-----RQKTGLDSTGIDFSD--ITANSFTVHWIAPRATIT 1477  
QY 742 GHHHHH 748  
Db 1478 GYRIRHH 1484

## RESULT 19

US-11-193-857-17  
Sequence 17, Application US/11193857  
Publication No. US20060024725A1  
GENERAL INFORMATION:  
APPLICANT: Hussa, Robert  
APPLICANT: Fisher-Colbrie, Mark  
APPLICANT: Hickok, Durlin  
APPLICANT: LaPointe, Jerome P.  
TITLE OF INVENTION: Oncofetal Fibronectin as Marker for Pregnancy-Related Indications  
FILE REFERENCE: 17101-026001/827  
CURRENT APPLICATION NUMBER: US/11/193,857  
CURRENT FILING DATE: 2005-07-29  
PRIOR APPLICATION NUMBER: 60/592,823  
PRIOR FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: 60/592,803  
PRIOR FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: 60/592,825  
PRIOR FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: 60/592,804  
PRIOR FILING DATE: 2004-07-30  
PRIOR APPLICATION NUMBER: 60/592,824  
PRIOR FILING DATE: 2004-07-30  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17  
LENGTH: 2421  
TYPE: PRT  
ORGANISM: Homo Sapiens  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: GenBank NM 212475  
DATABASE ENTRY DATE: 2005-06-10  
US-11-193-857-17

Query Match 3.0%; Score 118.5; DB 7; Length 2421;  
Best Local Similarity 18.9%; Pred. No. 1.3;  
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

19 SVSTTSTPGTPTVYLGAAS-----KTPASIFGPSAASHLLILFTLNFTITNLYE--- 67  
698 TTTTSTPTVNTVTGETTTPSPPLVATSEVTETASSFVSVWSASDITVSGFRVELS 757  
68 -----ENMFGSRKFNTERVQLGLRLPLFKNTSVGPLYSGRLT 107  
758 EGDPEQYLDLPSTATSVNIPDLLPGKRYVNVYQISEDEQSLILSTS----- 806  
108 LLRPEKDGATGVAICTHRPDPTGCLDREQLYLELSQLTHSITELGPVTLDRDSLX-- 165  
807 -----QTTAPDA-----PPDPTQVDDTTSIVVWRSRQAPIT---GYRI---VYSP 847

```
QY 166 -VNGFTHRSVPSTSTGVSEEBFTLNFTINRLYMADMGQSLKFNITDNVM---KHL 221
Db 848 SVESGSELNLPETANSV-----TLSDL-----QPG-VQYNTIYIAVEENQES 889
QY 222 LSLPFRSSLG-----ARYGCRVIALRSVKNGAET--RVDLLCTYLQPL 264
Db 890 TPVVIQOETTGTPRSPTVPSRDLQFVEVTDVKYIMWTPPESAVGYRVDVIVPNLPG 949
QY 265 SGPLPI-KQVFHELQOOTHGIT---RLGPSYDKDSLYLNGYNEPGDPEP-----PT 313
Db 950 HGQRLPISRNTFAEVTCGLSPGVYFKVFAVSHGRESKPLTAQOQTKLDAPTNLQFVNET 1009
QY 314 TPPEATFLPPLSEATAMGYHLKTLNFTINLQYSPDMGKSATFNSTEGVLQHLR 373
Db 1010 DSTVLVRWTTPRAQIT---GYRL-TVGLTRRGPRQY-----NVGPSVKYPLR 1054
QY 374 PLFQKSMGPFYLGCOLISLRPEKDG-AATGVDVDTCTYHDPDPVPGGLDIQOLYWELSQLT 432
Db 1055 NLQPAE-----YTVSLVAIKGNQESPKATGVFTT-----LQPGSSIPPYNTEVETT 1102
QY 433 HGVT-----QLGF-----YVL-----DR 445
Db 1103 IVITWTPAPRIGFKLGYRPSQGEAPREVTSDGSIIVVSGLTGPEVYVYTIQVLRDQGER 1162
QY 446 DSLFINGYA-----PQNLISIRGEYQINFIHVNMLSNPDPTSSEYITLLRDIQDKVTTYL 500
Db 1163 DAPIVNVKVTPLSPPTNLHLEANDPTGVLTVSWERSTTDPITGYRIT---TPPT 1213
QY 501 KGSQ-----LHDTFRCLVNTLT-----MDSVLVTVKALFSS 532
Db 1214 NGQGNLSLEEVHADQSSCTFDNLSPGLEYNVSVYTVKDKESVPSIDTIPEV-----1267
QY 533 NLDPQLVEQVFLDKT-LNASHFW--LGSTYQVLDIHVTEMESS-----VYQPTSSSSTQHF 585
Db 1268 ---POLTDLFSVDITDSSIGLRWTPLNSS-TIIGYRITVVAAGGIPFEDFVDSVGY- 1322
QY 586 YLNFITINLPSYQDKAQPGTNYQNRKNI-----EDALNQLFRNSSIKS-----YFSDQCV 637
Db 1323 ---YTVTGL-----EPG-IDYDISVITLNGESAPTTLTQQTAVPPPTDLRFTNIGP 1371
QY 638 STFRS--VPNRHHTGVDSLGNFSPARRVDRVAIYEEFLMRNQTQON-----FTLD 689
Db 1372 DTMRVTWAPPSIDLTNFLVRSYVKNKEED---VAELISPSDNAVLTNLLPGTEVVS 1428
QY 690 RSSVLVDGYSFNREPLTGNASADIQHGSGRSSLEGPRFEQKLISEEDLNMH-----T 741
Db 1429 VSSV---YEGHESTPLRG-----RQKTGLDSTPTGIDFSD--ITANSFTVHWIAPRATIT 1477
QY 742 GHHHHH 748
Db 1478 GYRIRHH 1484

RESULT 20
US-11-193-561-15
; Sequence 15, Application US/11193561
; Publication No. US20060024757A1
; GENERAL INFORMATION:
; APPLICANT: Husea, Robert
; TITLE OF INVENTION: Detection of Oncofetal Fibronectin for Selection of Concepti
; FILE REFERENCE: 17101-080001/831
; CURRENT APPLICATION NUMBER: US/11/193,561
; PRIOR FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: 60/592,823
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,803
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,825
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,804
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/592,824
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; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2477
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank NM 212482
; DATABASE ENTRY DATE: 2005-06-10
; US-11-193-561-15

Query Match 3.0%; Score 118.5; DB 7; Length 2477;
Best Local Similarity 18.9%; Pred. No. 1.4;
Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;

QY 19 SVSTTSTPGPTVYVLGAS-----KTPASIFGSPASASHLLILFTLNFTINLRYE---- 67
Db 698 TTTTSTPTVTSNTVTGTTTTPFPPLVATSESVTEITASSFVSVWSASDVTVSGRVEYELS 757
QY 68 -----ENMWPGSRKENTTTERVLQGLLRPLFKNTSVGPLYSGCLRT 107
Db 758 EGDPEQYLDLPSTATSVNIPDLLPGRKYIVNVYQISEDGEQSLILSTS----- 806
QY 108 LLRPEKDGATGVDAICTHRPDPTGCLDRQYLELSQLTHSITELGPTTLDRLSYL-- 165
Db 807 -----QTTAPDA-----PPDPTVOVDVTSIVVWSRPOAPIT---GYRI---VYSP 847
QY 166 -VNGFTHRSVPSTSTGVSEEBFTLNFTINRLYMADMGQSLKFNITDNVM---KHL 221
Db 848 SVESGSELNLPETANSV-----TLSDL-----QPG-VQYNTIYIAVEENQES 889
QY 222 LSLPFRSSLG-----ARYGCRVIALRSVKNGAET--RVDLLCTYLQPL 264
Db 890 TPVVIQOETTGTPRSPTVPSRDLQFVEVTDVKYIMWTPPESAVGYRVDVIVPNLPG 949
QY 265 SGPLPI-KQVFHELQOOTHGIT---RLGPSYDKDSLYLNGYNEPGDPEP-----PT 313
Db 950 HGQRLPISRNTFAEVTCGLSPGVYFKVFAVSHGRESKPLTAQOQTKLDAPTNLQFVNET 1009
QY 314 TPPEATFLPPLSEATAMGYHLKTLNFTINLQYSPDMGKSATFNSTEGVLQHLR 373
Db 1010 DSTVLVRWTTPRAQIT---GYRL-TVGLTRRGPRQY-----NVGPSVKYPLR 1054
QY 374 PLFQKSMGPFYLGCOLISLRPEKDG-AATGVDVDTCTYHDPDPVPGGLDIQOLYWELSQLT 432
Db 1055 NLQPAE-----YTVSLVAIKGNQESPKATGVFTT-----LQPGSSIPPYNTEVETT 1102
QY 433 HGVT-----QLGF-----YVL-----DR 445
Db 1103 IVITWTPAPRIGFKLGYRPSQGEAPREVTSDGSIIVVSGLTGPEVYVYTIQVLRDQGER 1162
QY 446 DSLFINGYA-----PQNLISIRGEYQINFIHVNMLSNPDPTSSEYITLLRDIQDKVTTYL 500
Db 1163 DAPIVNVKVTPLSPPTNLHLEANDPTGVLTVSWERSTTDPITGYRIT---TPPT 1213
QY 501 KGSQ-----LHDTFRCLVNTLT-----MDSVLVTVKALFSS 532
Db 1214 NGQGNLSLEEVHADQSSCTFDNLSPGLEYNVSVYTVKDKESVPSIDTIPEV-----1267
QY 533 NLDPQLVEQVFLDKT-LNASHFW--LGSTYQVLDIHVTEMESS-----VYQPTSSSSTQHF 585
Db 1268 ---POLTDLFSVDITDSSIGLRWTPLNSS-TIIGYRITVVAAGGIPFEDFVDSVGY- 1322
QY 586 YLNFITINLPSYQDKAQPGTNYQNRKNI-----EDALNQLFRNSSIKS-----YFSDQCV 637
Db 1323 ---YTVTGL-----EPG-IDYDISVITLNGESAPTTLTQQTAVPPPTDLRFTNIGP 1371
QY 638 STFRS--VPNRHHTGVDSLGNFSPARRVDRVAIYEEFLMRNQTQON-----FTLD 689
Db 1372 DTMRVTWAPPSIDLTNFLVRSYVKNKEED---VAELISPSDNAVLTNLLPGTEVVS 1428
QY 690 RSSVLVDGYSFNREPLTGNASADIQHGSGRSSLEGPRFEQKLISEEDLNMH-----T 741
```

Db	1429	VSSV----	YEQHES	PLRG-----	RQKTGLD	SPTGID	FSD--	ITANS	FTVH	WIAP	RATIT	1477
Qy	742	GHHHHH	748									
Db	1478	GYIRHH	1484									

Search completed: March 20, 2006, 07:32:41  
Job time : 15.0158 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:31:52 ; Search time 132.781 Seconds  
(without alignments)  
2353.772 Million cell updates/sec

Title: US-10-687-035-1

Perfect score: 3945

Sequence: 1 AAQARRARTKLFTHRSV.....QKLSEEDLNMHTGHHHHH 748

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications\_AA\_Main:\*

- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3945	100.0	748	5	US-10-687-035-1
2	3904.5	99.0	809	5	US-10-687-035-2
3	3665	92.9	6995	5	US-10-983-340-4
4	3663	92.9	833	3	US-09-884-441-389
5	3663	92.9	833	3	US-09-907-969-389
6	3663	92.9	833	3	US-09-827-271-389
7	3663	92.9	833	4	US-10-198-053-389
8	3663	92.9	833	5	US-10-860-790-389
9	3663	92.9	914	3	US-09-778-320-206
10	3663	92.9	914	3	US-09-910-689-206
11	3663	92.9	914	3	US-09-884-441-312
12	3663	92.9	914	3	US-09-884-441-478
13	3663	92.9	914	3	US-09-907-969-312
14	3663	92.9	914	3	US-09-907-969-478
15	3663	92.9	914	3	US-09-827-271-312
16	3663	92.9	914	4	US-10-010-742-206
17	3663	92.9	914	4	US-10-198-053-312
18	3663	92.9	914	4	US-10-198-053-478
19	3663	92.9	914	4	US-10-714-389-206
20	3663	92.9	914	4	US-10-717-296-206
21	3663	92.9	914	5	US-10-860-790-312
22	3663	92.9	914	5	US-10-860-790-478
23	3658	92.7	1899	4	US-10-142-515-5
24	3658	92.7	1890	4	US-10-097-340-217
25	3658	92.7	1890	4	US-10-245-871-314
26	3658	92.7	1890	4	US-10-253-286-314
27	3658	92.7	1890	6	US-11-050-926-217
28	3651	92.5	3451	3	US-09-907-969-595
29	3651	92.5	3451	4	US-10-198-053-595
30	3651	92.5	3451	5	US-10-860-790-595
31	3649	92.5	1148	3	US-09-965-738-48
32	3649	92.5	2248	3	US-09-965-738-50
33	3649	92.5	11721	3	US-09-965-738-162
34	3649	92.5	22152	4	US-10-715-066-5
35	3642	92.3	1148	3	US-09-884-441-458
36	3642	92.3	1148	3	US-09-884-441-479
37	3642	92.3	1148	3	US-09-907-969-458
38	3642	92.3	1148	3	US-09-907-969-479
39	3642	92.3	1148	3	US-09-827-271-458
40	3642	92.3	1148	4	US-10-097-340-216
41	3642	92.3	1148	4	US-10-198-053-458
42	3642	92.3	1148	4	US-10-198-053-479
43	3642	92.3	1148	4	US-10-257-021-56
44	3642	92.3	1148	4	US-10-383-368-2
45	3642	92.3	1148	4	US-10-734-564-131
46	3642	92.3	1148	5	US-10-860-790-458
47	3642	92.3	1148	5	US-10-860-790-479
48	3642	92.3	1148	5	US-10-936-626-129
49	3642	92.3	1148	5	US-10-938-061-129
50	3642	92.3	1148	6	US-11-050-926-216
51	3642	92.3	1156	3	US-09-884-441-459
52	3642	92.3	1156	3	US-09-907-969-459
53	3642	92.3	1156	3	US-09-827-271-459
54	3642	92.3	1156	4	US-10-198-053-459
55	3642	92.3	1156	5	US-10-860-790-459
56	3616	91.7	1148	3	US-09-932-419-2
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58	3189	80.8	772	3	US-09-907-969-388
59	3189	80.8	772	3	US-09-827-271-388
60	3189	80.8	772	4	US-10-198-053-388
61	3189	80.8	772	5	US-10-860-790-388
62	3166.5	80.3	1783	4	US-10-097-340-214
63	3166.5	80.3	1783	6	US-11-050-926-214
64	2743	69.5	583	4	US-10-142-515-4
65	2545	63.0	545	4	US-10-243-243A-4
66	2484	63.0	9799	3	US-09-965-738-146
67	2445	62.0	526	4	US-10-333-900-30
68	2018	51.2	2234	4	US-10-612-090-20
69	2000	50.7	439	3	US-09-965-738-148
70	1996	50.6	438	3	US-09-884-441-483
71	1996	50.6	438	3	US-09-907-969-483
72	1996	50.6	438	4	US-10-198-053-483
73	1996	50.6	438	5	US-10-860-790-483
74	1990	50.4	438	3	US-09-884-441-390
75	1990	50.4	438	3	US-09-907-969-390
76	1990	50.4	438	3	US-09-827-271-390
77	1990	50.4	438	4	US-10-198-053-390
78	1990	50.4	438	4	US-10-333-900-19
79	1990	50.4	438	5	US-10-860-790-390
80	1980.5	50.2	456	5	US-10-858-412-226
81	1931	48.9	367	4	US-10-333-900-27
82	1830	46.4	396	5	US-10-858-412-225
83	1615	40.9	5877	4	US-10-142-515-11
84	1615	40.9	5935	4	US-10-243-243A-8
85	1601.5	40.6	909	3	US-09-965-738-69
86	1591	40.3	1366	3	US-09-965-738-47
87	1558	39.5	1362	4	US-10-142-515-8
88	1542	39.1	780	3	US-09-965-738-159
89	1518	38.5	780	3	US-09-965-738-158
90	1436	36.4	304	3	US-09-884-441-486
91	1436	36.4	304	3	US-09-907-969-486
92	1436	36.4	304	4	US-10-198-053-486
93	1436	36.4	304	5	US-10-860-790-486
94	1406	35.6	624	3	US-09-965-738-160
95	1346.5	34.1	594	3	US-09-965-738-71
96	1345	34.1	318	3	US-09-907-969-594
97	1345	34.1	318	4	US-10-198-053-594
98	1345	34.1	318	5	US-10-860-790-594
99	1306	33.1	597	3	US-09-965-738-78
100	1284.5	32.6	525	3	US-09-965-738-70

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ALIGNMENTS
Db 541 QVFLDKTLNAGFWHLGSTYQLVDIHVTEMESSYQPTSSSTQHFYLNFTITNLPSYQDK 600
Qy 601 AOPGTNNYQNKENIEDALNQLFRNSSIKSYRSDCOVSTFRSPVNRHHTGVDLSLCPSP 660
Db 601 AOPGTNNYQNKENIEDALNQLFRNSSIKSYRSDCOVSTFRSPVNRHHTGVDLSLCPSP 660
Qy 661 ARVDRVAIYEELRMRTRNGTQLQNFTRDRSSVLDGYSNNRNEPLTGNASADIQHSGGRS 720
Db 661 ARVDRVAIYEELRMRTRNGTQLQNFTRDRSSVLDGYSNNRNEPLTGNASADIQHSGGRS 720
Qy 721 SLEGPREFEQLISEEDLNMTGHHHHH 748
Db 721 SLEGPREFEQLISEEDLNMTGHHHHH 748

RESULT 2
US-10-687-035-2
; Sequence 2, Application US/10687035
; Publication No. US20050064518A1
; GENERAL INFORMATION:
; APPLICANT: Albione, Earl F.
; APPLICANT: Soltis, Daniel A.
; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
; TITLE OF INVENTION: CA 125/0772P AND METHODS OF USE THEREOF
; FILE REFERENCE: 6750-214-999
; CURRENT APPLICATION NUMBER: US/10/687,035
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/485,986
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 60/418,828
; PRIOR FILING DATE: 2003-10-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CA 125/0772P 3-repeat TM
US-10-687-035-2

Query Match 99.0%; Score 3904.5; DB 5; Length 809;
Best Local Similarity 92.5%; Pred. No. 7e-309;
Matches 748; Conservative 0; Mismatches 0; Indels 61; Gaps 1;

Qy 1 AAQPARARATKLFTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFT 60
Db 1 AAQPARARATKLFTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFT 60
Qy 61 ITNLRYEENWMPGSRKENTTERRVLOGLLRPLFKNTSVGLYSGCRLTLRLPEKDGATGV 120
Db 61 ITNLRYEENWMPGSRKENTTERRVLOGLLRPLFKNTSVGLYSGCRLTLRLPEKDGATGV 120
Qy 121 DAICTHRPDPGPGLDREQLYLELSQTHSITELGPTVLDLDRSDLYVNGFTHRSSVPTTST 180
Db 121 DAICTHRPDPGPGLDREQLYLELSQTHSITELGPTVLDLDRSDLYVNGFTHRSSVPTTST 180
Qy 181 GVWSEEPFTLNFTINNRYMADMGQPSGLKFNITDNYMKHLLSPLFORSSIGARYTGCRV 240
Db 181 GVWSEEPFTLNFTINNRYMADMGQPSGLKFNITDNYMKHLLSPLFORSSIGARYTGCRV 240
Qy 241 IALRSVKNAGATRVLLCTYLOPLSGPGLPIKQVFHLSQOQTHGITRLGYSLDKDSL 300
Db 241 IALRSVKNAGATRVLLCTYLOPLSGPGLPIKQVFHLSQOQTHGITRLGYSLDKDSL 300
Qy 301 NGYNEPGDEPPTPKATTFPLPLSEATTAMGVHKLTLTNFTISNLQYSPDMGKGSAT 360
Db 301 NGYNEPGDEPPTPKATTFPLPLSEATTAMGVHKLTLTNFTISNLQYSPDMGKGSAT 360
Qy 361 FNSTEGVLOHLLRPLFOKSSMPYLGCOLISLPEKDGATGVDTTCTTHPDVPGGLD 420
Db 361 FNSTEGVLOHLLRPLFOKSSMPYLGCOLISLPEKDGATGVDTTCTTHPDVPGGLD 420
Qy 421 IQQLYWELSQLTHGVTOGLGFVLDLDRSLFINGYAPQNLISIRGEYQINFI VNNLNSNDP 480
Db 421 IQQLYWELSQLTHGVTOGLGFVLDLDRSLFINGYAPQNLISIRGEYQINFI VNNLNSNDP 480
Qy 481 TSSEYITLLRDIQKVITLYKGSQHLDTFRCLVNTLMDSVITVVKALFSSNLDPSLVE 540
Db 481 TSSEYITLLRDIQKVITLYKGSQHLDTFRCLVNTLMDSVITVVKALFSSNLDPSLVE 540
Qy 541 QVFLDKTLNAGFWHLGSTYQLVDIHVTEMESSYQPTSSSTQHFYLNFTITNLPSYQDK 600
Db 541 QVFLDKTLNAGFWHLGSTYQLVDIHVTEMESSYQPTSSSTQHFYLNFTITNLPSYQDK 600
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QY 421 IQQLYHLSQTHGVTQGLGPFYVLDRLSLFNGVAPQNLSTIRGEYQINFHIVNNLSNPD 480  
Db 421 IQQLYHLSQTHGVTQGLGPFYVLDRLSLFNGVAPQNLSTIRGEYQINFHIVNNLSNPD 480  
QY 481 TSSEYITLLRDIDQKVTLLKGSQSLDHTFRCLVTLNLTWDSVLVTVKALFSSNLDPSLVE 540  
Db 481 TSSEYITLLRDIDQKVTLLKGSQSLDHTFRCLVTLNLTWDSVLVTVKALFSSNLDPSLVE 540  
QY 541 QVFLDKTLNASFWLGSYQVLDIHTVEMESSYVQPTSSSTQHFLNFTITNLPSQDK 600  
Db 541 QVFLDKTLNASFWLGSYQVLDIHTVEMESSYVQPTSSSTQHFLNFTITNLPSQDK 600  
QY 601 AQPGTTNYQRKNIEDALNQLFRNSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNPSPL 660  
Db 601 AQPGTTNYQRKNIEDALNQLFRNSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNPSPL 660  
QY 661 ARVDRAVAYEEFLMTRNGTQNLFTLDRSSVLVDGYSNNRNEPLTG----- 708  
Db 661 ARVDRAVAYEEFLMTRNGTQNLFTLDRSSVLVDGYSNNRNEPLTG----- 708  
QY 709 -----NSADIQHSGR 719  
Db 721 GLAGLLGLITCLICGLVLTTRRRKGEYNNVQCCPGYQSHLDLQNSADIQHSGR 780  
QY 720 SSLEGRFQKLISEEDLNHHTGHHHH 748  
Db 781 SSLEGRFQKLISEEDLNHHTGHHHH 809

RESULT 3  
US-10-983-340-4  
; Sequence 4, Application US/10983340  
; Publication No. US20050238649A1  
; GENERAL INFORMATION:  
; APPLICANT: Doronina, Svetlana O.  
; APPLICANT: Toki, Brian E.  
; APPLICANT: Senter, Peter D.  
; APPLICANT: Ebens, Allen J.  
; APPLICANT: Polakis, Paul  
; APPLICANT: Sliwowski, Mark X.  
; APPLICANT: Spencer, Susan D.  
; APPLICANT: Kline, Toni Beth  
; TITLE OF INVENTION: MONOMETHYLVALINE COMPOUNDS CAPABLE OF CONJUGATION TO LIGANDS  
; FILE REFERENCE: 018991-001020US  
; CURRENT APPLICATION NUMBER: US/10/983,340  
; CURRENT FILING DATE: 2004-11-05  
; PRIOR FILING DATE: 2004-08-04  
; PRIOR APPLICATION NUMBER: US 60/598,899  
; PRIOR FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER: US 60/518,534  
; PRIOR FILING DATE: 2003-11-06  
; NUMBER OF SEQ ID NOS: 35  
; SEQ ID NO 4  
; LENGTH: 6995  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-983-340-4

Query Match 92.9%; Score 3665; DB 5; Length 6995;  
Best Local Similarity 99.9%; Pred. No. 6.8e-288;  
Matches 696; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTHRSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTNLFTITNLRYEENWPG 73  
Db 6240 FTHRSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTNLFTITNLRYEENWPG 6299  
QY 74 SRKFNTTERTVQLGLRPLFKNTSVGLYSGCRLLTLRPEKGEATGVDAICTHRPDPG 133  
Db 6300 SRKFNTTERTVQLGLRPLFKNTSVGLYSGCRLLTLRPEKGEATGVDAICTHRPDPG 6359  
QY 134 GLDRQLYLELSQTHSITELGPYTLDRSLYNGFTHRSSVPTTSTGVVSEBPFTLNFT 193

Db 6360 GLDRQLYLELSQTHSITELGPYTLDRSLYNGFTHRSSVPTTSTGVVSEBPFTLNFT 6419  
QY 194 INNLRYADMGGPGSLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNAGETR 253  
Db 6420 INNLRYADMGGPGSLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKNAGETR 6479  
QY 254 VDLCTYLOPLSGPGLPIKQVPHLSQQTHGTRGLPYSLDKDSLYNGNEPGBEPPT 313  
Db 6480 VDLCTYLOPLSGPGLPIKQVPHLSQQTHGTRGLPYSLDKDSLYNGNEPGBEPPT 6539  
QY 314 TRKPATTFPLPPISEATTANGYHLKTLTANFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 373  
Db 6540 TRKPATTFPLPPISEATTANGYHLKTLTANFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 6599  
QY 374 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIQQLYHLSQTH 433  
Db 6600 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIQQLYHLSQTH 6659  
QY 434 GVTQLGFFVLDRLDRLPFIYAPQNLSTIRGEYQINFHIVNNLSNPDPTSSSEYITLLRDIQ 493  
Db 6660 GVTQLGFFVLDRLDRLPFIYAPQNLSTIRGEYQINFHIVNNLSNPDPTSSSEYITLLRDIQ 6719  
QY 494 DKVTTLKGSQSLDHTFRCLVTLNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553  
Db 6720 DKVTTLKGSQSLDHTFRCLVTLNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 6779  
QY 554 WLGSTYQLVDIHTVEMESSYVQPTSSSTQHFLNFTITNLPSQDKAQPCTTNYQRNKR 613  
Db 6780 WLGSTYQLVDIHTVEMESSYVQPTSSSTQHFLNFTITNLPSQDKAQPCTTNYQRNKR 6839  
QY 614 NIEDALNQLFRNSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNPSPLARRVDRVAIYEEF 673  
Db 6840 NIEDALNQLFRNSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNPSPLARRVDRVAIYEEF 6899  
QY 674 LRWTRNGTOLQNLFTLDRSSVLVDGYSNNRNEPLTGNS 710  
Db 6900 LRWTRNGTOLQNLFTLDRSSVLVDGYSNNRNEPLTGNS 6936

RESULT 4  
US-09-884-441-389  
; Sequence 389, Application US/09884441  
; Patent No. US20020119158A1  
; GENERAL INFORMATION:  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Carter, Darrick  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C7  
; CURRENT APPLICATION NUMBER: US/09/884,441  
; CURRENT FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 489  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 389  
; LENGTH: 833  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-884-441-389

Query Match 92.9%; Score 3663; DB 3; Length 833;  
Best Local Similarity 99.9%; Pred. No. 3.6e-289;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTNLFTITNLRYEENWPG 73  
Db 78 FTHRSVSTSTPGTPTVYLGASKTPASIFGSPAASHLLILFTNLFTITNLRYEENWPG 137  
QY 74 SRKFNTTERTVQLGLRPLFKNTSVGLYSGCRLLTLRPEKGEATGVDAICTHRPDPG 133  
Db 138 SRKFNTTERTVQLGLRPLFKNTSVGLYSGCRLLTLRPEKGEATGVDAICTHRPDPG 197  
QY 134 GLDRQLYLELSQTHSITELGPYTLDRSLYNGFTHRSSVPTTSTGVVSEBPFTLNFT 193

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Db 198 GLDREQLYELSQLTHSITELGPTVTLDRDLSYNGFTHRSSVPTTSTGVVSEBPTTLNFT 257
Qy 194 INNLRYMADMGQPSGLKFNTIDNMVKHLLSPLFORSSLGARYTGCRRVIALRSVKNQGAETR 253
Db 258 INNLRYMADMGQPSGLKFNTIDNMVKHLLSPLFORSSLGARYTGCRRVIALRSVKNQGAETR 317
Qy 254 VDLCTYQLPSGPGPLPIKQVFHELSSQTHGIRLGPYSLDKDSLYLNGYNEPGPDEPPT 313
Db 318 VDLCTYQLPSGPGPLPIKQVFHELSSQTHGIRLGPYSLDKDSLYLNGYNEPGPDEPPT 377
Qy 314 TPXPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDMGKGSATFNSSTEGVLQHLR 373
Db 378 TPXPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDMGKGSATFNSSTEGVLQHLR 437
Qy 374 PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIOQLYWELSOLTH 433
Db 438 PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIOQLYWELSOLTH 497
Qy 434 GVTQLGYVLDROSLFNGVAPQNLISIRGEYQINFIHVNWNLSNPDPPTSSEYITLLRDIQ 493
Db 498 GVTQLGYVLDROSLFNGVAPQNLISIRGEYQINFIHVNWNLSNPDPPTSSEYITLLRDIQ 557
Qy 494 DKVTTLKYGSQLDHTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 558 DKVTTLKYGSQLDHTFRFCLVTNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 617
Qy 554 WLGSSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNYQRNKR 613
Db 618 WLGSSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNYQRNKR 677
Qy 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPNRHHTGVDSLCNFSPLARRVDRVAIYEEF 673
Db 678 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPNRHHTGVDSLCNFSPLARRVDRVAIYEEF 737
Qy 674 LRMRNGTQLQNFTLDRSSVLVDGYSPNRNEPLTGN 710
Db 738 LRMRNGTQLQNFTLDRSSVLVDGYSPNRNEPLTGN 774

RESULT 5
US-09-907-969-389
; Sequence 389, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Hill, Paul
; APPLICANT: Albone, Earl
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/09/907,969
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-907-969-389

Query Match 92.9%; Score 3663; DB 3; Length 833;
Best Local Similarity 99.9%; Pred. No. 3.6e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 14 FTHRSSVSTTSTPGTPTVYLGAASKTPASIFGSAASHLLILFTLNTITNLRBYENMWPG 73

RESULT 6
US-09-827-271-389
; Sequence 389, Application US/09827271
; Publication No. US20030165504A1
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-827-271-389

Query Match 92.9%; Score 3663; DB 3; Length 833;
Best Local Similarity 99.9%; Pred. No. 3.6e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 14 FTHRSSVSTTSTPGTPTVYLGAASKTPASIFGSAASHLLILFTLNTITNLRBYENMWPG 73
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Db 78 FTHRSSVTTSTPGTPTVYLGASKTSPASIFGPPSAASHLLILFTLNFTITNLRYEENWMPG 137  
Qy 74 SRKFNTERVLOGLRLRPLFKNTSVGPLYSGCRLTLRPEKDGATGVDALCTHRPDPGTP 133  
Db 138 SRKFNTERVLOGLRLRPLFKNTSVGPLYSGCRLTLRPEKDGATGVDALCTHRPDPGTP 197  
Qy 134 GLDREQLYLELSQTHSITELGPTTLDRDLSLYNGFTHRSSVPTTSTGVVSEBPPFTLNFT 193  
Db 198 GLDREQLYLELSQTHSITELGPTTLDRDLSLYNGFTHRSSVPTTSTGVVSEBPPFTLNFT 257  
Qy 194 INNLRYMADMGQPSGLKFNTDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 253  
Db 258 INNLRYMADMGQPSGLKFNTDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 317  
Qy 254 VDLCTYLOPLSGPLPIKQVPHLSQTHGIRLGPYSLDKDLSLYNGNBPDPBPPT 313  
Db 318 VDLCTYLOPLSGPLPIKQVPHLSQTHGIRLGPYSLDKDLSLYNGNBPDPBPPT 377  
Qy 314 TPXPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSMDMGKGSATFNSSTEGVLOHLR 373  
Db 378 TPXPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSMDMGKGSATFNSSTEGVLOHLR 437  
Qy 374 PLFQKSSMGPFYLGCOLISLRPEKDGATGVDCTTCTHPPDPVGPGLDIOQLYWELSQLTH 433  
Db 438 PLFQKSSMGPFYLGCOLISLRPEKDGATGVDCTTCTHPPDPVGPGLDIOQLYWELSQLTH 497  
Qy 434 GVTOLGFVLDRLSLFINGAPQNLISIRGEYQINFIHVNWNLNPNPDPSTSEYITLLRDIQ 493  
Db 498 GVTOLGFVLDRLSLFINGAPQNLISIRGEYQINFIHVNWNLNPNPDPSTSEYITLLRDIQ 557  
Qy 494 DKVTTLKGSQSLHDTFRCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553  
Db 558 DKVTTLKGSQSLHDTFRCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 617  
Qy 554 WLGSSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 613  
Db 618 WLGSSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 677  
Qy 614 NIEDALNQLFRNSIKSYFSDCQVSTFRSPNRRHTGVDLSLNCNPSPLARVDRVAIYEEF 673  
Db 678 NIEDALNQLFRNSIKSYFSDCQVSTFRSPNRRHTGVDLSLNCNPSPLARVDRVAIYEEF 737  
Qy 674 LRMRNGTQLQNFTRDRSSVLVDGYSNRPNEPLTGN 710  
Db 738 LRMRNGTQLQNFTRDRSSVLVDGYSNRPNEPLTGN 774

## RESULT 7

US-10-198-053-389  
; Sequence 389, Application US/10198053  
; Publication No. US20030124140A1  
; GENERAL INFORMATION:  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Hill, Paul  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C9  
; CURRENT APPLICATION NUMBER: US/10/198,053  
; CURRENT FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 624  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 389  
; LENGTH: 833  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-198-053-389

Query Match 92.9%; Score 3663; DB 4; Length 833;  
Best Local Similarity 99.9%; Pred. No. 3.6e-289;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVTTSTPGTPTVYLGASKTSPASIFGPPSAASHLLILFTLNFTITNLRYEENWMPG 73  
Db 78 FTHRSSVTTSTPGTPTVYLGASKTSPASIFGPPSAASHLLILFTLNFTITNLRYEENWMPG 137  
Qy 74 SRKFNTERVLOGLRLRPLFKNTSVGPLYSGCRLTLRPEKDGATGVDALCTHRPDPGTP 133  
Db 138 SRKFNTERVLOGLRLRPLFKNTSVGPLYSGCRLTLRPEKDGATGVDALCTHRPDPGTP 197  
Qy 134 GLDREQLYLELSQTHSITELGPTTLDRDLSLYNGFTHRSSVPTTSTGVVSEBPPFTLNFT 193  
Db 198 GLDREQLYLELSQTHSITELGPTTLDRDLSLYNGFTHRSSVPTTSTGVVSEBPPFTLNFT 257  
Qy 194 INNLRYMADMGQPSGLKFNTDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 253  
Db 258 INNLRYMADMGQPSGLKFNTDNVMKHLSPFORSSLGARYTGCRRVIALRSVKNAGETR 317  
Qy 254 VDLCTYLOPLSGPLPIKQVPHLSQTHGIRLGPYSLDKDLSLYNGNBPDPBPPT 313  
Db 318 VDLCTYLOPLSGPLPIKQVPHLSQTHGIRLGPYSLDKDLSLYNGNBPDPBPPT 377  
Qy 314 TPXPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSMDMGKGSATFNSSTEGVLOHLR 373  
Db 378 TPXPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSMDMGKGSATFNSSTEGVLOHLR 437  
Qy 374 PLFQKSSMGPFYLGCOLISLRPEKDGATGVDCTTCTHPPDPVGPGLDIOQLYWELSQLTH 433  
Db 438 PLFQKSSMGPFYLGCOLISLRPEKDGATGVDCTTCTHPPDPVGPGLDIOQLYWELSQLTH 497  
Qy 434 GVTOLGFVLDRLSLFINGAPQNLISIRGEYQINFIHVNWNLNPNPDPSTSEYITLLRDIQ 493  
Db 498 GVTOLGFVLDRLSLFINGAPQNLISIRGEYQINFIHVNWNLNPNPDPSTSEYITLLRDIQ 557  
Qy 494 DKVTTLKGSQSLHDTFRCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553  
Db 558 DKVTTLKGSQSLHDTFRCLVNTLWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 617  
Qy 554 WLGSSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 613  
Db 618 WLGSSTYQLVDIHVTMESSYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 677  
Qy 614 NIEDALNQLFRNSIKSYFSDCQVSTFRSPNRRHTGVDLSLNCNPSPLARVDRVAIYEEF 673  
Db 678 NIEDALNQLFRNSIKSYFSDCQVSTFRSPNRRHTGVDLSLNCNPSPLARVDRVAIYEEF 737  
Qy 674 LRMRNGTQLQNFTRDRSSVLVDGYSNRPNEPLTGN 710  
Db 738 LRMRNGTQLQNFTRDRSSVLVDGYSNRPNEPLTGN 774

## RESULT 8

US-10-860-790-389  
; Sequence 389, Application US/10860790  
; Publication No. US20050031634A1  
; GENERAL INFORMATION:  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Hill, Paul  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C11  
; CURRENT APPLICATION NUMBER: US/10/860,790  
; CURRENT FILING DATE: 2004-06-02  
; NUMBER OF SEQ ID NOS: 624  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 389  
; LENGTH: 833  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-860-790-389

Query Match 92.9%; Score 3663; DB 5; Length 833;

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; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-778-320-206

Query Match      92.9%; Score 3663; DB 3; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPGSAASHLLILFTLNTITNLRVEENWMPG 73
Db 78 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPGSAASHLLILFTLNTITNLRVEENWMPG 137
Qy 74 SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGDAICTHRPDPTGP 133
Db 138 SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGDAICTHRPDPTGP 197
Qy 134 GLDREQLYLELSQTHSITELGPTTLDRLSYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 198 GLDREQLYLELSQTHSITELGPTTLDRLSYNGFTHRSSVPTTSTGVVSEEPFTLNFT 257
Qy 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTGCRIALRSVKNQGAETR 253
Db 258 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTGCRIALRSVKNQGAETR 317
Qy 254 VLLCTYLOPLSGPLPIKQVFHELSTQTHGITRLGFSYLDKDSLYLNGYNEPGDEPPT 313
Db 318 VLLCTYLOPLSGPLPIKQVFHELSTQTHGITRLGFSYLDKDSLYLNGYNEPGDEPPT 377
Qy 314 TPKEPATTFLPPLSEATTAMGYHLKTLTNTFTISNLQYSPDMGKGSATFNSSTGVLOHLLR 373
Db 378 TPKEPATTFLPPLSEATTAMGYHLKTLTNTFTISNLQYSPDMGKGSATFNSSTGVLOHLLR 437
Qy 374 PLFQKSSMGPFYLGCLISLRPEKDGATGVTCTTCTVHPDPVGPGLDIQQLYWELSQLTH 433
Db 438 PLFQKSSMGPFYLGCLISLRPEKDGATGVTCTTCTVHPDPVGPGLDIQQLYWELSQLTH 497
Qy 434 GVTOLGFVLDRLSLFNGVAPQNLISIRGEYQINFIHVNWNLSPDPTSEYITLLRDIQ 493
Db 498 GVTOLGFVLDRLSLFNGVAPQNLISIRGEYQINFIHVNWNLSPDPTSEYITLLRDIQ 557
Qy 494 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTLNASFH 553
Db 558 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTLNASFH 617
Qy 554 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 613
Db 618 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 677
Qy 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLGNFPLARRVDRVAIYEFP 673
Db 678 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLGNFPLARRVDRVAIYEFP 737
Qy 674 LRMTNRGTQLQNFTLDRSSVLVDGYFPNREPLTGN 710
Db 738 LRMTNRGTQLQNFTLDRSSVLVDGYFPNREPLTGN 774

RESULT 9
US-09-778-320-206
; Sequence 206, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongrong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C5
; CURRENT APPLICATION NUMBER: US/09/778,320
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 914

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; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-778-320-206

Query Match      92.9%; Score 3663; DB 3; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPGSAASHLLILFTLNTITNLRVEENWMPG 73
Db 159 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPGSAASHLLILFTLNTITNLRVEENWMPG 218
Qy 74 SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGDAICTHRPDPTGP 133
Db 219 SRKFNTERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGDAICTHRPDPTGP 278
Qy 134 GLDREQLYLELSQTHSITELGPTTLDRLSYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPTTLDRLSYNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
Qy 194 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTGCRIALRSVKNQGAETR 253
Db 339 INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSLGARYTGCRIALRSVKNQGAETR 398
Qy 254 VLLCTYLOPLSGPLPIKQVFHELSTQTHGITRLGFSYLDKDSLYLNGYNEPGDEPPT 313
Db 399 VLLCTYLOPLSGPLPIKQVFHELSTQTHGITRLGFSYLDKDSLYLNGYNEPGDEPPT 458
Qy 314 TPKEPATTFLPPLSEATTAMGYHLKTLTNTFTISNLQYSPDMGKGSATFNSSTGVLOHLLR 373
Db 459 TPKEPATTFLPPLSEATTAMGYHLKTLTNTFTISNLQYSPDMGKGSATFNSSTGVLOHLLR 518
Qy 374 PLFQKSSMGPFYLGCLISLRPEKDGATGVTCTTCTVHPDPVGPGLDIQQLYWELSQLTH 433
Db 519 PLFQKSSMGPFYLGCLISLRPEKDGATGVTCTTCTVHPDPVGPGLDIQQLYWELSQLTH 578
Qy 434 GVTOLGFVLDRLSLFNGVAPQNLISIRGEYQINFIHVNWNLSPDPTSEYITLLRDIQ 493
Db 579 GVTOLGFVLDRLSLFNGVAPQNLISIRGEYQINFIHVNWNLSPDPTSEYITLLRDIQ 638
Qy 494 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTLNASFH 553
Db 639 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTLNASFH 698
Qy 554 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 613
Db 699 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 758
Qy 614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLGNFPLARRVDRVAIYEFP 673
Db 759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDLSLGNFPLARRVDRVAIYEFP 818
Qy 674 LRMTNRGTQLQNFTLDRSSVLVDGYFPNREPLTGN 710
Db 819 LRMTNRGTQLQNFTLDRSSVLVDGYFPNREPLTGN 855

RESULT 10
US-09-910-689-206
; Sequence 206, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongrong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C6

```

; CURRENT APPLICATION NUMBER: US/09/910,689  
; CURRENT FILING DATE: 2001-07-20  
; NUMBER OF SEQ ID NOS: 307  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 206  
; LENGTH: 914  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-910-689-206

Query Match 92.9%; Score 3663; DB 3; Length 914;  
Best Local Similarity 99.9%; Pred. No. 4.2e-289;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	14	FTHRSSVSTTSGTPTVYLGASKTPASIFGSAASHLLILFTLNTITNLRYEENWPG	73
DB	159	FTHRSSVSTTSGTPTVYLGASKTPASIFGSAASHLLILFTLNTITNLRYEENWPG	218
QY	74	SRKFNTERVLOGLLRPLPKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDP	133
DB	219	SRKFNTERVLOGLLRPLPKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDP	278
QY	134	GLDREQLYLELSQTHSITELGPTTLDRDLSLVNGFTHRSSVPTTSTGVVSEBEP	193
DB	279	GLDREQLYLELSQTHSITELGPTTLDRDLSLVNGFTHRSSVPTTSTGVVSEBEP	338
QY	194	INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKGAE	253
DB	339	INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKGAE	398
QY	254	VDLLCTYQLPSGPGPLPIKQVFHELSQOHTGITRLGPYSLDKDSLYLNGYNE	313
DB	399	VDLLCTYQLPSGPGPLPIKQVFHELSQOHTGITRLGPYSLDKDSLYLNGYNE	458
QY	314	TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSPDMGKGSATFNS	373
DB	459	TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSPDMGKGSATFNS	518
QY	374	PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIO	433
DB	519	PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIO	578
QY	434	GVTLGFGYVLDRLDPLFNGYAPQNLISIRGEYQINFIHVNWNLSPDPTSE	493
DB	579	GVTLGFGYVLDRLDPLFNGYAPQNLISIRGEYQINFIHVNWNLSPDPTSE	638
QY	494	DKVTTLKGSQSLDHTFRCLVNTLTMDSVLVTVKALFSSNLDPSLYEQVFL	553
DB	639	DKVTTLKGSQSLDHTFRCLVNTLTMDSVLVTVKALFSSNLDPSLYEQVFL	698
QY	554	WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAOPGT	613
DB	699	WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAOPGT	758
QY	614	NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLNCNFSPLARR	673
DB	759	NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLNCNFSPLARR	818
QY	674	LRMTRNGTOLQNFTRDRSSVLVDGYSPNRNEPLTGNS	710
DB	819	LRMTRNGTOLQNFTRDRSSVLVDGYSPNRNEPLTGNS	855

RESULT 11  
US-09-884-441-312  
; Sequence 312, Application US/09884441  
; Patent No. US20020119158A1  
; GENERAL INFORMATION:  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Carter, Darrick  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C7

; CURRENT APPLICATION NUMBER: US/09/884,441.  
; CURRENT FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 489  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 312  
; LENGTH: 914  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-884-441-312

Query Match 92.9%; Score 3663; DB 3; Length 914;  
Best Local Similarity 99.9%; Pred. No. 4.2e-289;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	14	FTHRSSVSTTSGTPTVYLGASKTPASIFGSAASHLLILFTLNTITNLRYEENWPG	73
DB	159	FTHRSSVSTTSGTPTVYLGASKTPASIFGSAASHLLILFTLNTITNLRYEENWPG	218
QY	74	SRKFNTERVLOGLLRPLPKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDP	133
DB	219	SRKFNTERVLOGLLRPLPKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDP	278
QY	134	GLDREQLYLELSQTHSITELGPTTLDRDLSLVNGFTHRSSVPTTSTGVVSEBEP	193
DB	279	GLDREQLYLELSQTHSITELGPTTLDRDLSLVNGFTHRSSVPTTSTGVVSEBEP	338
QY	194	INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKGAE	253
DB	339	INNLRYMADMGQPSGLKFNITDNVMKHLSPFORSSLGARYTGCRIALRSVKGAE	398
QY	254	VDLLCTYQLPSGPGPLPIKQVFHELSQOHTGITRLGPYSLDKDSLYLNGYNE	313
DB	399	VDLLCTYQLPSGPGPLPIKQVFHELSQOHTGITRLGPYSLDKDSLYLNGYNE	458
QY	314	TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSPDMGKGSATFNS	373
DB	459	TPKPATTFPLPSEATTAMGYHLKTLTLNFTISNLOYSPDMGKGSATFNS	518
QY	374	PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIO	433
DB	519	PLFQKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIO	578
QY	434	GVTLGFGYVLDRLDPLFNGYAPQNLISIRGEYQINFIHVNWNLSPDPTSE	493
DB	579	GVTLGFGYVLDRLDPLFNGYAPQNLISIRGEYQINFIHVNWNLSPDPTSE	638
QY	494	DKVTTLKGSQSLDHTFRCLVNTLTMDSVLVTVKALFSSNLDPSLYEQVFL	553
DB	639	DKVTTLKGSQSLDHTFRCLVNTLTMDSVLVTVKALFSSNLDPSLYEQVFL	698
QY	554	WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAOPGT	613
DB	699	WLGSTYQLVDIHVTMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAOPGT	758
QY	614	NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLNCNFSPLARR	673
DB	759	NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLNCNFSPLARR	818
QY	674	LRMTRNGTOLQNFTRDRSSVLVDGYSPNRNEPLTGNS	710
DB	819	LRMTRNGTOLQNFTRDRSSVLVDGYSPNRNEPLTGNS	855

RESULT 12  
US-09-884-441-478  
; Sequence 478, Application US/09884441  
; Patent No. US20020119158A1  
; GENERAL INFORMATION:  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Carter, Darrick  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C7

; CURRENT APPLICATION NUMBER: US/09/884,441  
; CURRENT FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 489  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 478  
; LENGTH: 914  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-884-441-478

Query Match 92.9%; Score 3663; DB 3; Length 914;  
Best Local Similarity 99.9%; Pred. No. 4.2e-289;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 14 FTHRSSVSTTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLFTITNLRYEENWPG 73
DB 159 FTHRSSVSTTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLFTITNLRYEENWPG 218

QY 74 SRKFNTTVERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 133
DB 219 SRKFNTTVERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 278

QY 134 GLDREQLYLELSQTHSITELGPTVYLDRLDSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
DB 279 GLDREQLYLELSQTHSITELGPTVYLDRLDSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 338

QY 194 INNLRYMADWQPGSLAKFNITDNVMKHLSPFORSSIGARYTCRVIARSVKNGAETR 253
DB 339 INNLRYMADWQPGSLAKFNITDNVMKHLSPFORSSIGARYTCRVIARSVKNGAETR 398

QY 254 VDLCTVLOPLSGPLPIKOVFHELQOOTHGITRLGYSYLDKSLYNGYNEPDPDEPPT 313
DB 399 VDLCTVLOPLSGPLPIKOVFHELQOOTHGITRLGYSYLDKSLYNGYNEPDPDEPPT 458

QY 314 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
DB 459 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518

QY 374 PLFKSSMGPFYLGCLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 433
DB 519 PLFKSSMGPFYLGCLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 578

QY 434 GVTQLGYVLDRLDSLFINGYAPQNLSIRGEYQINFHIVNNLNSNPDPPTSSEYITLLRDIQ 493
DB 579 GVTQLGYVLDRLDSLFINGYAPQNLSIRGEYQINFHIVNNLNSNPDPPTSSEYITLLRDIQ 638

QY 494 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTLNASFH 553
DB 639 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTLNASFH 698

QY 554 WLGSYQLVDIHVTMESSYVQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNYQRNKR 613
DB 699 WLGSYQLVDIHVTMESSYVQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNYQRNKR 758

QY 614 NIEDALNQLFRNSIKSYFSDCVSTFRSPNRHHTGVDLSLNCNFSPLARRVDRVAIYEEF 673
DB 759 NIEDALNQLFRNSIKSYFSDCVSTFRSPNRHHTGVDLSLNCNFSPLARRVDRVAIYEEF 818

QY 674 LRMTNRGTQLQNFTLDRSSVLVDGYSNRPNEPLTGN 710
DB 819 LRMTNRGTQLQNFTLDRSSVLVDGYSNRPNEPLTGN 855
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## RESULT 13

US-09-907-969-312  
; Sequence 312, Application US/09907969  
; Publication No. US20030091580A1  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Fling, Steven P.  
; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary Richard  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Hill, Paul  
; APPLICANT: Albone, Earl  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.462C8  
; CURRENT APPLICATION NUMBER: US/09/907,969  
; CURRENT FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 596  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 312  
; LENGTH: 914  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-907-969-312

Query Match 92.9%; Score 3663; DB 3; Length 914;  
Best Local Similarity 99.9%; Pred. No. 4.2e-289;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 14 FTHRSSVSTTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLFTITNLRYEENWPG 73
DB 159 FTHRSSVSTTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLFTITNLRYEENWPG 218

QY 74 SRKFNTTVERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 133
DB 219 SRKFNTTVERVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGVDAICTHRPDPGP 278

QY 134 GLDREQLYLELSQTHSITELGPTVYLDRLDSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
DB 279 GLDREQLYLELSQTHSITELGPTVYLDRLDSLYNGFTHRSSVPTTSTGVVSEEPFTLNFT 338

QY 194 INNLRYMADWQPGSLAKFNITDNVMKHLSPFORSSIGARYTCRVIARSVKNGAETR 253
DB 339 INNLRYMADWQPGSLAKFNITDNVMKHLSPFORSSIGARYTCRVIARSVKNGAETR 398

QY 254 VDLCTVLOPLSGPLPIKOVFHELQOOTHGITRLGYSYLDKSLYNGYNEPDPDEPPT 313
DB 399 VDLCTVLOPLSGPLPIKOVFHELQOOTHGITRLGYSYLDKSLYNGYNEPDPDEPPT 458

QY 314 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
DB 459 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518

QY 374 PLFKSSMGPFYLGCLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 433
DB 519 PLFKSSMGPFYLGCLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 578

QY 434 GVTQLGYVLDRLDSLFINGYAPQNLSIRGEYQINFHIVNNLNSNPDPPTSSEYITLLRDIQ 493
DB 579 GVTQLGYVLDRLDSLFINGYAPQNLSIRGEYQINFHIVNNLNSNPDPPTSSEYITLLRDIQ 638

QY 494 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTLNASFH 553
DB 639 DKVTTLKGSQQLHDTFRFCLVTNLTMDSVLVTKALFSSNLDPSLVQVFLDKTLNASFH 698

QY 554 WLGSYQLVDIHVTMESSYVQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNYQRNKR 613
DB 699 WLGSYQLVDIHVTMESSYVQPTSSSTQHFYLNFTITNLPSQDKAQPGTTNYQRNKR 758

QY 614 NIEDALNQLFRNSIKSYFSDCVSTFRSPNRHHTGVDLSLNCNFSPLARRVDRVAIYEEF 673
DB 759 NIEDALNQLFRNSIKSYFSDCVSTFRSPNRHHTGVDLSLNCNFSPLARRVDRVAIYEEF 818

QY 674 LRMTNRGTQLQNFTLDRSSVLVDGYSNRPNEPLTGN 710
DB 819 LRMTNRGTQLQNFTLDRSSVLVDGYSNRPNEPLTGN 855
```

## RESULT 14

US-09-907-969-478  
; Sequence 478, Application US/09907969  
; Publication No. US20030091580A1  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Fling, Steven P.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary Richard  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Hill, Paul  
; APPLICANT: Albone, Earl  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C8  
; CURRENT APPLICATION NUMBER: US/09/907,969  
; CURRENT FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 596  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 478  
; LENGTH: 914  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-907-969-478

Query Match 92.9%; Score 3663; DB 3; Length 914;  
Best Local Similarity 99.9%; Pred. No. 4.2e-289;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	14	FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG	73
DB	159	FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG	218
QY	74	SRKFNTERVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDAICTHRPDPTGP	133
DB	219	SRKFNTERVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDAICTHRPDPTGP	278
QY	134	GLDREQLYLELSQTHSITELGPTTLDRLSLYNGFTHRSSVPTTSTGVVSEBPTLNFT	193
DB	279	GLDREQLYLELSQTHSITELGPTTLDRLSLYNGFTHRSSVPTTSTGVVSEBPTLNFT	338
QY	194	INNLRYMADMGQPSGLKFNTITDNVMKHLSPFORSSLGARYTGCRIALRSVKNCAETR	253
DB	339	INNLRYMADMGQPSGLKFNTITDNVMKHLSPFORSSLGARYTGCRIALRSVKNCAETR	398
QY	254	VDLLCTYLQPLSGPLPIKQVFHELSSQTHGITRLGPIYSLDKDSLXLYNGNEPDEPPT	313
DB	399	VDLLCTYLQPLSGPLPIKQVFHELSSQTHGITRLGPIYSLDKDSLXLYNGNEPDEPPT	458
QY	314	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOQSPDMGKSATFNSTEGVLOHLR	373
DB	459	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOQSPDMGKSATFNSTEGVLOHLR	518
QY	374	PLFQKSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDVPVPGGLDIOQLYWELSQLTH	433
DB	519	PLFQKSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDVPVPGGLDIOQLYWELSQLTH	578
QY	434	GVTLQGFYVLDRLSLFNGYAPQNLISIRGEYQINFIHNVNMLSNPDPTSEYITLLRDIQ	493
DB	579	GVTLQGFYVLDRLSLFNGYAPQNLISIRGEYQINFIHNVNMLSNPDPTSEYITLLRDIQ	638
QY	494	DKVTTLTKGSQLHDTFRFCLVNTLMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH	553
DB	639	DKVTTLTKGSQLHDTFRFCLVNTLMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH	698
QY	554	WLGSTYQLVDIHVTENESSVYQPTSSSTQHFYLNFTITNLRYSQDKAQPCTTNYQRNKR	613
DB	699	WLGSTYQLVDIHVTENESSVYQPTSSSTQHFYLNFTITNLRYSQDKAQPCTTNYQRNKR	758
QY	614	NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF	673

Db 759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF 818  
QY 674 LRMRNGTQLOQNTFLDRSSVLVDGYSPPNEPLTGNS 710  
Db 819 LRMRNGTQLOQNTFLDRSSVLVDGYSPPNEPLTGNS 855

RESULT 15  
US-09-827-271-312  
; Sequence 312, Application US/09827271  
; Publication No. US20030165504A1  
; GENERAL INFORMATION:  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.462C6  
; CURRENT APPLICATION NUMBER: US/09/827,271  
; CURRENT FILING DATE: 2001-04-04  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 312  
; LENGTH: 914  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-827-271-312

Query Match 92.9%; Score 3663; DB 3; Length 914;  
Best Local Similarity 99.9%; Pred. No. 4.2e-289;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	14	FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG	73
DB	159	FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG	218
QY	74	SRKFNTERVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDAICTHRPDPTGP	133
DB	219	SRKFNTERVLOGLLRPLFKNTSVGLYSGCRITLLRPEKDGATGVDAICTHRPDPTGP	278
QY	134	GLDREQLYLELSQTHSITELGPTTLDRLSLYNGFTHRSSVPTTSTGVVSEBPTLNFT	193
DB	279	GLDREQLYLELSQTHSITELGPTTLDRLSLYNGFTHRSSVPTTSTGVVSEBPTLNFT	338
QY	194	INNLRYMADMGQPSGLKFNTITDNVMKHLSPFORSSLGARYTGCRIALRSVKNCAETR	253
DB	339	INNLRYMADMGQPSGLKFNTITDNVMKHLSPFORSSLGARYTGCRIALRSVKNCAETR	398
QY	254	VDLLCTYLQPLSGPLPIKQVFHELSSQTHGITRLGPIYSLDKDSLXLYNGNEPDEPPT	313
DB	399	VDLLCTYLQPLSGPLPIKQVFHELSSQTHGITRLGPIYSLDKDSLXLYNGNEPDEPPT	458
QY	314	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOQSPDMGKSATFNSTEGVLOHLR	373
DB	459	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLOQSPDMGKSATFNSTEGVLOHLR	518
QY	374	PLFQKSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDVPVPGGLDIOQLYWELSQLTH	433
DB	519	PLFQKSMGPFYLGCOLISLRPEKDGATGVDTTCTTHPDVPVPGGLDIOQLYWELSQLTH	578
QY	434	GVTLQGFYVLDRLSLFNGYAPQNLISIRGEYQINFIHNVNMLSNPDPTSEYITLLRDIQ	493
DB	579	GVTLQGFYVLDRLSLFNGYAPQNLISIRGEYQINFIHNVNMLSNPDPTSEYITLLRDIQ	638
QY	494	DKVTTLTKGSQLHDTFRFCLVNTLMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH	553
DB	639	DKVTTLTKGSQLHDTFRFCLVNTLMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH	698
QY	554	WLGSTYQLVDIHVTENESSVYQPTSSSTQHFYLNFTITNLRYSQDKAQPCTTNYQRNKR	613
DB	699	WLGSTYQLVDIHVTENESSVYQPTSSSTQHFYLNFTITNLRYSQDKAQPCTTNYQRNKR	758
QY	614	NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIYEEF	673



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||||| 759 NIEDALNQLFRNSSIKSYFSDCQVSIFSRVSPNRHHTGVDLSLNFSPLARVDRVAIYEEF 818
Db
Qy 674 LRMRNGTQLONFTRDRSSVLVDGYSNRPNEPLTGNS 710
Db 819 LRMRNGTQLONFTRDRSSVLVDGYSNRPNEPLTGNS 855

RESULT 16
US-10-010-742-206
; Sequence 206, Application US/10010742
; Publication No. US20020146727A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Bennington, Angela Ann
; APPLICANT: Zehentner, Barbara
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C7
; CURRENT APPLICATION NUMBER: US/10/010,742
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-742-206

Query Match 92.9%; Score 3663; DB 4; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLYEENWMPG 73
Db 159 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLYEENWMPG 218
Qy 74 SRKFNTTERTVQLGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 133
Db 219 SRKFNTTERTVQLGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 278
Qy 134 GLDREQLYLELSQLTSHITELGPYTLDRDSLIVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQLTSHITELGPYTLDRDSLIVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
Qy 194 INNLRVMDMGQPSGLKFNITDNNMKHLLPLFORSSIGARYTCRVALRSVKNGAETR 253
Db 339 INNLRVMDMGQPSGLKFNITDNNMKHLLPLFORSSIGARYTCRVALRSVKNGAETR 398
Qy 254 VDLICTYQLPLSGPLPIKQVFHELSSQTHGITRLGPSYLDKSLYLYNGNEPDPDEPPT 313
Db 399 VDLICTYQLPLSGPLPIKQVFHELSSQTHGITRLGPSYLDKSLYLYNGNEPDPDEPPT 458
Qy 314 TPKPATTFPLPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
Db 459 TPKPATTFPLPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518
Qy 374 PLFOKSSMGPPYLGQQLISLRPEKDGATGVDTTCTVHPDPVGPGLDIQQLYWELSOLTH 433
Db 519 PLFOKSSMGPPYLGQQLISLRPEKDGATGVDTTCTVHPDPVGPGLDIQQLYWELSOLTH 578
Qy 434 GVTQLGFVLDRLDSLFINGYAPQNLISIRGEQINFIHVNWNLSPDPPTSSEYITLLRDIQ 493
Db 579 GVTQLGFVLDRLDSLFINGYAPQNLISIRGEQINFIHVNWNLSPDPPTSSEYITLLRDIQ 638
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Qy 494 DKVTTLVKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
Db 639 DKVTTLVKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698
Qy 554 WLGSTYQLVDIHVTEMESSYQPTSSSTOHFYLNFTITNLYSQDKAQPGTTNYQNKR 613
Db 699 WLGSTYQLVDIHVTEMESSYQPTSSSTOHFYLNFTITNLYSQDKAQPGTTNYQNKR 758
Qy 614 NIEDALNQLFRNSSIKSYFSDCQVSIFSRVSPNRHHTGVDLSLNFSPLARVDRVAIYEEF 673
Db 759 NIEDALNQLFRNSSIKSYFSDCQVSIFSRVSPNRHHTGVDLSLNFSPLARVDRVAIYEEF 818
Qy 674 LRMRNGTQLONFTRDRSSVLVDGYSNRPNEPLTGNS 710
Db 819 LRMRNGTQLONFTRDRSSVLVDGYSNRPNEPLTGNS 855

RESULT 17
US-10-198-053-312
; Sequence 312, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-312

Query Match 92.9%; Score 3663; DB 4; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLYEENWMPG 73
Db 159 FTHRSSVSTSTPGTPTVYLGAASKTPASIFGPSAASHLLILFTLNFTITNLYEENWMPG 218
Qy 74 SRKFNTTERTVQLGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 133
Db 219 SRKFNTTERTVQLGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 278
Qy 134 GLDREQLYLELSQLTSHITELGPYTLDRDSLIVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
Db 279 GLDREQLYLELSQLTSHITELGPYTLDRDSLIVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
Qy 194 INNLRVMDMGQPSGLKFNITDNNMKHLLPLFORSSIGARYTCRVALRSVKNGAETR 253
Db 339 INNLRVMDMGQPSGLKFNITDNNMKHLLPLFORSSIGARYTCRVALRSVKNGAETR 398
Qy 254 VDLICTYQLPLSGPLPIKQVFHELSSQTHGITRLGPSYLDKSLYLYNGNEPDPDEPPT 313
Db 399 VDLICTYQLPLSGPLPIKQVFHELSSQTHGITRLGPSYLDKSLYLYNGNEPDPDEPPT 458
Qy 314 TPKPATTFPLPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
Db 459 TPKPATTFPLPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518
Qy 374 PLFOKSSMGPPYLGQQLISLRPEKDGATGVDTTCTVHPDPVGPGLDIQQLYWELSOLTH 433
Db 519 PLFOKSSMGPPYLGQQLISLRPEKDGATGVDTTCTVHPDPVGPGLDIQQLYWELSOLTH 578
Qy 434 GVTQLGFVLDRLDSLFINGYAPQNLISIRGEQINFIHVNWNLSPDPPTSSEYITLLRDIQ 493
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Db 579 GVTQLGFYVLDRLDSLFINGVAPQNLISIRGEYQINFIHVNWLSNPDPSTSEYITLLRDIQ 638
Qy 494 DKVTTLTKGSQLHDTFRFCLVTLNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553
Db 639 DKVTTLTKGSQLHDTFRFCLVTLNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 698
Qy 554 WLGSTVQLVDIHVTMESSYQPTSSSTQHFLNFTIITNLPSYQDKAQPGTTNYQRNKR 613
Db 699 WLGSTVQLVDIHVTMESSYQPTSSSTQHFLNFTIITNLPSYQDKAQPGTTNYQRNKR 758
Qy 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIEEP 673
Db 759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIEEP 818
Qy 674 LWMTRNGTQLQNFLLDRSSVLVDGYFPNNEPLTGN 710
Db 819 LWMTRNGTQLQNFLLDRSSVLVDGYFPNNEPLTGN 855

RESULT 18
US-10-198-053-478
; Sequence 478, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-478

Query Match 92.9%; Score 3663; DB 4; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLRYENMMWPG 73
Db 159 FTHRSSVSTTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLRYENMMWPG 218
Qy 74 SRKNTTERTVLQGLRLPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 133
Db 219 SRKNTTERTVLQGLRLPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 278
Qy 134 GLDREQLYLELSQTHSITELGPTLDRDSLTVNGFTHRSPVTTSTGVWSEEPFTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPTLDRDSLTVNGFTHRSPVTTSTGVWSEEPFTLNFT 338
Qy 194 INNLRYMADMGQPSGLKFNITDNVMKLLSLPLFORSSIGARYTCGRVIALSVKNGAETR 253
Db 339 INNLRYMADMGQPSGLKFNITDNVMKLLSLPLFORSSIGARYTCGRVIALSVKNGAETR 398
Qy 254 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGYSLDKDSLYLNGYNEPCPDPT 313
Db 399 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGYSLDKDSLYLNGYNEPCPDPT 458
Qy 314 TPXPATTFPLPLSATTAMGYHLKTLITLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
Db 459 TPXPATTFPLPLSATTAMGYHLKTLITLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518
Qy 374 PLFOKSMGPPYLGCQLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 433
Db 519 PLFOKSMGPPYLGCQLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 578
```

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Qy 434 GVTQLGFYVLDRLDSLFINGVAPQNLISIRGEYQINFIHVNWLSNPDPSTSEYITLLRDIQ 493
Db 579 GVTQLGFYVLDRLDSLFINGVAPQNLISIRGEYQINFIHVNWLSNPDPSTSEYITLLRDIQ 638
Qy 494 DKVTTLTKGSQLHDTFRFCLVTLNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 553
Db 639 DKVTTLTKGSQLHDTFRFCLVTLNLTWDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH 698
Qy 554 WLGSTVQLVDIHVTMESSYQPTSSSTQHFLNFTIITNLPSYQDKAQPGTTNYQRNKR 613
Db 699 WLGSTVQLVDIHVTMESSYQPTSSSTQHFLNFTIITNLPSYQDKAQPGTTNYQRNKR 758
Qy 614 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIEEP 673
Db 759 NIEDALNQLFRNSSIKSYFSDCOVSTFRSPVNRHHTGVDSLNCNFSPLARRVDRVAIEEP 818
Qy 674 LWMTRNGTQLQNFLLDRSSVLVDGYFPNNEPLTGN 710
Db 819 LWMTRNGTQLQNFLLDRSSVLVDGYFPNNEPLTGN 855
```

```
RESULT 19
US-10-714-389-206
; Sequence 206, Application US/10714389
; Publication No. US20040101899A1
; GENERAL INFORMATION:
; APPLICANT: Dallon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, TongTong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491D1
; CURRENT APPLICATION NUMBER: US/10/714,389;
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-714-389-206
```

```
Query Match 92.9%; Score 3663; DB 4; Length 914;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 FTHRSSVSTTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLRYENMMWPG 73
Db 159 FTHRSSVSTTSTPGTPTVYLKASCTPASIFGPSAASHLLILFTLNFTITNLRYENMMWPG 218
Qy 74 SRKNTTERTVLQGLRLPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 133
Db 219 SRKNTTERTVLQGLRLPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 278
Qy 134 GLDREQLYLELSQTHSITELGPTLDRDSLTVNGFTHRSPVTTSTGVWSEEPFTLNFT 193
Db 279 GLDREQLYLELSQTHSITELGPTLDRDSLTVNGFTHRSPVTTSTGVWSEEPFTLNFT 338
Qy 194 INNLRYMADMGQPSGLKFNITDNVMKLLSLPLFORSSIGARYTCGRVIALSVKNGAETR 253
Db 339 INNLRYMADMGQPSGLKFNITDNVMKLLSLPLFORSSIGARYTCGRVIALSVKNGAETR 398
Qy 254 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGYSLDKDSLYLNGYNEPCPDPT 313
Db 399 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGYSLDKDSLYLNGYNEPCPDPT 458
Qy 314 TPXPATTFPLPLSATTAMGYHLKTLITLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 373
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Mon Mar 20 08:49:44 2006

459 TPXPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 518  
374 PLFOKSSMGPFYLGCGQLISLRPEKDGAAATGVDTTCTTHPDPVPGGLDIQQLYWELSOLTH 433  
519 PLFOKSSMGPFYLGCGQLISLRPEKDGAAATGVDTTCTTHPDPVPGGLDIQQLYWELSOLTH 578  
434 GVTOLGFFVLDRDLSLFINGYAPQNLISIRGEYQINFIHVNMLSNPDPTSSSEYITLLRDIQ 493  
579 GVTOLGFFVLDRDLSLFINGYAPQNLISIRGEYQINFIHVNMLSNPDPTSSSEYITLLRDIQ 638  
494 DKVTTLKGSQSLHDTFRCLVTNLTMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH 553  
639 DKVTTLKGSQSLHDTFRCLVTNLTMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH 698  
554 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQRNKR 613  
699 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQRNKR 758  
614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLCNFSPFLARRVDRVAIYEEF 673  
759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLCNFSPFLARRVDRVAIYEEF 818  
674 LMRTRNGTQLQNFTLDRSSVLVDGYFPNNEPLTGNS 710  
819 LMRTRNGTQLQNFTLDRSSVLVDGYFPNNEPLTGNS 855

Search completed: March 20, 2006, 07:35:08  
Job time : 137.781 secs

459 TPXPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 518  
374 PLFOKSSMGPFYLGCGQLISLRPEKDGAAATGVDTTCTTHPDPVPGGLDIQQLYWELSOLTH 433  
519 PLFOKSSMGPFYLGCGQLISLRPEKDGAAATGVDTTCTTHPDPVPGGLDIQQLYWELSOLTH 578  
434 GVTOLGFFVLDRDLSLFINGYAPQNLISIRGEYQINFIHVNMLSNPDPTSSSEYITLLRDIQ 493  
579 GVTOLGFFVLDRDLSLFINGYAPQNLISIRGEYQINFIHVNMLSNPDPTSSSEYITLLRDIQ 638  
494 DKVTTLKGSQSLHDTFRCLVTNLTMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH 553  
639 DKVTTLKGSQSLHDTFRCLVTNLTMDSVLTVKALFSSNLDPSLVEQVFLDKTLNASFH 698  
554 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQRNKR 613  
699 WLGSTYQLVDIHVTEMESVYQPTSSSTQHFYLNFTITNLPSQDKAQPCTTNYQRNKR 758  
614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLCNFSPFLARRVDRVAIYEEF 673  
759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSPVNRHHTGVDSLCNFSPFLARRVDRVAIYEEF 818  
674 LMRTRNGTQLQNFTLDRSSVLVDGYFPNNEPLTGNS 710  
819 LMRTRNGTQLQNFTLDRSSVLVDGYFPNNEPLTGNS 855

RESULT 20  
US-10-717-296-206  
; Sequence 206, Application US/10717296  
; Publication No. US20040142361A1  
; GENERAL INFORMATION:  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Jiang, Yuqiu  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.491C8  
; CURRENT APPLICATION NUMBER: US/10717,296  
; NUMBER OF SEQ ID NOS: 313  
; CURRENT FILING DATE: 2003-11-19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 206  
; LENGTH: 914  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-717-296-206

Query Match 92.9%; Score 3663; DB 4; Length 914;  
Best Local Similarity 99.9%; Pred. No. 4.2e-289;  
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 FTHRSSVSTTTPGTPTYLGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENMWP 73  
DB 159 FTHRSSVSTTTPGTPTYLGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENMWP 218  
QY 74 SRKFNTTERRVLOGLRPLFKNTSVGPLYSGCRLLLRPEKDGAAATGVDICTHRRDPTGP 133  
DB 219 SRKFNTTERRVLOGLRPLFKNTSVGPLYSGCRLLLRPEKDGAAATGVDICTHRRDPTGP 278  
QY 134 GLDREQLYLELSQLTHSITELGPYTLDRDLSLVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193  
DB 279 GLDREQLYLELSQLTHSITELGPYTLDRDLSLVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338  
QY 194 INNLRYMADMGQPSLKFNITDVMKHLSPFORSLGARYTGCRIALRSVKNGAETR 253  
DB 339 INNLRYMADMGQPSLKFNITDVMKHLSPFORSLGARYTGCRIALRSVKNGAETR 398  
QY 254 VDLICTYLOPLSGPLPIKOVFHELSSQTHGITRLGPYSIDKDSLVLNGYNEPGDEPPT 313  
DB 399 VDLICTYLOPLSGPLPIKOVFHELSSQTHGITRLGPYSIDKDSLVLNGYNEPGDEPPT 458  
QY 314 TPXPATTFPLPSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 373

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:28:38 ; Search time 26.0454 Seconds  
(without alignments)  
3765.293 Million cell updates/sec

Title: US-10-687-035-34

Perfect score: 758

Sequence: 1 MGWSWIFLLSCTAGVHSE.....FGSGYFYDYGQGTTLTVSS 139

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	601.5	79.4	472	2	Q6PJA7_MOUSE
2	596.5	78.7	483	2	Q4VAB6_MOUSE
3	585.5	77.2	470	2	Q7TKM1_MOUSE
4	579	76.4	117	1	HV14_MOUSE
5	575.5	75.9	477	2	Q58E56_MOUSE
6	564	74.4	481	2	Q8VCV5_MOUSE
7	555	73.2	488	2	Q91WR1_MOUSE
8	533.5	70.4	481	2	Q91WT1_MOUSE
9	532.5	70.3	140	1	HV02_MOUSE
10	531	70.1	465	2	Q6PJB2_MOUSE
11	525.5	69.3	488	2	Q569W9_MOUSE
12	522	68.9	139	1	HV07_MOUSE
13	514.5	67.9	136	1	HV15_MOUSE
14	512	67.5	485	2	Q58E61_MOUSE
15	512	67.5	590	2	Q4V9V8_MOUSE
16	508.5	67.1	480	2	Q8K0Z4_MOUSE
17	502.5	66.3	473	2	Q9D8L4_MOUSE
18	501.5	66.2	458	2	Q5BUZ2_RAT
19	499	65.8	137	1	HV11_MOUSE
20	499	65.8	613	2	Q8VCX7_MOUSE
21	498.5	65.8	614	2	Q7TWT6_MOUSE
22	497.5	65.6	475	2	Q5FVP3_RAT
23	495	65.3	118	2	Q5R3X0_MOUSE
24	493	65.0	463	2	Q991C4_MOUSE
25	492.5	65.0	117	2	Q9QXF0_MOUSE
26	490.5	64.7	464	2	Q6PF95_MOUSE
27	489	64.5	598	2	Q568Y0_RAT
28	488.5	64.4	168	2	Q8VDC9_MOUSE
29	486.5	64.2	489	2	Q8VCX4_MOUSE
30	485	64.0	591	2	Q4QQW0_RAT
31	484	63.9	617	2	Q4KML5_MOUSE

32	480	63.3	487	2	Q65ZL2_MOUSE
33	479.5	63.3	134	2	Q65ZR6_MOUSE
34	479	63.2	482	2	Q8K172_MOUSE
35	476	62.8	117	1	HV52_MOUSE
36	475	62.7	486	2	Q5HZV6_MOUSE
37	471	62.1	118	1	HV51_MOUSE
38	470.5	62.1	117	1	HV12_MOUSE
39	470.5	62.1	616	2	Q504M7_MOUSE
40	470	62.0	488	2	Q8K0F2_MOUSE
41	469.5	61.9	117	1	HV13_MOUSE
42	469.5	61.9	117	1	Q9QXK9_MOUSE
43	469.5	61.9	138	1	HV48_MOUSE
44	460	60.7	145	2	Q924Q7_MOUSE
45	458.5	60.5	170	2	Q925S2_MOUSE
46	458.5	60.5	458	2	Q5BK05_RAT
47	457.5	60.4	146	2	Q924R8_MOUSE
48	456.5	60.2	483	2	Q52L51_MOUSE
49	455.5	60.1	120	1	HV03_MOUSE
50	449.5	59.3	120	2	Q920E8_MOUSE
51	445	58.7	145	2	Q924R1_MOUSE
52	444	58.6	143	2	Q924R0_MOUSE
53	443.5	58.5	123	2	Q8V1J1_MOUSE
54	441	58.2	145	2	Q924R4_MOUSE
55	438	57.8	137	2	Q924R6_MOUSE
56	437.5	57.7	140	2	Q924P8_MOUSE
57	437	57.7	117	1	HV09_MOUSE
58	436.5	57.6	481	2	Q91WT3_MOUSE
59	435.5	57.5	474	2	Q8R3H6_MOUSE
60	435	57.4	145	2	Q924R3_MOUSE
61	434.5	57.3	146	2	Q924Q3_MOUSE
62	434	57.3	117	1	HV04_MOUSE
63	434	57.3	143	2	Q924Q0_MOUSE
64	434	57.3	145	2	Q924P7_MOUSE
65	433.5	57.2	142	2	Q924Q1_MOUSE
66	431	56.9	117	1	HV06_MOUSE
67	431	56.9	145	2	Q924Q6_MOUSE
68	430.5	56.8	144	2	Q924P5_MOUSE
69	430.5	56.8	468	2	Q505N9_MOUSE
70	428	56.5	120	1	HV50_MOUSE
71	428	56.5	141	2	Q924Q4_MOUSE
72	428	56.5	145	2	Q924Q9_MOUSE
73	426	56.2	117	1	HV05_MOUSE
74	424	55.9	117	1	HV49_MOUSE
75	424	55.9	143	2	Q924Q5_MOUSE
76	423	55.8	243	2	Q7TQM2_MOUSE
77	422.5	55.7	147	2	Q925S3_MOUSE
78	422	55.7	143	2	Q924P9_MOUSE
79	421	55.5	109	2	Q9JL75_MOUSE
80	420.5	55.5	140	2	Q924R2_MOUSE
81	420.5	55.5	480	2	Q6P089_HUMAN
82	420.5	55.5	500	2	Q6N091_HUMAN
83	416.5	54.9	146	2	Q924Q8_MOUSE
84	416.5	54.9	208	2	Q62P87_HUMAN
85	416	54.9	136	2	Q7TPE3_MOUSE
86	416	54.9	143	2	Q924R7_MOUSE
87	415	54.7	117	1	HV10_MOUSE
88	413.5	54.6	121	1	HV01_MOUSE
89	411	54.2	143	2	Q91V67_MOUSE
90	411	54.2	143	2	Q91VA2_MOUSE
91	410.5	54.2	142	2	Q924Q2_MOUSE
92	408.5	53.9	120	2	Q5F211_MOUSE
93	408	53.8	118	2	Q921C4_MOUSE
94	407	53.7	143	2	Q924P6_MOUSE
95	406	53.6	518	2	Q6N030_HUMAN
96	404.5	53.4	497	2	Q8WY24_HUMAN
97	404	53.3	114	2	Q8JL81_MOUSE
98	403	53.2	498	2	Q6N041_HUMAN
99	402	53.0	147	1	HV1C_HUMAN
100	400.5	52.8	476	2	Q569X1_MOUSE

ALIGNMENTS

Qy	1	MGWSIFLFLLSGTAGVHSEVQLQOSPELVKPGASVKISCKASGYTFTDYNIIHWVKQSH
h	1	MGWSMIFLFLISGTAGVISEVQLQOSPELVKPGASVKMSCKASGYTFDYNIIHWVKQSH

QY	121	-GSGYFDFWGCITLTVSS	139
DB	121	SGSYWYFDWGCAGTITVSS	140
RESULT 4			
ID	HV14_MOUSE	STANDARD;	PRT; 117 AA.
AC	P01758;		
DT	21-JUL-1986	(Rel. 01, Created)	
DT	21-JUL-1986	(Rel. 01, Last sequence update)	
DT	10-MAY-2005	(Rel. 47, Last annotation update)	
DE	Ig heavy chain V region 108A precursor.		
GN	Name=Igh-VJ558;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muroidea; Muridae; Murinae; Mus.		
OC	NCBI_TaxID=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RP	MEDLINE=81245215; PubMed=6789211;		
RA	Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.;		
RT	"Diversity of germ-line immunoglobulin VH genes";		
RL	Nature 292:428-430(1981).		
CC	-1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.		
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use as long as its content is in no way modified and this statement is not		
CC	removed.		
CC	-----		
DR	EMBL; J00488; AAA38519.1; -; Genomic_DNA.		
DR	PIR; A02041; HVMS8A.		
DR	HSSP; P01751; 1NOB.		
DR	SMR; P01758; 20-116.		
DR	MGI; MGI:96486; Igh-VJ558.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003596; Ig_v.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
KW	Immunoglobulin domain; Immunoglobulin V region; Signal.		
FT	SIGNAL 1 19		
FT	CHAIN 20 117 Ig heavy chain V region 108A.		
FT	DOMAIN 20 >117 Ig-like.		
FT	NON_TER 117 117		
SQ	SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;		
Query Match 76.4%; Score 579; DB 1; Length 117;			
Best Local Similarity 92.3%; Pred. No. 3.9e-47;			
Matches 108; Conservative 3; Mismatches 6; Indels 0; Gaps 0;			
QY	1	MCMSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISCKASGYFTDYNHWKQSH	60
DB	1	MCMSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISCKASGYFTDYNHWKQSH	60
QY	61	GKLEWIGIYYPNGVSDYNQNFKSKATLIVDNSNTAYMELRLSITSDSAVYCAR	117
DB	61	GKLEWIGIYYPNGVSDYNQNFKSKATLIVDNSNTAYMELRLSITSDSAVYCAR	117
RESULT 5			
ID	Q58E56_MOUSE	PRELIMINARY;	PRT; 477 AA.
AC	Q58E56;		
DT	10-MAY-2005	(TREMELrel. 30, Created)	
DT	10-MAY-2005	(TREMELrel. 30, Last sequence update)	
DT	10-MAY-2005	(TREMELrel. 30, Last annotation update)	
DE	Igh-1a protein.		
GN	Name=Igh-1a;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		

QY	121	-GSGYFDFWGCITLTVSS	139
DB	121	SGSYWYFDWGCAGTITVSS	140
RESULT 4			
ID	HV14_MOUSE	STANDARD;	PRT; 117 AA.
AC	P01758;		
DT	21-JUL-1986	(Rel. 01, Created)	
DT	21-JUL-1986	(Rel. 01, Last sequence update)	
DT	10-MAY-2005	(Rel. 47, Last annotation update)	
DE	Ig heavy chain V region 108A precursor.		
GN	Name=Igh-VJ558;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muroidea; Muridae; Murinae; Mus.		
OC	NCBI_TaxID=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RP	MEDLINE=81245215; PubMed=6789211;		
RA	Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.;		
RT	"Diversity of germ-line immunoglobulin VH genes";		
RL	Nature 292:428-430(1981).		
CC	-1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.		
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use as long as its content is in no way modified and this statement is not		
CC	removed.		
DR	EMBL; J00488; AAA38519.1; -; Genomic_DNA.		
DR	PIR; A02041; HVMS8A.		
DR	HSSP; P01751; 1NOB.		
DR	SMR; P01758; 20-116.		
DR	MGI; MGI:96486; Igh-VJ558.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003596; Ig_v.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
KW	Immunoglobulin domain; Immunoglobulin V region; Signal.		
FT	SIGNAL 1 19		
FT	CHAIN 20 117 Ig heavy chain V region 108A.		
FT	DOMAIN 20 >117 Ig-like.		
FT	NON_TER 117 117		
SQ	SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;		
Query Match 76.4%; Score 579; DB 1; Length 117;			
Best Local Similarity 92.3%; Pred. No. 3.9e-47;			
Matches 108; Conservative 3; Mismatches 6; Indels 0; Gaps 0;			
QY	1	MCMSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISCKASGYFTDNIHWKQSH	60
DB	1	MCMSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISCKASGYFTDNIHWKQSH	60
QY	61	GKLEWIGIYYPNGVSDYNQNFKSKATLIVDNSNTAYMELRLSITSDSAVVCAR	117
DB	61	GKLEWIGIYYPNGVSDYNQNFKSKATLIVDNSNTAYMELRLSITSDSAVVCAR	117
RESULT 5			
ID	Q58E56_MOUSE	PRELIMINARY;	PRT; 477 AA.
AC	Q58E56;		
DT	10-MAY-2005	(TREMELrel. 30, Created)	
DT	10-MAY-2005	(TREMELrel. 30, Last sequence update)	
DT	10-MAY-2005	(TREMELrel. 30, Last annotation update)	
DE	Igh-1a protein.		
GN	Name=Igh-1a;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		



```
Best Local Similarity 75.5%; Pred. No. 5.1e-45;
Matches 105; Conservative 13; Mismatches 19; Indels 2; Gaps 1;

QY 1 MGWSWIFLLSSTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGWSWIFLLSSTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GKLEWIGYTPYNGVSDYNQFKSKATLVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GKLEWIGYTPYNGVSDYNQFKSKATLVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GSGYFDPYNGGQFTLTVSS 139
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GA--WFAFWGQGLTVTVA 137

RESULT 7
Q91WRI_MOUSE
ID Q91WRI_MOUSE PRELIMINARY; PRT; 488 AA.
AC Q91WRI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013539; AAH13539.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR Ensembl; ENSMUSG000000021155; Mus musculus.
DR MGI; MGI:96486; Igh-VJ558.
DR GO; GO:0003823; P:antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.

SQ SEQUENCE 488 AA; 52965 MW; F12068460B400B9D CRC64;
Query Match 73.2%; Score 555; DB 2; Length 488;
Best Local Similarity 72.6%; Pred. No. 3.7e-44;
Matches 106; Conservative 13; Mismatches 17; Indels 10; Gaps 2;

QY 1 MGWSWIFLLSSTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGWSWIFLLSSTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GKLEWIGYTPYNGVSDYNQFKSKATLVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GKLEWIGYTPYNGVSDYNQFKSKATLVDNSSNTAYMELSLTSEDSAVYYCARWDF 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GSGYFDPYNGGQFTLTVSS 139
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 118 GPVYYSFSDYRCDYWGQGLTVTVA 143

RESULT 8
Q91WRI_MOUSE
ID Q91WRI_MOUSE PRELIMINARY; PRT; 481 AA.
AC Q91WRI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR Ensembl; ENSMUSG000000021155; Mus musculus.
DR GO; GO:0003823; P:antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
```

```
KW Immunoglobulin domain.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 70.4%; Score 533.5; DB 2; Length 481;
Best Local Similarity 74.1%; Pred. No. 4e-42;
Matches 103; Conservative 9; Mismatches 24; Indels 3; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVQLOQSGPELVKPGASVKISCKASGYTFTDYNHWVKQSH 60
Db 1 MGWRWIFLLSGTAGVQCCVQLQSGPELVKPGASVKISCKASGYTFTSYIHWVKQRP 60
Qy 61 GKILEWIGYIPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRLSLTSDSAVYFCARWDF 120
Db 61 GQGLWIGWIPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRLSLTSDSAVYFCARWDF 120
Qy 121 GSGYFDYWGQGTTLTVSS 139
Db 118 GGGWAFDYWGQGTTLTVSS 136

RESULT 9
HV02 MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP STRAIN=A/J;
RC MEDLINE=92152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RL immunoglobulin heavy chain."
CC Science 216:309-311(1982).
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; J00493; AAA38128.1; -; mRNA.
DR HSSP; P01747; 1UFQ.
DR SMR; P01746; 20-140.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19
FT DOMAIN 20 140 Ig heavy chain V region 93G7.
FT NON_TER 20 139 Ig-like.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 70.3%; Score 532.5; DB 1; Length 140;
Best Local Similarity 74.3%; Pred. No. 1.3e-42;
Matches 104; Conservative 12; Mismatches 23; Indels 1; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVQLOQSGPELVKPGASVKISCKASGYTFTDYNHWVKQSH 60
Db 1 MGWSWIFLLSGTAGVHSEVQLOQSGPELVKPGASVKISCKASGYTFTSYIHWVKQRP 60
Qy 61 GKILEWIGYIPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRLSLTSDSAVYFCARWDF 119
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Query Match 70.1%; Score 531; DB 2; Length 465;  
 Best Local Similarity 72.9%; Pred. No. 6.7e-42;  
 Matches 102; Conservative 11; Mismatches 21; Indels 6; Gaps 2;

QY 1 MGWSWIFLLSSTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHIVKQSH 60  
 DB 1 MGWSWIFLLSSTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHIVKQSH 60  
 QY 61 GKILEWIGYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120  
 DB 61 GKILEWIGYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120  
 QY 121 GSGYI-FDYWGQGTTLTVSS 139  
 DB 118 -GYVFDYWGQGTTLTVSS 135

RESULT 11  
 Q569W9 MOUSE PRELIMINARY; PRT; 468 AA.  
 AC Q569W9;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Hypothetical protein.  
 GN Name=Igh-1a;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CZECH II;  
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
 RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CZECH II;  
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
 RG NTH MGC Project;  
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC092271; AAH92271.1; -; mRNA.  
 DR SRR: Q569W9; 20-464.  
 DR MGI: MGI:96443; Igh-1a.  
 DR GO: GO:0003823; F:antigen binding; IEA.  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF07654; Cl-set; 3.

DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 468 AA; 51666 MW; 5BF6E527329F8461 CRC64;

Query Match 69.3%; Score 525.5; DB 2; Length 468;  
 Best Local Similarity 72.3%; Pred. No. 2.3e-41;  
 Matches 102; Conservative 15; Mismatches 19; Indels 5; Gaps 2;

QY 1 MGWSWIFLLSSTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHIVKQSH 60  
 DB 1 MGWSWIFLLSSTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHIVKQSH 60  
 QY 61 GKILEWIGYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120  
 DB 61 GKILEWIGYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120  
 QY 121 GSGYI-FDYWGQGTTLTVSS 139  
 DB 118 TGGYDGYVFDYWGQGTTLTVSS 138

RESULT 12  
 HV07 MOUSE STANDARD; PRT; 139 AA.  
 AC P01751; P01752;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 07, Last annotation update)  
 DE Ig heavy chain V region B1-8/186-2 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;  
 RA Bothwell A.L.M., Faskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NPB family of  
 antibodies: somatic mutation evident in a gamma 2a variable region."  
 RL Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: The B1-8 mu chain mRNA was cloned from a hybridoma  
 making antibodies to the hepten (4-hydroxy-3-nitrophenyl)acetyl  
 (NPB antibodies).  
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC EMBL: J00529; AAA38170.1; -; mRNA.  
 DR PIR: A90809; MEMS18.  
 DR PDB: 1AGU; X-ray; H=20-139.  
 DR PDB: 1AGV; X-ray; H/I/J=20-139.  
 DR PDB: 1AGW; X-ray; H=20-139.  
 DR PDB: 1NGP; X-ray; H=20-139.  
 DR PDB: 1NGQ; X-ray; H=20-139.  
 DR PDB: 1NQB; X-ray; A/C=20-139.  
 DR Ensemble: ENSMUSG0000063737; Mus musculus.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_v.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR SMART; SM00406; IGV; 1.  
 KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 139 Ig heavy chain V region B1-8/186-2.

```

FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT REGION 118 124 D segment.
FT REGION 125 139 JH2 segment.
FT DISULFID 41 115 By similarity.
FT NON_TER 139 139
FT STRAND 22 24
FT STRAND 28 31
FT TURN 33 34
FT TURN 37 38
FT STRAND 48 50
FT HELIX 48 50
FT STRAND 52 58
FT TURN 60 61
FT STRAND 64 70
FT TURN 72 74
FT STRAND 77 79
FT STRAND 81 83
FT HELIX 84 86
FT TURN 87 92
FT STRAND 93 96
FT TURN 97 102
FT STRAND 107 109
FT STRAND 111 118
FT TURN 120 123
FT STRAND 129 129
FT STRAND 133 137
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 68.9%; Score 522; DB 1; Length 139;
Best Local Similarity 71.9%; Pred. No. 1.2e-41;
Matches 100; Conservative 12; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNIHVKQSH 60
Db 1 MGWSCIMFLAATATGATGHSVQLQSGPELVKPGASVKISCKASGYTFSTYMHVVKQRP 60

Qy 61 GKILEWIGIYYPYNGVSDYNQNFKSKATLIVDSSNTAYMELRLSTSEDSAVYYCARWDF 120
Db 61 GRGLEWIGRIDPNSGTYKNEKFSKATLIVDKPSSTAYMQLSLTSEDSAVYYCARYDY 120

Qy 121 GSGYFDYWGQGTTLTVSS 139
Db 121 YGSSYFDYWGQGTTLTVSS 139

RESULT 13
HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=8222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared by
RT two adjacent CH genes."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

CC -----  
 CC EMBL; J00494; AAA38130.1; -; Genomic\_DNA.

CC PIR; A02042; HVMSB1.

CC HSP; P01751; INQB.

CC SMR; P01759; 20-136.

CC Ensembl; ENSMUSG00000063048; Mus musculus.

CC InterPro; IPR007110; Ig-like.

CC InterPro; IPR003596; Ig\_V.

CC SMART; SM00406; IGV; 1.

CC PROSITE; PS50835; IG\_LIKE; 1.

CC Immunoglobulin domain; Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 136 Ig heavy chain V region BCL1.

FT DOMAIN 20 135 Ig-like.

FT NON\_TER 136 136

SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 67.9%; Score 514.5; DB 1; Length 136;

Best Local Similarity 70.5%; Pred. No. 6.2e-41;

Matches 98; Conservative 11; Mismatches 27; Indels 3; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNIHVKQSH 60

Db 1 MGWSCIIFFLVATATGATGHSVQLQSGPELVKPGASVKISCKASGYTFDYNIHVKQSH 60

Qy 61 GKILEWIGIYYPYNGVSDYNQNFKSKATLIVDSSNTAYMELRLSTSEDSAVYYCARWDF 120

Db 61 AKSLEWIGIVSTYNGVSTYNGKPKGATMTVDKSSSTVHMLARLTSEDSANLYCARY-- 118

Qy 121 GSGYFDYWGQGTTLTVSS 139

Db 119 -YGYFDYWGQGTTLTVSS 136

RESULT 14

Q5861\_MOUSE

ID Q5861\_MOUSE PRELIMINARY; PRT; 485 AA.

AC Q5861;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Igh-VJ558 protein.

GN Name=Igh-VJ558;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Mus.

OC NCBI\_TaxID=10090;

OC [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Czech II;

RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.

RC Expression driven by an MMTV-LTR enhancer.

RX MEDLINE=22388252; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=Czech II;  
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.  
 RC Expression driven by an MMTV-LTR enhancer.;  
 RG NIH MGC Project;  
 RG Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC092056; AA092056.1; -, mRNA.  
 DR GO; GO:0003823; F:antigen binding; IEA.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00407; IGC1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 SQ SEQUENCE 485 AA; 52628 MW; F08C1FB47C4E44EC CRC64;  
 Query Match 67.5%; Score 512; DB 2; Length 485;  
 Best Local Similarity 71.5%; Pred. No. 4.5e-40;  
 Matches 103; Conservative 10; Mismatches 23; Indels 8; Gaps 2;  
 QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNIHWKQSH 60  
 DB 1 MEWRWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNIHWKQSH 60  
 QY 61 GKLEWIGIYYPNGVDYNNQPKSKATLIVDSSNTAYMELSLTSEDSAVTYCARWDF 120  
 DB 61 GRSLWIGNINPNYDSTIYNQKPKGKATLTVEKSSSTAYMELSLTSDSDSAVTYCARTE- 119  
 QY 121 GSGYY-----FDYWGQGTTLTVSS 139  
 DB 120 --TYYSYDGGFAWGRTLVTSVA 141  
 RESULT 15  
 Q4V9V8 MOUSE  
 ID Q4V9V8\_MOUSE PRELIMINARY; PRT; 590 AA.  
 AC Q4V9V8;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DE Hypothetical protein.  
 GN Name-Igh-6;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Mammary gland;  
 RC MEDLINS=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,  
 RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.J., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

PAhey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Mammary gland;  
 RC NIH MGC Project;  
 RG Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC096667; AA096667.1; -, mRNA.  
 DR MGI; MGI:96448; Igh-6.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 590 AA; 64892 MW; D425318F9A188B14 CRC64;  
 Query Match 67.5%; Score 512; DB 2; Length 590;  
 Best Local Similarity 70.5%; Pred. No. 5.6e-40;  
 Matches 98; Conservative 16; Mismatches 21; Indels 4; Gaps 1;  
 QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNIHWKQSH 60  
 DB 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNIHWKQSH 60  
 QY 61 GKLEWIGIYYPNGVDYNNQPKSKATLIVDSSNTAYMELSLTSEDSAVTYCARWDF 120  
 DB 61 GGQLEWIAIYPCSGNTYNEKFGKATLTAEKSSSTAYMELSLTSEDSAVTYCAR--- 117  
 QY 121 GSGYYFDYWGQGTTLTVSS 139  
 DB 118 -TGTGMDYWGQGTSTVSS 135  
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 Q8K0Z4 MOUSE  
 ID Q8K0Z4\_MOUSE PRELIMINARY; PRT; 480 AA.  
 AC Q8K0Z4;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE LOC238447 protein.  
 GN Name-LOC238447;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Mix FVB/N;  
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
 RX MEDLINS=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.J., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumarane P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny K.D., Sodergren E.J., Lu X.N., Gibbs R.A.,
RA Fahy J., Helton E., Ketting A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RG NIH MGC Project;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029188; AAT29188.1; -; mRNA.
DR SMR; Q8K024; 20-238.
DR Ensemble; ENSMUSG00000021155; Mus musculus.
DR GO; GO:0003823; F-antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 480 AA; 51646 MW; 8690A63C669CDBED CRC64;
Query Match 67.1%; Score 508.5; DB 2; Length 480;
Best Local Similarity 70.5%; Pred. No. 9.6e-40;
Matches 98; Conservative 13; Mismatches 25; Indels 3; Gaps 1;
Qy 1 MGWEIFLLSLGSGTAGVHSEYVQLQSGPELVKPGASVKISCKASGYTFTDYNHIVKQSH 60
Db 1 MGWEIFLLSLGSGTAGVHSCVQLQSGPELVKPGALVKISCKASGYTFTSPDISMWKQRP 60
Qy 61 GKILEWGIYIPYNGVDYNGNPFKSKATLIVDNSNTAYMELRLSLTSDSNAVYCARWDF 120
Db 61 GQGPWEIWTISPGDSEYNEKFKGKATLTADKSSNTAYMELSLTSENSAVYFCARSKL 120
Qy 121 GSGYFYDVGQGTTLTVSS 139
Db 121 GG---FAYWGGTTLTVSA 136
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AC Q9D8L4_MOUSE PRELIMINARY; PRT; 473 AA.
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
DE library, clone:191060009 product:immunoglobulin heavy chain 6 (heavy
DE chain of IgM), full insert sequence.
GN Name=Igh-1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Pancreas;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
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RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Pancreas;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ighii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojbori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavani T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohseki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
[3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Pancreas;
RC The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Pancreas;
RC MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
[5]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Pancreas;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Pancreas;
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akahira S., Fukuda S., Fukunishi Y., Furuno M.,
RA Arakawa T., Bono H., Carninci P., Hiramoto K., Hiraoka T., Hori F.,
RA Hanagaki T., Hara A., Hayatsu N., Izawa M., Kasukawa T., Kato H.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamoto T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK007918; BAB25349.1; -; mRNA.
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DR PIR; PH1165; PH1165.  
 DR PIR; S19966; S19966.  
 DR PIR; S26746; S26746.  
 DR HSP; P01864; 180G.  
 DR SMR; Q9D814; 20-469.  
 DR Ensembl; ENSMUSG00000054328; Mus musculus.  
 DR MGI; MGI:96443; Igh-1a.  
 DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.  
 DR GO; GO:005771; C:multivesicular body; IDA.  
 DR GO; GO:0003823; P:antigen binding; IDA.  
 DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.  
 DR GO; GO:0006958; P:antigen processing; IDA.  
 DR GO; GO:0006958; P:antigen processing; IDA.  
 DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.  
 DR GO; GO:0008333; P:endosome to lysosome transport; IDA.  
 DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.  
 DR GO; GO:0006910; P:phagocytosis, recognition; IDA.  
 DR GO; GO:0050871; P:positive regulation of B cell activation; IDA.  
 DR GO; GO:0050778; P:positive regulation of immune response; IDA.  
 DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.  
 DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.  
 DR GO; GO:0001798; P:positive regulation of type IIA hypersensitivity; IDA.  
 DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; IDA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Immunoglobulin domain.  
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 Query Match 66.3%; Score 502.5; DB 2; Length 473;  
 Best Local Similarity 70.4%; Pred. No. 3.5e-39;  
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 DB 1 MEWSWFLFLSAGTAGVHSEVQLQSGPVLKPGASVKISKASGYFTFTDYNHWKQRP 60  
 QY 61 GKLEWIGIYYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYFCARWDF 120  
 DB 61 GQGLEWIGIKPGSGSTYNEKFGKATLTADKSSSTAYMQLSLTSEDSAVYFCAR--- 117  
 QY 121 GSGY---YFDYWGQGTTLTVSS 139  
 DB 118 -SGDYDWFAYWGQGTTLTVSSA 138  
  
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 AC Q5BJZ2;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE LOC367586 protein.  
 GN Name=LOC367586;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
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 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Thymus;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner C.M., Shenmen C.F., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
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 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
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 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Vallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
 Schnerf A., Schein J.E., Jones S.J.M., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [2]  
 NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Thymus;  
 RC NIH MGC Project;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major  
 CC histocompatibility complex class I molecules (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC EMBL; BC091272; AAH91272.1; -; mRNA.  
 DR InterPro; IPR003597; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 3.  
 DR SMART; SM00409; IG; 3.  
 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR Immunoglobulin domain; Repeat.  
 KW Immunoglobulin domain; Repeat.  
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 Query Match 66.2%; Score 501.5; DB 2; Length 458;  
 Best Local Similarity 69.8%; Pred. No. 4.2e-39;  
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 DB 1 MGWSWFLFLSAGTAGVHSEVQLQSGPVLKPGASVKISKASGYFTFTDYNHWKQRP 60  
 QY 61 GKLEWIGIYYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYFCARWDF 120  
 DB 61 GNGLEWIGIYYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYFCAR-DY 119  
 QY 121 GSGYFYDYGQGTTLTVSS 139  
 DB 120 FDGY--DYWGQGVMTVSS 136  
  
 RESULT 19  
 HV11 MOUSE  
 ID HV11 MOUSE STANDARD; PRT; 137 AA.  
 AC P01755;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig heavy chain V region S43 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Thymus;  
 RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;  
 RA Bothwell A.L.M., Paskind M., Rath M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;

RT "Heavy chain variable region contribution to the NPb family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RL Cell 24:625-637(1981).  
 CC -1- MTSCELLANEUS: The gamma-2a chain mRNA was cloned from a hybridoma  
 CC making antibodies to the haptens (4-hydroxy-3-nitrophenyl)acetyl  
 CC (NPB antibodies).  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----

DR EMBL; J00539; AAA38172.1; -; mRNA.  
 DR PIR; A02038; G2MS43.  
 DR HSSP; P01751; IAGW.  
 DR SMR; P01755; 20-137.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR Immunoglobulin domain; Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 137 Ig heavy chain V region S43.  
 FT REGION 20 49 Framework-1.  
 FT REGION 50 54 Complementarity-determining-1.  
 FT REGION 55 68 Framework-2.  
 FT REGION 65 85 Complementarity-determining-2.  
 FT REGION 86 117 Framework-3.  
 FT REGION 118 122 D segment.  
 FT REGION 123 137 JH2 segment.  
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 FT NON TER 137 137  
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Query Match 65.8%; Score 499; DB 1; Length 137;  
 Best Local Similarity 69.1%; Pred. No. 1.9e-39;  
 Matches 96; Conservative 14; Mismatches 27; Indels 2; Gaps 1;  
 Oy 1 MGWSWIFLFLSLGAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDNIHNVKQSH 60  
 Db 1 MGWSWIFLFLSLGAGVHSEVQLQSGPELVKPGASVKISKASGYTFTSILMHWVQRP 60  
 Oy 61 GKILEWIGYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRLSLTSDSAVYVCARWDF 120  
 Db 61 GRGLEWIGRIDPNSGGTYNEHFRSKATLTIDKPSSTAYMQLSLTSDSAVYVCARYL 120  
 Oy 121 GSGYFYDWGGTTLTVSS 139  
 Db 121 GR--YFDYWGQGTTLTVSS 137

RESULT 20  
 Q8VCX7\_MOUSE PRELIMINARY; PRT; 613 AA.  
 AC Q8VCX7;  
 DT 01-MAR-2002 (TRENBLrel. 20, Created)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Igh-6 protein.  
 GN Name=Igh-6;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N; TISSUE=Salivary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiehl F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=FVB/N; TISSUE=Salivary gland;  
 RA Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 RL [3]  
 RN NUCLEOTIDE SEQUENCE.  
 RP PubMed=2464031;  
 RX Sikder S.K., Borden P., Gruzo F., Akolkar P.N., Bhattacharya S.B.,  
 RA Morrison S.L., Kabat E.A.,  
 RT "Amino acid substitutions in VH CDR2 change the idiotype but not the  
 RT antigen-binding of monoclonal antibodies to alpha(1----6)dextran.";  
 RL J. Immunol. 142:888-893(1989).  
 DR EMBL; BC018315; AAH18315.1; -; mRNA.  
 DR PIR; C30562; C30562.  
 DR HSSP; P01751; IAGW.  
 DR Ensembl; ENSMUSG0000054328; Mus musculus.  
 DR MGI; MGI:96448; Igh-6.  
 DR GO; GO:0019815; C:B cell receptor complex; IDA.  
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.  
 DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.  
 DR GO; GO:0048471; C:perinuclear region; IDA.  
 DR GO; GO:0003823; F:antigen binding; IDA.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0004888; F:transmembrane receptor activity; IDA.  
 DR GO; GO:000187; P:activation of MAPK activity; IDA.  
 DR GO; GO:000333; P:antigen processing; IDA.  
 DR GO; GO:0050853; P:B cell receptor signaling pathway; IDA.  
 DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.  
 DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.  
 DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.  
 DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.  
 DR GO; GO:0050731; P:positive regulation of peptidyl-tyrosine ph. .; IDA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; C1-set; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Immunoglobulin domain.  
 SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 65.8%; Score 499; DB 2; Length 613;  
 Best Local Similarity 68.5%; Pred. No. 1e-38;  
 Matches 98; Conservative 12; Mismatches 23; Indels 10; Gaps 2;  
 Oy 1 MGWSWIFLFLSLGAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDNIHNVKQSH 60  
 Db 1 MEWTWVFLFLSLGAGVHSEVQLQSGPELVKPGASVKISKATGYTFTSILMHWVQRP 60  
 Oy 61 GKILEWIGYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRLSLTSDSAVYVCARWDF 116  
 Db 61 GHGLEWIGIILPGSGSTNYNEKFKGATFTADTSNTAYMQLSLTSDSAVYVCARL 120

Oy 117 RWDFSGYFYFDYWGOGTTLTVSS 139  
||  
121 RW-----YFDVWGAGTTTVSS 137

Search completed: March 20, 2006, 07:32:04  
Job time : 26.0454 secs

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Result No.	Query	Score	Match	Length	DB	ID	Description
1	597	78.8	139	2	A27609	Ig heavy chain pre	
2	585	77.2	137	2	H32513	Ig heavy chain pre	
3	579	76.4	117	1	HVWS8A	Ig heavy chain pre	
4	566.5	74.7	151	2	PL0011	Ig heavy chain pre	
5	565.5	74.6	140	2	T01407	Ig heavy chain (my	
6	559	73.7	469	2	S37483	Ig gamma-2a chain	
7	548.5	72.4	138	2	PH0105	anti-digoxin trans	
8	547.5	72.2	140	2	PH1482	Ig heavy chain v r	
9	547	72.2	135	2	PS0057	Ig heavy chain pre	
10	544	71.8	150	2	PN0444	Ig heavy chain v r	
11	535.5	70.6	138	2	S45249	Ig heavy chain pre	
12	532.5	70.3	140	1	HVMSG7	Ig heavy chain pre	
13	531.5	70.1	140	2	PH1489	Ig heavy chain v r	
14	530.5	70.0	166	2	PL0012	Ig heavy chain pre	
15	525.5	69.3	140	2	PH1484	Ig heavy chain v r	
16	522	68.9	139	1	HVWS18	Ig heavy chain pre	
17	521.5	68.8	135	2	PH1493	Ig heavy chain v r	
18	520.5	68.7	140	2	PH1498	Ig heavy chain v r	
19	520.5	68.7	140	2	PH1483	Ig heavy chain v r	
20	520.5	68.7	140	2	PH1488	Ig heavy chain v r	
21	520	68.6	474	1	G2MSW11	Ig gamma-2b chain	
22	517.5	68.3	138	2	S21810	Ig heavy chain v r	
23	514.5	67.9	136	1	HVMSB1	Ig heavy chain pre	
24	512.5	67.6	140	2	PH1486	Ig heavy chain v r	
25	506.5	66.8	140	2	A36194	Ig heavy chain v r	
26	505.5	66.7	135	2	PH1492	Ig heavy chain v r	
27	503	66.4	139	2	PS0024	Ig heavy chain pre	
28	502.5	66.3	136	2	PL0208	Ig heavy chain pre	
29	499	65.8	128	2	I37267	Ig heavy chain v r	

## ALIGNMENTS

```
RESULT 1
A27609
Ig heavy chain precursor V region (I29) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: A27609
R;Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A;Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain switch
A;Reference number: A27609; MUID:88154467; PMID:3126234
A;Accession: A27609
A;Molecule type: DNA
A;Residues: 1-139 <KLE>
A;Cross-references: UNIPARC:UPI0000114D5D; EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PTD
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/DNA: signal sequence #status predicted <SIG>
F;20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>
F;34-117/DNA: immunoglobulin homology <IMV>

Query Match 78.8%; Score 597; DB 2; Length 139;
Best Local Similarity 80.6%; Pred. No. 4.3e-44;
Matches 112; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60
Db 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60

Qy 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSDSAVYCARWDF 120
Db 61 GKSLEWIGIYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSDSAVYCARWDF 120

Qy 121 GSGYFDYWGQGTTLTVSS 139
Db 121 YSYAMDYWGQGTSTVSS 139

RESULT 2
H32513
Ig heavy chain precursor V region (BXW16) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: H32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and
A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Accession: H32513
A;Molecule type: DNA
A;Residues: 1-137 <KOF>
A;Cross-references: UNIPARC:UPI0000114D9A; GB:M20831; NID:g196949; PIDN:AAA38848.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/DNA: immunoglobulin homology <IMV>

Query Match 77.2%; Score 585; DB 2; Length 137;
Best Local Similarity 80.6%; Pred. No. 4.4e-43;
Matches 112; Conservative 9; Mismatches 16; Indels 2; Gaps 1;

Qy 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60
Db 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60

Qy 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSDSAVYCARWDF 120
Db 61 GKSLEWIGIYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSDSAVYCARWDF 120

Qy 121 GSGYFDYWGQGTTLTVSS 139
```

Db 121 GSS--FDYWGQGTTLTVSS 137

## RESULT 3

```
HVMS8A
Ig heavy chain precursor V region (108A) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 09-Jul-2004
C;Accession: A02041
R;Givol, D.; Zakut, R.; Effron, K.; Rechavi, G.; Ram, D.; Cohen, J.B.
Nature 292, 426-430, 1981
A;Title: Diversity of germ-line immunoglobulin V-H genes.
A;Reference number: A02041; MUID:81245215; PMID:6789211
A;Accession: A02041
A;Molecule type: DNA
A;Residues: 1-117 <GIV>
A;Cross-references: UNIPROT:P01758; UNIPARC:UPI00000270F3
A;Note: the sequence was determined from the germline gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/DNA: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (108A) #status predicted <MAT>
F;34-117/DNA: immunoglobulin homology <IMV>

Query Match 76.4%; Score 579; DB 1; Length 117;
Best Local Similarity 92.3%; Pred. No. 1.2e-42;
Matches 108; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60
Db 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60

Qy 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSDSAVYCAR 117
Db 61 GKSLEWIGIYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSDSAVYCAR 117

RESULT 4
PL0011
Ig heavy chain precursor V region (4C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0011
R;Cheng, H.I.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
A;Accession: PL0011
A;Molecule type: mRNA
A;Residues: 1-151 <CHE>
A;Cross-references: UNIPARC:UPI0000176D36
A;Experimental source: cell line 4C11
A;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcholine
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/DNA: signal sequence #status predicted <SIG>
F;20-136/Product: Ig heavy chain V region 4C11 #status predicted <MAT>
F;34-117/DNA: immunoglobulin homology <IMV>
F;50-54/Region: complementarity-determining 1
F;69-85/Region: complementarity-determining 2
F;118-125/Region: complementarity-determining 3
F;137-151/DNA: C region (fragment) #status predicted <COR>

Query Match 74.7%; Score 566.5; DB 2; Length 151;
Best Local Similarity 78.4%; Pred. No. 1.9e-41;
Matches 109; Conservative 9; Mismatches 18; Indels 3; Gaps 1;

Qy 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60
Db 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60

Qy 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSDSAVYCARWDF 120
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Db 61 GKSLEWIGGDPNVDNFFYNEKFKDKATLTVDKSSSTAYMELSLTSEDSAVVYCASDY 120  
Qy 121 GSGYFDYWGQGTTLTVSS 139  
Db 121 GA---LDYWGQGTSTVTVSS 136

RESULT 5  
T01407  
Ig heavy chain (myeloma M104E) - mouse (fragment)  
C:Species: Mus sp. (mouse)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Jun-2000  
C:Accession: T01407  
R;Takahashi, S.; Matsura, Y.; Taniguchi, T.; Tamura, H.; Bitoh, S.; Onishi, S.; Yamamoto  
Microbiol. Immunol. 36, 855-863, 1992  
A:Title: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and  
A:Reference number: Z14317; MUID:93116638; PMID:1474935  
A:Accession: T01407  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-140 <TAK>  
A:Cross-references: UNIPARC:UPI00011B29E; EMBL:S51851; NID:g262657  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 74.6%; Score 565.5; DB 2; Length 140;  
Best Local Similarity 79.9%; Pred. No. 2.1e-41;  
Matches 111; Conservative 8; Mismatches 17; Indels 3; Gaps 2;

Qy 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60  
Db 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60  
Qy 61 GKLEWIGIYYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120  
Db 61 GKSLEWIGDINPNNGGTSYNGKPKGKATLTVDKSSSTAYMQLSLTSEDSAVVYCAR-DY 119  
Qy 121 GSGYFDYWGQGTTLTVSS 139  
Db 120 --DWYFDVWGAGTTVTVSS 136

RESULT 6  
S37483  
Ig gamma-2a chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S37483  
R;Ducancel, F.F.D.  
submitted to the EMBL Data Library, February 1993  
A:Reference number: S37483  
A:Accession: S37483  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-469 <DUC>  
A:Cross-references: UNIPARC:UPI000002FB47; EMBL:X70423; NID:g406252; PIDN:CAA49868.1; P  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 559; DB 2; Length 469;  
Best Local Similarity 75.5%; Pred. No. 2.8e-40;  
Matches 105; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60  
Db 1 MGWSWIFLLSCTAGVHSCIQIQSGPELVKPGASVKISCKASGYTFTDYNHWKQKP 60  
Qy 61 GKLEWIGIYYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120  
Db 61 GQGLKIGIYYPASGNTKYNFKGKATLTVDTSSTAYMQLSLTSEDSAVVYFCARMG 120  
Qy 121 GSGYFDYWGQGTTLTVSS 139

Db 121 ATATLLDYWGQGTTLTVSS 139

RESULT 7  
PH0105  
anti-digoxin transfectoma antibody light chain V region precursor - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
C:Accession: PH0105  
R;Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G.  
Mol. Immunol. 27, 901-909, 1990  
A:Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chain  
A:Reference number: PH0105; MUID:91015092; PMID:2120577  
A:Accession: PH0105  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-138 <NEA>  
A:Cross-references: UNIPARC:UPI000115EC4; GB:X56622; GB:S44836; NID:g49875; PIDN:CAA399;  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.4%; Score 548.5; DB 2; Length 138;  
Best Local Similarity 74.8%; Pred. No. 5.8e-40;  
Matches 104; Conservative 16; Mismatches 18; Indels 1; Gaps 1;

Qy 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60  
Db 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60  
Qy 61 GKLEWIGIYYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120  
Db 61 GKSLDVIYISPYSGVGYNGKPKGKATLTVDKSSSTAYMELSLTSEDSAVVYCA-GSS 119  
Qy 121 GSGYFDYWGQGTTLTVSS 139  
Db 120 GNKWMADYWGHSASVTVSS 138

RESULT 8  
PH1482  
Ig heavy chain V region (clones 36-35 [TG] and X7-TG) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C:Accession: PH1482; PH1495  
R;Giusti, A.M.; Manser, T.  
J. Exp. Med. 177, 797-809, 1993  
A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have  
d for somatic mutation.  
A:Reference number: PH1482; MUID:93171820; PMID:8436910  
A:Accession: PH1482  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-140 <GIU>  
A:Cross-references: UNIPARC:UPI0000176BA2  
A:Experimental source: hybridoma cell  
C:Genetics:  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.2%; Score 547.5; DB 2; Length 140;  
Best Local Similarity 75.7%; Pred. No. 7.2e-40;  
Matches 106; Conservative 12; Mismatches 21; Indels 1; Gaps 1;

Qy 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60  
Db 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTSYGINWYKQRP 60  
Qy 61 GKLEWIGIYYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCAR-WD 119  
Db 61 GQGLWIGIYINFGNGYTKYNEKFKGKATLTVDKSSSTAYMQLSLTSEDSAVVYFCARSVY 120

```
QY 120 FGSYYFDYWGQGTTLTVSS 139
Db 121 YGGSYYFDYWGQGTTLTVSS 140

RESULT 9
PS0057
Ig heavy chain precursor V region (PAR) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
C;Accession: PS0057
R;Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.
J. Biochem. 104, 337-343, 1988
A;Title: Biased expression of variable region gene families of the immunoglobulin heavy
A;Reference number: PS0057; MUID:89197817; PMID:2467902
A;Accession: PS0057
A;Molecule type: DNA
A;Residues: 1-135 <YAO>
A;Cross-references: UNIPARC:UPI000011B257; GB:D00307; NID:G220448; PIDN:BAA00213.1; PID:
A;Note: The authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly
C;Comment: The gene encoding this protein was isolated from a hybridoma that produces an
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-135/Product: Ig heavy chain V region PAR #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.2%; Score 547; DB 2; Length 135;
Best Local Similarity 77.0%; Pred. No. 7.7e-40;
Matches 107; Conservative 10; Mismatches 18; Indels 4; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNIHVKQSH 60
Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYSTGYFMNWKQSH 60

QY 61 GKILEWIGYYPNGVDYNGNFKSKATLVDNSNTAYMELRSLTSEDSAVVYCARWDF 120
Db 61 GKSLEWIGRINPYNGDFTPNQKFGKATLVDKSSSTAHEMLRSLTSEDSAVVYCARLNY 120

QY 121 GSGYYFDYWGQGTTLTVSS 139
Db 121 RGA-----YWGQGTTLTVSA 135

RESULT 10
PN0444
Ig heavy chain V region precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PN0444
R;Kaluza, B.; Betz, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A;Title: A general method for chimerization of monoclonal antibodies by inverse polymers
A;Reference number: PN0444; MUID:93138402; PMID:1339379
A;Accession: PN0444
A;Molecule type: mRNA
A;Residues: 1-150 <KAL>
A;Cross-references: UNIPARC:UPI0000176A08; GB:L02346
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-150/Product: Ig heavy chain V region #status predicted <MAT>
F;20-117/Domain: variable region <VRG>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.8%; Score 544; DB 2; Length 150;
Best Local Similarity 78.4%; Pred. No. 1.5e-39;
Matches 109; Conservative 4; Mismatches 29; Indels 2; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNIHVKQSH 60
Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYIFTDYNMDVKQSH 60
```

```
QY 61 GKILEWIGYYPNGVDYNGNFKSKATLVDNSNTAYMELRSLTSEDSAVVYCARWDF 120
Db 61 GKSLEWIGDIDPNFSSSSNQKFGKATLVDKSSNTAYMELRSLTSEDSAVVYCARGGF 120

QY 121 GSGYYFDYWGQGTTLTVSS 139
Db 121 --PYGMDYWGQGTSTVTVSS 137
```

## RESULT 11

```
S45249
Ig heavy chain precursor V region (Mab 1G3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1998 #sequence_revision 15-May-1998 #text_change 21-Jan-2000
C;Accession: S45249; S41429
R;Sassano, M.; Repetto, M.; Cassani, G.; Corti, A.
Nucleic Acids Res. 22, 1768-1769, 1994
A;Title: PCR amplification of antibody variable regions using primers that anneal to conserved regions
A;Reference number: S45249; MUID:94261453; PMID:8202386
A;Accession: S45249
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-138 <SAS>
A;Cross-references: UNIPARC:UPI00001161D5; EMBL:X77230; NID:G452273; PIDN:CAA54447.1; PFI:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
```

```
Query Match 70.6%; Score 535.5; DB 2; Length 138;
Best Local Similarity 72.4%; Pred. No. 7.5e-39;
Matches 105; Conservative 10; Mismatches 17; Indels 13; Gaps 2;
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QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNIHVKQSH 60
Db 1 MGWSWIFLLSGTAGVLSAVQLQSGPELVKPGASVKISKASGDSFTGNDLHWVRQSH 60

QY 61 GKILEWIGYYPNGVDYNGNFKSKATLVDNSNTAYMELRSLTSEDSAVVYCAR--- 117
Db 61 VRSLEWIGRISPYNGVTSYKNFKDKATLVDSESSNTAYMELSLTSEDSAVVYCTRPTT 120

QY 118 ---WDFGSGYYFDYWGQGTTLTVSS 139
Db 121 VDTW-----FPYWGQGTTLTVSA 138
```

## RESULT 12

## HVMSG7

```
Ig heavy chain precursor V region (93G7, 36-65) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A94264; A91261; A02028
R;Sims, J.; Rabbitts, T.H.; Estess, P.; Slaughter, C.; Tucker, P.W.; Capra, J.D.
Science 216, 309-311, 1982
A;Title: Somatic mutation in genes for the variable portion of the immunoglobulin heavy
A;Reference number: A94264; MUID:82152818; PMID:6801765
A;Accession: A94264
A;Molecule type: mRNA
A;Residues: 1-140 <SIM>
A;Cross-references: UNIPROT:P01746; UNIPARC:UPI00000270DA; GB:J00493; NID:G195006; PIDN:
A;Experimental source: strain A/J, hybridoma 93G7
R;Stekevitz, M.; Geffter, M.L.; Brodeur, P.; Riblet, R.; Marshak-Rothstein, A.
Eur. J. Immunol. 12, 1023-1032, 1982
A;Title: The genetic basis of antibody production: the dominant anti-arsenate idiotype
A;Reference number: A91261; MUID:83131846; PMID:6186498
A;Accession: A91261
A;Molecule type: DNA
A;Residues: 20-76, 'TK', 79-118, 'V', 120-125, 'Y', 127-134, 'T', 136-140 <SIE>
A;Cross-references: UNIPARC:UPI0000114D5B; GB:M19292; NID:G196201; PIDN:AAA38625.1; PID:
A;Experimental source: strain A/J, hybridoma 36-65
A;Note: the sequence was determined from the differentiated gene
A;Note: from analysis of the sizes of several other differentiated genes that hybridize
```

## C;Genetics:

A;Introns: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; hybridoma; immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-140/Product: Ig heavy chain V region (93GT) #status predicted <MAT>  
F;34-117/Domain: immunoglobulin homology <IMM>  
F;41-115/Diulfide bonds: #status predicted

Query Match 70.3%; Score 532.5; DB 1; Length 140;  
Best Local Similarity 74.3%; Pred. No. 1.4e-38;  
Matches 104; Conservative 12; Mismatches 23; Indels 1; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVOLQQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60

DB 1 MGWSWIFLLSVTAGVHSEVOLQQSGAELVRAGSSVMSCKASGYTFTSYGINWVKQRP 60

QY 61 GKILEWIGYIYPNGVSDYNQNFPSKATLIVDSSNTAYMELSLTSEDSAVTYCARWD- 119

DB 61 GQGLEWIGYINPGNGIYAYNEKFKGKTLTVDKSSSTAYMQLRSLTSEDSAVTYCARSHY 120

QY 120 FGSYYFDYWGQGTTLTVSS 139

DB 121 YGGSYFDYWGQGTTLTVSS 140

## RESULT 13

PH1489

Ig heavy chain V region (clone X41-2) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C;Accession: PH1489  
R;Giusti, A.M.; Manser, T.  
J. Exp. Med. 177, 797-809, 1993  
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.

A;Reference number: PH1482; MUID:93171820; PMID:8436910

A;Accession: PH1489

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-140 <GIU>

A;Cross-references: UNIPARC:UPI0000176BA8

A;Experimental source: hybridoma cell

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.1%; Score 531.5; DB 2; Length 140;  
Best Local Similarity 73.6%; Pred. No. 1.7e-38;  
Matches 103; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVOLQQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60

DB 1 MGWSWIFLLSVTAGVHSEVOLQQSGAELVRAGSSVMSCKASGYTFTSYGINWVKQRP 60

QY 61 GKILEWIGYIYPNGVSDYNQNFPSKATLIVDSSNTAYMELSLTSEDSAVTYCAR-WD 119

DB 61 GQGLEWIGYINPGNGIYAYNEKFKGKTLTVDKSSSTAYMQLRSLTSEDSAVTYCARSHY 120

QY 120 FGSYYFDYWGQGTTLTVSS 139

DB 121 YGGSYFDYWGQGTTLTVSS 140

## RESULT 14

PL0012

Ig heavy chain precursor V region (F6-3) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000  
C;Accession: PL0012  
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.  
Mol. Immunol. 25, 33-40, 1988  
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.

A;Reference number: PL0011; MUID:88142863; PMID:3125424

A;Accession: PL0012

A;Molecule type: mRNA

A;Residues: 1-166 <CHE>

A;Cross-references: UNIPARC:UPI0000176DJ3C

A;Experimental source: cell line F6-3

C;Comment: This protein is an anti-idiotypic antibody which induces an anti-phosphorylch

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-32/Domain: signal sequence #status predicted <SIG>

F;33-151/Product: Ig heavy chain V region 4C11 #status predicted <MAT>

F;47-130/Domain: immunoglobulin homology <IMM>

F;63-67/Region: complementarity-determining 1

F;82-98/Region: complementarity-determining 2

F;131-140/Region: complementarity-determining 3

F;152-166/Domain: C region(fragment) #status predicted <COR>

Query Match 70.0%; Score 530.5; DB 2; Length 166;  
Best Local Similarity 72.7%; Pred. No. 2.4e-38;  
Matches 101; Conservative 14; Mismatches 23; Indels 1; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVOLQQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60

DB 14 MGWSWIFLLSGTAGVLSQVQLQQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 73

QY 61 GKILEWIGYIYPNGVSDYNQNFPSKATLIVDSSNTAYMELSLTSEDSAVTYCARWDF 120

DB 74 GKLEWIGSTNPVIDYTNKENFKGRATVVDKSSSTAYMQLNSLTSEDSAVTYCAR-EG 132

QY 121 GSGYYFDYWGQGTTLTVSS 139

DB 133 GFGNSLDYWGQGTSTVNVSS 151

## RESULT 15

PH1484

Ig heavy chain V region (clones X7-3C5 and X7-3C5H) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999

C;Accession: PH1484; PH1497

R;Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A;Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.

A;Reference number: PH1482; MUID:93171820; PMID:8436910

A;Accession: PH1484

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-140 <GIU>

A;Cross-references: UNIPARC:UPI0000176BA4

A;Experimental source: hybridoma cell

C;Genetics: 16/1

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 69.3%; Score 525.5; DB 2; Length 140;  
Best Local Similarity 73.6%; Pred. No. 5.4e-38;  
Matches 103; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVOLQQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60

DB 1 MGWSWIFLLSVTAGVHSEVOLQQSGAELVRAGSSVMSCKASGYTFTSYGINWVKQRP 60

QY 61 GKILEWIGYIYPNGVSDYNQNFPSKATLIVDSSNTAYMELSLTSEDSAVTYCAR-WD 119

DB 61 GQGLEWIGYINPGNDYIYNEKFKGKTLTVDKSSSTAYMQLRSLTSEDSAVTYCARSHY 120

QY 120 FGSYYFDYWGQGTTLTVSS 139

DB 121 YGGSYFDYWGQGTTLTVSS 140



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d for somatic mutation.  
A;Reference number: PH1482; MUID:93171820; PMID:8436910  
A;Accession: PH1483  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-140 <GIU>  
A;Cross-references: UNIPARC:UPI0000176BA3  
A;Experimental source: hybridoma cell  
C;Genetics:  
A;Introns: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match	68.7%;	Score 520.5;	DB 2;	Length 140;
Best Local Similarity	72.9%;	Pred. No. 1.5e-37;		
Matches 102;	Conservative 12;	Mismatches 25;	Indels 1;	Gaps 1;

  

Qy	1	MGWSWIFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHVWKQSH 60
Db	1	MGWSFIFLLSVTAGVHSEVQLQQSGVEQVRTGSSVKMSCKASGYTFTSYGINVWKQRP 60

  

Qy	61	GKILEWIGIYPYNGVSDYNQNFKSKATLIYDSSNTAYMELSLTSEDSAVYYCAR-WD 119
Db	61	GQGLEWIGIYHPGKGYYHYSEKFKDKTTLTVDKSSSTAYNQRLSLTSEDSAVYLCARSVY 120

  

Qy	120	FGSGYYPDYWGQGTTLTVSS 139
Db	121	YGSYYFDYWAQGTTLTVSS 140

## RESULT 20

PH1488  
Ig heavy chain V region (clone X41-1) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C;Accession: PH1488  
R;Giusti, A.M.; Manser, T.  
J. Exp. Med. 177, 797-809, 1993  
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that have  
d for somatic mutation.  
A;Reference number: PH1482; MUID:93171820; PMID:8436910  
A;Accession: PH1488  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-140 <GIU>  
A;Cross-references: UNIPARC:UPI0000176BA7  
A;Experimental source: hybridoma cell  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match	68.7%;	Score 520.5;	DB 2;	Length 140;
Best Local Similarity	71.4%;	Pred. No. 1.5e-37;		
Matches 100;	Conservative 16;	Mismatches 23;	Indels 1;	Gaps 1;

  

Qy	1	MGWSWIFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHVWKQSH 60
Db	1	MGWSFIFLLSVTAGVHSEVQLQQFGAELVRAGSSVKMSCKASGYTFTSYGINVWKQRP 60

  

Qy	61	GKILEWIGIYPYNGVSDYNQNFKSKATLIYDSSNTAYMELSLTSEDSAVYYCAR-WD 119
Db	61	GQGLEWIGIYINPGYIKYNEKPKGKTTTLTVDKSASTAYNQVRSLSLTSSEDSAVYFCRSRVY 120

  

Qy	120	FGSGYYPDYWGQGTTLTVSS 139
Db	121	YGSYYFDYWGQGTTLTVSS 140

Search completed: March 20, 2006, 07:36:25  
Job time : 5.07199 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:32:13 ; Search time 2.60454 Seconds  
(without alignments)  
1527.558 Million cell updates/sec

Title: US-10-687-035-34

Perfect score: 758

Sequence: 1 MGMSWIFLLSCTAGVHSE.....FGSGYFYDYGQCTTLTVSS 139

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications\_AA\_New:\*  
1: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pdb:\*  
2: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pdb:\*  
3: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pdb:\*  
4: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pdb:\*  
5: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pdb:\*  
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7: /cgn2\_6/ptodata/2/pubppaa/US11\_NEW\_PUB.pdb:\*  
8: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pdb:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	577	76.1	139	6	US-10-504-389A-28
2	562	74.1	137	7	US-11-074-373-39
3	543.5	71.7	138	7	US-11-125-837-22
4	537.5	70.9	140	7	US-11-193-512-27
5	536	70.7	592	6	US-10-016-686-4
6	518.5	68.4	136	7	US-11-250-411-88
7	518.5	68.4	142	7	US-11-170-453-7
8	513	67.7	293	7	US-11-116-939-10
9	513	67.7	824	7	US-11-116-939-12
10	513	67.7	824	7	US-11-116-939-11
11	505.5	66.7	140	7	US-11-193-512-63
12	496.5	65.5	136	7	US-11-250-411-91
13	495.5	65.4	136	7	US-11-250-411-95
14	494.5	65.2	140	7	US-11-183-205-62
15	493.5	65.1	140	7	US-11-193-512-74
16	488	64.4	145	6	US-10-504-389A-45
17	487.5	64.3	140	7	US-11-193-512-78
18	487	64.2	143	6	US-10-932-334-52
19	485.5	64.1	462	7	US-11-177-648-9
20	482.5	63.7	140	7	US-11-193-512-83
21	478	63.1	138	7	US-11-089-872-3
22	477	62.9	153	7	US-11-126-798-4
23	477	62.9	488	6	US-10-016-686-3
24	475.5	62.7	462	7	US-11-177-648-30
25	475.5	62.7	462	7	US-11-177-648-33

139	7	US-11-226-325-34	Sequence 34, Appl
130	7	US-11-179-820-6	Sequence 6, Appl
119	7	US-11-154-337-2	Sequence 2, Appl
119	7	US-11-182-908-2	Sequence 2, Appl
119	7	US-11-102-120-2	Sequence 2, Appl
119	7	US-11-223-361-2	Sequence 1, Appl
243	6	US-10-016-686-1	Sequence 4, Appl
117	7	US-11-087-528-4	Sequence 4, Appl
117	7	US-11-122-622-4	Sequence 4, Appl
139	7	US-11-226-325-4	Sequence 26, Appl
139	7	US-11-226-325-26	Sequence 2, Appl
139	7	US-11-226-325-44	Sequence 2, Appl
232	7	US-11-173-564-2	Sequence 32, Appl
462	7	US-11-177-648-32	Sequence 30, Appl
139	7	US-11-226-325-30	Sequence 16, Appl
115	7	US-11-165-023-16	Sequence 100, Appl
139	7	US-11-226-325-100	Sequence 36, Appl
139	7	US-11-226-325-36	Sequence 35, Appl
121	7	US-11-107-028-35	Sequence 31, Appl
462	7	US-11-177-648-31	Sequence 97, Appl
462	7	US-11-177-648-97	Sequence 74, Appl
120	6	US-10-932-334-74	Sequence 24, Appl
139	7	US-11-226-325-24	Sequence 7, Appl
114	7	US-11-102-743-7	Sequence 32, Appl
139	7	US-11-226-325-32	Sequence 98, Appl
139	7	US-11-226-325-98	Sequence 96, Appl
462	7	US-11-177-648-96	Sequence 50, Appl
120	6	US-10-932-334-71	Sequence 71, Appl
139	7	US-11-226-325-40	Sequence 40, Appl
139	7	US-11-226-325-42	Sequence 42, Appl
139	7	US-11-226-325-46	Sequence 46, Appl
139	7	US-11-226-325-50	Sequence 50, Appl
139	7	US-11-226-325-127	Sequence 137, Appl
462	7	US-11-177-648-29	Sequence 29, Appl
122	7	US-11-107-028-39	Sequence 39, Appl
139	7	US-11-226-325-18	Sequence 18, Appl
139	7	US-11-226-325-22	Sequence 22, Appl
139	7	US-11-226-325-48	Sequence 48, Appl
462	7	US-11-158-505-72	Sequence 72, Appl
119	7	US-11-097-812-71	Sequence 71, Appl
119	7	US-11-097-812-73	Sequence 73, Appl
119	7	US-11-097-812-74	Sequence 74, Appl
119	7	US-11-097-812-76	Sequence 76, Appl
462	7	US-11-177-648-28	Sequence 28, Appl
120	6	US-10-932-334-72	Sequence 72, Appl
138	7	US-11-250-411-90	Sequence 90, Appl
139	7	US-11-226-325-38	Sequence 38, Appl
117	6	US-10-932-334-76	Sequence 76, Appl
119	6	US-10-507-662-22	Sequence 22, Appl
130	7	US-11-188-187A-3	Sequence 3, Appl
139	7	US-11-226-325-16	Sequence 16, Appl
139	7	US-11-226-325-20	Sequence 20, Appl
471	7	US-11-106-820-25	Sequence 25, Appl
471	7	US-11-106-820-27	Sequence 27, Appl
471	7	US-11-190-364-22	Sequence 22, Appl
471	7	US-11-190-364-23	Sequence 23, Appl
471	7	US-11-147-780-22	Sequence 23, Appl
471	7	US-11-147-780-23	Sequence 23, Appl
139	7	US-11-226-325-28	Sequence 28, Appl
467	7	US-11-158-505-5	Sequence 5, Appl
467	7	US-11-158-505-13	Sequence 13, Appl
467	7	US-11-158-505-15	Sequence 15, Appl
467	7	US-11-158-505-21	Sequence 21, Appl
467	7	US-11-158-505-23	Sequence 23, Appl
467	7	US-11-158-505-29	Sequence 29, Appl
467	7	US-11-158-505-31	Sequence 31, Appl
120	7	US-11-097-812-144	Sequence 144, Appl
138	7	US-11-250-411-86	Sequence 86, Appl
462	7	US-11-177-648-95	Sequence 95, Appl
115	7	US-11-165-023-31	Sequence 31, Appl
119	7	US-11-097-812-66	Sequence 66, Appl
119	7	US-11-097-812-67	Sequence 67, Appl

99 454.5 60.0 120 7 US-11-097-812-136 Sequence 136, App  
100 454.5 60.0 120 7 US-11-097-812-145 Sequence 145, App

## ALIGNMENTS

## RESULT 1

US-10-504-389A-28  
; Sequence 28, Application US/10504389A  
; Publication No. US20060045876A1  
; GENERAL INFORMATION:  
; APPLICANT: Renner, Christoph  
; APPLICANT: Scott, Andrew  
; TITLE OF INVENTION: FUSION PROTEINS OF HUMANIZED G250 SPECIFIC  
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF  
; FILE REFERENCE: LUD 5821  
; CURRENT APPLICATION NUMBER: US/10/504,389A  
; CURRENT FILING DATE: 2004-08-10  
; PRIOR APPLICATION NUMBER: PCT/US03/04243  
; PRIOR FILING DATE: 2002-02-12  
; NUMBER OF SEQ ID NOS: 56  
; SEQ ID NO 28  
; LENGTH: 139  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; OTHER INFORMATION: amino acid sequence for murine 19/2 heavy chain variable region  
US-10-504-389A-28

Query Match 76.1%; Score 577; DB 6; Length 139;  
Best Local Similarity 83.6%; Pred. No. 4.7e-41;  
Matches 112; Conservative 7; Mismatches 13; Indels 2; Gaps 1;

Qy 6 IFLLSGTAGVHSEVOLQSGPELVKPGASVKISCKASGYTFDYNHIVKQSHGKILE 65  
Db 4 IMFLSGTAGVHSEVOLQSGPELVKPGASVKISCKASGYTFDYNHIVKQSHGKSLD 63  
Qy 66 WIGYIYPNGVSDYNQNFKSKATLIVDSSNTAYMELRLTSDSAVYCARWDFGSGY 125  
Db 64 WIGYIAPSGGTGYNQFKNRATLTVKSSSTAYMELRLTSDSAVYCARRD--RFPY 121  
Qy 126 FDYWGQGTTLTVSS 139  
Db 122 FDYWGQGTTLTVSS 135

## RESULT 2

US-11-074-373-39  
; Sequence 39, Application US/11074373  
; Publication No. US20060024302A1  
; GENERAL INFORMATION:  
; APPLICANT: Achen et al.  
; TITLE OF INVENTION: CHIMERIC ANTI-VEGF-D ANTIBODIES AND HUMANIZED ANTI-VEGF-D ANTIBODIES  
; TITLE OF INVENTION: AND METHODS OF USING SAME  
; FILE REFERENCE: 28967/39969A  
; CURRENT APPLICATION NUMBER: US/11/074,373  
; CURRENT FILING DATE: 2005-03-07  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 39  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-074-373-39

Query Match 74.1%; Score 562; DB 7; Length 137;  
Best Local Similarity 74.8%; Pred. No. 8e-40;  
Matches 104; Conservative 15; Mismatches 18; Indels 2; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVOLQSGPELVKPGASVKISCKASGYTFDYNHIVKQSH 60  
Db 1 MGWSGVFLLLSGTAGVHSEVOLQSGPELVKPGASVKISCKASGYTFDYNHIVKQSH 60

Qy 61 GKLEWIGYIYPNGVSDYNQNFKSKATLIVDSSNTAYMELRLTSDSAVYCARWDF 120  
Db 61 GKLEWIGYIDPNGDTTNNQKFKGKATLTVKSSSTAFMHLNLSLTSDESAVYCAR 120  
Qy 121 GSGYFDYWGQGTTLTVSS 139  
Db 121 YGG--MDYWGQGTSLTVSS 137

## RESULT 3

US-11-125-837-22  
; Sequence 22, Application US/11125837  
; Publication No. US20050266003A1  
; GENERAL INFORMATION:  
; APPLICANT: Lin, Rong-Hwa  
; APPLICANT: Chang, Chung Nan  
; APPLICANT: Chen, Pei-Jiun  
; APPLICANT: Huang, Chiu-Chen  
; TITLE OF INVENTION: ANTIBODIES  
; FILE REFERENCE: 13062-011001  
; CURRENT APPLICATION NUMBER: US/11/125,837  
; CURRENT FILING DATE: 2005-05-10  
; PRIOR APPLICATION NUMBER: US 60/569,892  
; PRIOR FILING DATE: 2004-05-10  
; NUMBER OF SEQ ID NOS: 100  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-125-837-22

Query Match 71.7%; Score 543.5; DB 7; Length 138;  
Best Local Similarity 77.1%; Pred. No. 2.7e-38;  
Matches 108; Conservative 7; Mismatches 22; Indels 3; Gaps 2;

Qy 1 MGWSWIFLLSGTAGVHSEVOLQSGPELVKPGASVKISCKASGYTFDYNHIVKQSH 60  
Db 1 MEWSWVFLLLSVTTGVHSEVOLQSGPELVKPGALVKISCKASGYFTAYYIHVKQSH 60  
Qy 61 GKLEWIGYIYPNGVSDYNQNFKSKATLIVDSSNTAYMELRLTSDSAVYCARWDF 120  
Db 61 GKLEWIGRVNPTNGTSTYNNPKFKKAILNVKSSSTAYMELRLTSDSAVYCAR--S 118  
Qy 121 GSGYFDYWGQGTTLTVSS 139  
Db 119 GSPYRYDDWGQGTTLTVSS 138

## RESULT 4

US-11-193-512-27  
; Sequence 27, Application US/11193512  
; Publication No. US20050272918A1  
; GENERAL INFORMATION:  
; APPLICANT: KOIKE, Masamichi  
; FURUYA, Akiko  
; NAKAMURA, Kazuyasu  
; IIDA, Akihiro  
; ANAZAWA, Hideharu  
; HANAI, Nobuo  
; TAKATSU, Kiyoshi  
; TITLE OF INVENTION: Antibody Against Human Interleukin-5  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/11/193,512
;   FILING DATE: 01-AUG-2005
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/10/283,349
;   FILING DATE: 29-Oct-2002
;   APPLICATION NUMBER: US/08/836,561
;   FILING DATE: 09-MAY-1997
;   APPLICATION NUMBER: JP 232384/95
;   FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Lawrence, III, Stanton T
;   REGISTRATION NUMBER: 25,736
;   REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-790-9090
;   TELEFAX: 212-869-9741
;   TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 140 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-11-193-512-27

Query Match      70.9%; Score 537.5; DB 7; Length 140;
Best Local Similarity 76.1%; Pred. No. 8.5e-38;
Matches 108; Conservative 5; Mismatches 24; Indels 5; Gaps 2;

QY 1 MGWSWIFLLSGTAGVHSEVOLQSGPBLVPGASVKISCKASGYTFDYNHWKQSH 60
DB 1 MEWSWIFLLSGTAGVHSEVOLQSGPBLVPGASVKMSCKASGYTFSTYVHWKQRP 60
QY 61 GKILEWIGYIPYNGVDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVVYCARWDF 120
DB 61 GQGLWIGYIPYNGVDYTKYRKATLTSDRSSVTVMELSSLTSEDSAVVYLCGR--E 118
QY 121 GSGYY---PDYWGQGTTLTVSS 139
DB 119 GIRYGLLDYWGQGTTLTVSS 140

RESULT 5
US-10-016-686-4
; Sequence 4, Application US/10016686
; Publication No. US2006001422A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; APPLICANT: Kingsman, Alan
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Bebbington, Christopher Robert
; APPLICANT: Carroll, Miles William
; APPLICANT: Ellard, Fiona Margaret
; APPLICANT: Myers, Kevin Alan
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 674523-2012
; CURRENT APPLICATION NUMBER: US/10/016,686
; PRIOR FILING DATE: 2002-11-02
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 592
; TYPE: PRT

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/11/193,512
;   FILING DATE: 01-AUG-2005
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/10/283,349
;   FILING DATE: 29-Oct-2002
;   APPLICATION NUMBER: US/08/836,561
;   FILING DATE: 09-MAY-1997
;   APPLICATION NUMBER: JP 232384/95
;   FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Lawrence, III, Stanton T
;   REGISTRATION NUMBER: 25,736
;   REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-790-9090
;   TELEFAX: 212-869-9741
;   TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 140 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-11-193-512-27

Query Match      70.9%; Score 536; DB 6; Length 592;
Best Local Similarity 74.8%; Pred. No. 4.2e-37;
Matches 104; Conservative 9; Mismatches 26; Indels 0; Gaps 0;

QY 1 MGWSWIFLLSGTAGVHSEVOLQSGPBLVPGASVKISCKASGYTFDYNHWKQSH 60
DB 1 MGWSWIFLLSGTAGVHSEVOLQSGPBLVPGASVKISCKASGYTFDYNHWKQSH 60
QY 61 GKILEWIGYIPYNGVDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVVYCARWDF 120
DB 61 GKSLEWIGIRINPNNGVTLNQKFKKAILTVDKSSSTAYMELSLTSEDSAVVYCARSTM 120
QY 121 GSGYYFDYWGQGTTLTVSS 139
DB 121 ITNYVMDYWGQVTSVTSS 139

RESULT 6
US-11-250-411-88
; Sequence 88, Application US/11250411
; Publication No. US2006003483A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR PUT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/11/250,411
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 88
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-88

Query Match      68.4%; Score 518.5; DB 7; Length 136;
Best Local Similarity 72.7%; Pred. No. 3.1e-36;
Matches 101; Conservative 13; Mismatches 22; Indels 3; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVOLQSGPBLVPGASVKISCKASGYTFDYNHWKQSH 60
DB 1 MGFSRIFLLSVTTGVHSGAFLQSGAELVRPGASVKMSCKASGYTFINYNHWYKQTP 60
QY 61 GKILEWIGYIPYNGVDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVVYCARWDF 120
DB 61 RQGLEWIGAIPGNGFTSYNQKFKKAILTVDKSSSTVMQRLSLTSEDSAVVYFCAR--- 117
QY 121 GSGYYFDYWGQGTTLTVSS 139
DB 118 DGDYVFDYWGQGTTLTVSS 136

RESULT 7
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US-11-170-453-7
; Sequence 7, Application US/11170453
; Publication No. US20060039913A1
; GENERAL INFORMATION:
; APPLICANT: Das, Anuk
; APPLICANT: Carton, Jill
; APPLICANT: Tsui, Ping
; TITLE OF INVENTION: ANTI-MCP1 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5068
; CURRENT APPLICATION NUMBER: US/11/170,453
; CURRENT FILING DATE: 2005-06-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-170-453-7

Query Match      58.4%; Score 518.5; DB 7; Length 142;
Best Local Similarity 70.4%; Pred. No. 3.2e-36;
Matches 100; Conservative 15; Mismatches 24; Indels 3; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
DB 1 MGWSWIFLLSGTAGVHSCVQLKQSGAEIVRPGASVKLSCKASGYFTFDYNIHWKQRP 60
QY 61 GKILEWIGIYYPNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWD- 119
DB 61 GQGLEWIAIYVPGTGYNNENFKGKATLTAEKSSSTAYVQLSLSLTSEDSAVYFCARSGS 120
QY 120 --FGSGIYFDYWGQGTTLTVSS 139
DB 121 TVVGNYYGMDYWGQGTSTVTVSS 142

RESULT 8
US-11-116-939-10
; Sequence 10, Application US/11116939
; Publication No. US20050265995A1
; GENERAL INFORMATION:
; APPLICANT: Stephen Tomlinson
; APPLICANT: Richard J. Quigg
; TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
; FILE REFERENCE: 19113.0115U2
; CURRENT APPLICATION NUMBER: US/11/116,939
; CURRENT FILING DATE: 2005-04-28
; PRIOR FILING DATE: 2005-04-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
US-11-116-939-10

Query Match      67.7%; Score 513; DB 7; Length 293;
Best Local Similarity 69.9%; Pred. No. 1.7e-35;
Matches 100; Conservative 12; Mismatches 27; Indels 4; Gaps 2;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
DB 151 MGWSVLMFLVATATGVHSGVQLQSGPELVKPGASVKISKASGYFTFDYAIHWKQSH 210
QY 61 GKILEWIGIYYPNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCAR- 119
DB 211 AKSLEWIGVISTYGHYTHNQKFGKATLTVDKSSNTAYMELARLTSEDSAIYYCARPNN 270
QY 120 FGSG---YYPFDYWGQGTTLTVSS 139
DB 121 TVVGNYYGMDYWGQGTSTVTVSS 142

US-11-116-939-12
; Sequence 12, Application US/11116939
; Publication No. US20050265995A1
; GENERAL INFORMATION:
; APPLICANT: Stephen Tomlinson
; APPLICANT: Richard J. Quigg
; TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
; FILE REFERENCE: 19113.0115U2
; CURRENT APPLICATION NUMBER: US/11/116,939
; CURRENT FILING DATE: 2005-04-28
; PRIOR FILING DATE: 2005-04-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
US-11-116-939-12

Query Match      67.7%; Score 513; DB 7; Length 412;
Best Local Similarity 69.9%; Pred. No. 2.4e-35;
Matches 100; Conservative 12; Mismatches 27; Indels 4; Gaps 2;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
DB 151 MGWSVLMFLVATATGVHSGVQLQSGPELVKPGASVKISKASGYFTFDYAIHWKQSH 210
QY 61 GKILEWIGIYYPNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCAR- 119
DB 211 AKSLEWIGVISTYGHYTHNQKFGKATLTVDKSSNTAYMELARLTSEDSAIYYCARPNN 270
QY 120 FGSG---YYPFDYWGQGTTLTVSS 139
DB 271 YGSSPPYYAMDCWGQGTSTVTVSS 293

RESULT 10
US-11-116-939-11
; Sequence 11, Application US/11116939
; Publication No. US20050265995A1
; GENERAL INFORMATION:
; APPLICANT: Stephen Tomlinson
; APPLICANT: Richard J. Quigg
; TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
; FILE REFERENCE: 19113.0115U2
; CURRENT APPLICATION NUMBER: US/11/116,939
; CURRENT FILING DATE: 2005-04-28
; PRIOR FILING DATE: 2005-04-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note=synthetic
US-11-116-939-11

Query Match      67.7%; Score 513; DB 7; Length 824;
Best Local Similarity 69.9%; Pred. No. 4.4e-35;
Matches 100; Conservative 12; Mismatches 27; Indels 4; Gaps 2;
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1	MGWSIFIFLLSGTAGHSEVLOCSGPELYKPGASVKISCKASGYTFDTYNLHWKQSH	60
	:     :     :     :     :     :     :     :     :     :	
151	MGWSCVPLFVATATGVHSQVQLSGSGPELVKPGSVKISKSGYTFDTYALHWKQSH	210
	:     :     :     :     :     :     :     :     :	
61	GKILWIGVYYPNGVSDYNQFKSKATLIVDNSNTAYMELRSLTSEDSAVYTCAR-WD	119
	:     :     :     :     :     :     :     :     :	
211	AKSLWIGVISTYYGTHYNGKFGKATLVDKSSNTAYMELARLTSEDSAIYTCARPNN	270
	:     :     :     :     :     :     :     :     :	
120	FGSG---YYFDYWGQGTLTVSS	139
	:     :     :     :     :     :     :     :     :	
271	YGSSPPYYAMDCWGQTSVTVSS	293
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Qy 1 MGSWIFLLFLLSTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNIIHWKQSH 60
Db 1 MEWSWIFLLFLLSTAGVHSEVQLVQSGAEVKYKPGASVKSKASGYTFTSVIIHWKQAP 60
Qy 61 GKILEWIGIYTPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSGEDSAVYYCARWDF 120
Db 61 GQGLEWNGWYINPYNDGTYKNERKGRVTITADTSTSTAYMELSSURSEDYAVYYCAR--E 118
Qy 121 GSGYY---FDYWGQGTTLTVSS 139
Db 119 GIRYGLLDYWGQGLTVTVSS 140
RESULT 12
US-11-250-411-91
; Sequence 91, Application US/11250411
; Publication No. US20060034838A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/11/250,411
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-91

```

QY 1 MGSWTFLLSCTAGVHSEVOLQQSGPELVKPGASVKISKASGYTFTDYNIIHWKQSH 60  
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
Db 1 MGFSRIFLFLSVTTGVHSQVLVQSAGAEVKVPKPGASVKSKASGYTFINNMHVQRAP 60  
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
QY 61 GKILEWIGIYYPNVGSDNYNQNPFSKATLIVDNSSNTAYNELRSLTSEDGSAVYTCARWDF 120  
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
Db 61 GCGLEWGAIIPGNGSTSYNKFEGKRVITVDKSTSTAYNELSLSRSEDTA VYVCAR --- 117  
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
QY 121 GSGYYEDYWGQGTTLTVSS 139  
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :  
Db 118 DGDYEDYWGQGTTLTVSS 136  
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 13

US-11-250-411-95

; Sequence 95, Application US/11250411

; Publication No. US20060034838A1

; GENERAL INFORMATION:

; APPLICANT: SHITARA, KENYA

; APPLICANT: ITO, MIKITO

; APPLICANT: HANAI, NOBUO

; APPLICANT: KAWADA, YOKO

; APPLICANT: NAKAMURA, KAZUYASU

```
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/11/250,411
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
; US-11-250-411-95

Query Match      65.4%; Score 495.5; DB 7; Length 136;
Best Local Similarity 66.9%; Pred. No. 2.4e-34;
Matches 93; Conservative 20; Mismatches 23; Indels 3; Gaps 1;

QY 1 MGWSWIFLLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
DB 1 MGFSRIEFLLSVTTGVHSSQVLQSGAEVKKPGASVKVSKASGYFTFDYNIHWVRQAP 60
QY 61 GKILEWIGYIYPNGVDYQNFKSKATLIVDNNSNTAYMELRSLTSDSAVYYCARWDF 120
DB 61 GQGLEWGAIFPGNGFTSYNQKFGKATLTVDKSTAYMQLRSRSEDYAVYFCAR--- 117
QY 121 GSGYYFDYWGQGTTLTVSS 139
DB 118 DGDYFDYWGQGTTLTVSS 136

RESULT 14
US-11-183-205-62
; Sequence 62, Application US/11/183205
; Publication No. US2006030521A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bove, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-US01
; CURRENT APPLICATION NUMBER: US/11/183,205
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 11/183,205
; PRIOR FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/US2002/032263
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; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 10/287,994
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Mus musculus
; US-11-183-205-62

Query Match      65.2%; Score 494.5; DB 7; Length 140;
Best Local Similarity 68.6%; Pred. No. 3e-34;
Matches 96; Conservative 15; Mismatches 28; Indels 1; Gaps 1;

QY 1 MGWSWIFLLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
DB 1 MGWSLILLFLVAVATRVLSQVLQSGAEVKKPGASVKVSKASGYFTFDYNIHWVQKTP 60
QY 61 GKILEWIGYIYPNGVDYQNFKSKATLIVDNNSNTAYMELRSLTSDSAVYYCARWD- 119
DB 61 GRGLEWIGALYIPNGDTSYNQKFGKATLTADKSSSTAYMQLSLSLTSDSAVYYCARSTY 120
QY 120 FSGYYFDYWGQGTTLTVSS 139
DB 121 YGDDWYFNVWGAGTTVTUSA 140

RESULT 15
US-11-193-512-74
; Sequence 74, Application US/11/193512
; Publication No. US20050272918A1
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; FURUYA, Akiko
; NAKAMURA, Kazuyasu
; IIDA, Akihiro
; ANAZAWA, Hideharu
; HANAI, Nobuo
; TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; Receptor Alpha Chain
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/193,512
; FILING DATE: 01-AUG-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,349
; FILING DATE: 29-Oct-2002
; APPLICATION NUMBER: US/08/836,561
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: JP 232384/95
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, III, Stanton T
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-115-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
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;       TELEX: 66141 PENNIE
;
; INFORMATION FOR SEQ ID NO: 74:
;
;   SEQUENCE CHARACTERISTICS:
;
;     LENGTH: 140 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;
;   MOLECULE TYPE: peptide
;
;   SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-11-193-512-74

Query Match          65.1%;   Score 493.5;   DB 7;   Length 140;
Best Local Similarity 67.6%;   Pred. No. 3.6e-34;
Matches 96; Conservative 14; Mismatches 27; Indels 5; Gaps 2;

QY      1  MCWSWIFLLSLGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHWKQSH 60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  MEWSWIFLLSLGTAGVHSEVQLVQSGAEVKPGASVKISCKASGYTFYIHWVRQAP 60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      61  GKLEWIGYIYPYGVSDYNQFNKSKATLIVDSSNTAYMELRSLTSEDSAVVYCARWDF 120
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61  GQGLEWVGVIYNDYDGTKYNERFKGRVTITADTSTAYMELSSLSESDTAVYLGR--E 118
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      121  GSGYY---FDYWGQGTTLTVSS 139
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Db      119  GIRYVGLLGDYWGQGTTLTVSS 140
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RESULT 16
US-10-504-389A-45
; Sequence 45, Application US/10504389A
; Publication NO. US20060045876A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Christoph
; APPLICANT: Scott, Andrew
; TITLE OF INVENTION: FUSION PROTEINS OF HUMANIZED G250 SPECIFIC
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: LUD 5821
; CURRENT APPLICATION NUMBER: US/10/504,389A
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US03/04243
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 56
; SEQ ID NO 45
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: amino acid sequence for murine heavy chain variable region
US-10-504-389A-45

```

RESULT 17  
US-11-193-512-78  
; Sequence 78, Application US/11193512  
; Publication No. US20050272918A1  
; GENERAL INFORMATION:

APPLICANT: KOIKE, Masamichi  
FURUYA, Akiko  
NAKAMURA, Kazuyasu  
IIDA, Akihiro  
ANAZAWA, Hideharu  
HANAI, Nobuo  
TAKATSU, Kiyoshi  
TITLE OF INVENTION: Antibody Against Human Interleukin-5  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION NUMBER:  
APPLICATION NUMBER: US/11/193,512  
FILING DATE: 01-Aug-2005  
CLASSIFICATION: <Unknown>

RESULT 18  
US-10-932-334-52  
; Sequence 52, Application US/10932334  
; Publication No. US20050249728A1  
; GENERAL INFORMATION:

APPLICANT: ImmunoGen, Inc.  
 TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY  
 FILE REFERENCE: A8689  
 CURRENT APPLICATION NUMBER: US/10/932,334  
 CURRENT FILING DATE: 2004-09-02  
 PRIOR APPLICATION NUMBER: US/10/729,441  
 PRIOR FILING DATE: 2003-12-08  
 PRIOR APPLICATION NUMBER: 10/170,390  
 PRIOR FILING DATE: 2002-06-14  
 NUMBER OF SEQ ID NOS: 96  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 52  
 LENGTH: 143  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-10-932-334-52

Query Match 64.2%; Score 487; DB 6; Length 143;  
 Best Local Similarity 68.5%; Pred. No. 1.3e-33;  
 Matches 98; Conservative 15; Mismatches 26; Indels 4; Gaps 2;  
 QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60  
 DB 1 MGWSWIFLLSVATATEVHSGVQLQSGAELVKPGASVKISKASGYTFTSYMMHWKQRP 60  
 QY 61 GKILEWIGYIPYNGVDYNGNFKSKATLIIVDSSNTAYMELRLSLTSDSAVYYCARW-- 118  
 DB 61 GQGLEWIGINPNSNGRTNYNEKFKRATLVKSSSTAYMQLSSLTSDSAVYYFARGRP 120  
 QY 119 DF--GSGYYPDYWGQGTTLTVSS 139  
 DB 121 DYGGSKWYFDVWGAGTTVTSS 143

RESULT 19  
 US-11-177-648-9  
 Sequence 9, Application US/11177648  
 Publication No. US20060029603A1  
 GENERAL INFORMATION:  
 APPLICANT: Jonathon Henry ELLIS  
 APPLICANT: Paul Andrew HAMBLIN  
 APPLICANT: Paul Alexander WILSON  
 APPLICANT: Alan Peter LEWIS  
 TITLE OF INVENTION: IMMUNOGLOBULINS  
 FILE REFERENCE: PB60608-2  
 CURRENT APPLICATION NUMBER: US/11/177,648  
 CURRENT FILING DATE: 2005-07-06  
 PRIOR APPLICATION NUMBER: PCT/GB2004/005325  
 PRIOR FILING DATE: 2004-12-20  
 PRIOR APPLICATION NUMBER: GB0329711.6  
 PRIOR FILING DATE: 2003-12-22  
 PRIOR APPLICATION NUMBER: GB0329684.5  
 PRIOR FILING DATE: 2003-12-22  
 NUMBER OF SEQ ID NOS: 113  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 9  
 LENGTH: 462  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-11-177-648-9

Query Match 64.1%; Score 485.5; DB 7; Length 462;  
 Best Local Similarity 69.1%; Pred. No. 4.8e-33;  
 Matches 96; Conservative 13; Mismatches 23; Indels 7; Gaps 2;  
 QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60  
 DB 1 MGWSWIFLLVAATAGVHSEVQLQSGPELVKPGASVKISKASGYTFTSYMMHWKQRP 60  
 QY 61 GKILEWIGYIPYNGVDYNGNFKSKATLIIVDSSNTAYMELRLSLTSDSAVYYCARWDF 120  
 DB 61 GQGLEWIGINPNSNGRTNYNEKFKSKATLVKSSSTAYMQLSSLTSDSAVYYC--EL 117

QY 121 GSGYYPDYWGQGTTLTVSS 139  
 DB 118 GQG---YWGQGTTLTVSS 132  
 RESULT 20  
 US-11-193-512-83  
 Sequence 83, Application US/11193512  
 Publication No. US20050272918A1  
 GENERAL INFORMATION:  
 APPLICANT: KOIKE, Masamichi  
 FURUYA, Akiko  
 NAKAMURA, Kazuyasu  
 IIDA, Akihiko  
 ANAZAWA, Hideharu  
 HANAI, Nobuo  
 TAKATSU, Kiyoshi  
 TITLE OF INVENTION: Antibody Against Human Interleukin-5  
 Receptor Alpha Chain  
 NUMBER OF SEQUENCES: 106  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/11/193,512  
 FILING DATE: 01-Aug-2005  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/10/283,349  
 FILING DATE: 29-Oct-2002  
 APPLICATION NUMBER: US/08/836,561  
 FILING DATE: 09-MAY-1997  
 APPLICATION NUMBER: JP 232384/95  
 FILING DATE: 11-SEP-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lawrence, III, Stanton T  
 REGISTRATION NUMBER: 25,736  
 REFERENCE/DOCKET NUMBER: 7005-115-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-790-9090  
 TELEFAX: 212-869-9741  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 83:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 140 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 83:  
 US-11-193-512-83

Query Match 63.7%; Score 482.5; DB 7; Length 140;  
 Best Local Similarity 66.9%; Pred. No. 2.9e-33;  
 Matches 95; Conservative 12; Mismatches 30; Indels 5; Gaps 2;  
 QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60  
 DB 1 MGWSWIFLLSGTAGVHSEVQLQSGAELVKPGASVKISKASGYTFTSYMMHWKQRP 60  
 QY 61 GKILEWIGYIPYNGVDYNGNFKSKATLIIVDSSNTAYMELRLSLTSDSAVYYCARWDF 120  
 DB 61 GQGLEWIGYIPYNDGTYNEKFKRATLVKSSSTAYMELRLSLTSDSAVYYCGR--E 118



Search completed: March 20, 2006, 07:32:42  
Job time : 2.60454 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:31:52 ; Search time 24.6746 Seconds  
(without alignments)  
2353.772 Million cell updates/sec

Title: US-10-687-035-34

Perfect score: 758

Sequence: 1 MGWSWIFLPLLSCTAGVHSE.....FGSGYYPYWGQGTTLTVSS 139

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	758	100.0	139	5	US-10-687-035-34
2	625	82.5	135	4	US-10-389-155-60
3	625	82.5	135	4	US-10-389-417-60
4	625	82.5	135	4	US-10-452-357-69
5	616	81.3	137	4	US-10-462-062-153
6	616	81.3	137	4	US-10-462-062-154
7	613.5	80.9	132	3	US-09-982-107-14
8	613.5	80.9	132	5	US-10-781-989-14
9	600.5	79.2	438	3	US-09-903-327A-6
10	600.5	79.2	456	3	US-09-903-327A-2
11	600.5	79.2	493	3	US-09-903-327A-13
12	600.5	79.2	510	3	US-09-903-327A-12
13	600.5	79.2	597	3	US-09-903-327A-11
14	600.5	79.2	613	3	US-09-903-327A-14
15	585.5	77.2	136	4	US-10-768-193-7
16	578.5	76.3	139	4	US-10-774-076-8
17	577	76.1	139	4	US-10-365-123-28
18	568	74.9	137	4	US-10-462-062-158
19	567	74.8	135	5	US-10-837-904-27
20	565.5	74.6	138	4	US-10-389-155-72
21	565.5	74.6	138	4	US-10-389-417-72
22	565.5	74.6	138	4	US-10-452-357-85
23	564	74.4	143	3	US-09-301-593-26
24	564	74.4	143	4	US-10-159-006-26
25	564	74.4	472	3	US-09-301-593-30
26	564	74.4	472	4	US-10-159-006-30
27	559	73.7	137	4	US-10-462-062-157

28	557	73.5	133	5	US-10-810-861A-79	Sequence 79, Appl
29	555.5	73.3	462	5	US-10-828-782A-18	Sequence 18, Appl
30	552	72.8	467	5	US-10-500-696-2	Sequence 2, Appl
31	551.5	72.8	136	4	US-10-138-505-12	Sequence 12, Appl
32	551.5	72.8	136	4	US-10-257-864A-88	Sequence 88, Appl
33	551.5	72.8	136	4	US-10-221-131-93	Sequence 93, Appl
34	551.5	72.8	136	4	US-10-399-518-117	Sequence 117, App
35	551.5	72.8	136	5	US-10-399-585-117	Sequence 117, App
36	551.5	72.8	136	5	US-10-645-085A-88	Sequence 88, Appl
37	550	72.6	152	4	US-10-642-120-2	Sequence 2, Appl
38	550	72.6	152	4	US-10-642-060-2	Sequence 2, Appl
39	550	72.6	152	4	US-10-642-122-2	Sequence 2, Appl
40	550	72.6	152	4	US-10-642-059-2	Sequence 2, Appl
41	550	72.6	152	4	US-10-642-124-2	Sequence 2, Appl
42	550	72.6	152	4	US-10-621-269-2	Sequence 2, Appl
43	550	72.6	152	4	US-10-620-850-2	Sequence 2, Appl
44	550	72.6	152	4	US-10-642-118-2	Sequence 2, Appl
45	550	72.6	152	4	US-10-642-119-2	Sequence 2, Appl
46	550	72.6	152	4	US-10-642-117-2	Sequence 2, Appl
47	550	72.6	152	5	US-10-642-099-2	Sequence 2, Appl
48	550	72.6	152	5	US-10-642-064-2	Sequence 2, Appl
49	550	72.6	152	5	US-10-642-116-2	Sequence 2, Appl
50	550	72.6	152	5	US-10-642-100-2	Sequence 2, Appl
51	550	72.6	152	5	US-10-642-058-2	Sequence 2, Appl
52	550	72.6	152	5	US-10-642-121-2	Sequence 2, Appl
53	550	72.6	152	5	US-10-642-065-2	Sequence 2, Appl
54	550	72.6	152	5	US-10-642-071-2	Sequence 2, Appl
55	545.5	72.0	142	3	US-09-772-120-8	Sequence 8, Appl
56	545	71.9	144	4	US-10-195-752-112	Sequence 112, App
57	540.5	71.3	136	4	US-10-138-505-8	Sequence 8, Appl
58	540.5	71.3	136	4	US-10-257-864A-86	Sequence 86, Appl
59	540.5	71.3	136	4	US-10-221-131-91	Sequence 91, Appl
60	540.5	71.3	136	4	US-10-399-518-115	Sequence 115, App
61	540.5	71.3	136	5	US-10-399-585-115	Sequence 115, App
62	540.5	71.3	136	5	US-10-645-085A-86	Sequence 86, Appl
63	539.5	71.2	138	5	US-10-723-003-8	Sequence 8, Appl
64	539.5	71.2	138	6	US-11-004-639-8	Sequence 8, Appl
65	539.5	71.2	468	5	US-10-723-003-12	Sequence 12, Appl
66	539.5	71.2	468	6	US-11-004-639-12	Sequence 12, Appl
67	539.5	71.2	624	5	US-10-723-003-30	Sequence 30, Appl
68	539.5	71.2	624	6	US-11-004-639-30	Sequence 30, Appl
69	539.5	71.2	639	5	US-10-723-003-32	Sequence 32, Appl
70	539.5	71.2	639	5	US-11-004-639-32	Sequence 32, Appl
71	538	71.0	137	5	US-10-687-035-30	Sequence 30, Appl
72	537.5	70.9	136	5	US-09-956-206A-47	Sequence 47, Appl
73	537.5	70.9	136	5	US-10-965-616-47	Sequence 47, Appl
74	537.5	70.9	140	4	US-10-283-349-27	Sequence 27, Appl
75	537	70.8	139	4	US-10-006-773-13	Sequence 13, Appl
76	536	70.7	600	4	US-10-334-235-38	Sequence 38, Appl
77	531	70.1	135	4	US-10-389-155-32	Sequence 32, Appl
78	531	70.1	135	4	US-10-389-417-32	Sequence 32, Appl
79	531	70.1	135	4	US-10-452-357-19	Sequence 19, Appl
80	529.5	69.9	138	2	US-08-779-784-31	Sequence 31, Appl
81	529.5	69.9	138	4	US-10-010-729-67	Sequence 67, Appl
82	526.5	69.5	146	3	US-09-791-551-111	Sequence 111, App
83	525.5	69.3	130	3	US-09-929-665-4	Sequence 4, Appl
84	525.5	69.3	130	3	US-09-929-546-4	Sequence 4, Appl
85	522	68.9	118	4	US-10-462-062-139	Sequence 139, App
86	522	68.9	118	4	US-10-462-062-140	Sequence 140, App
87	521.5	68.8	138	4	US-10-682-845-40	Sequence 40, Appl
88	521.5	68.8	147	3	US-09-797-481-4	Sequence 4, Appl
89	521.5	68.8	147	3	US-09-844-736-6	Sequence 6, Appl
90	521.5	68.8	147	3	US-10-162-396-6	Sequence 6, Appl
91	521.5	68.8	147	5	US-10-819-493-6	Sequence 6, Appl
92	521.5	68.8	669	3	US-09-807-721-2	Sequence 2, Appl
93	519.5	68.5	140	5	US-10-723-003-36	Sequence 36, Appl
94	519.5	68.5	140	6	US-11-004-639-36	Sequence 36, Appl
95	519.5	68.5	152	3	US-09-881-823-20	Sequence 20, Appl
96	519.5	68.5	470	5	US-10-723-003-40	Sequence 40, Appl
97	519.5	68.5	470	6	US-11-004-639-40	Sequence 40, Appl
98	519.5	68.5	626	5	US-10-723-003-44	Sequence 44, Appl
99	519.5	68.5	626	6	US-11-004-639-44	Sequence 44, Appl
100	519.5	68.5	641	5	US-10-723-003-46	Sequence 46, Appl

## ALIGNMENTS

RESULT 1  
US-10-687-035-34  
; Sequence 34, Application US/10687035  
; Publication No. US20050064518A1  
; GENERAL INFORMATION:  
; APPLICANT: Albione, Earl F.  
; APPLICANT: Soltis, Daniel A.  
; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED  
; TITLE OF INVENTION: CA 125/0772P AND METHODS OF USE THEREOF  
; FILE REFERENCE: 6750-214-999  
; CURRENT APPLICATION NUMBER: US/10/687,035  
; CURRENT FILING DATE: 2003-10-15  
; PRIOR FILING DATE: 2003-07-10  
; PRIOR FILING DATE: 2003-07-10  
; PRIOR FILING DATE: 2003-07-10  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 139  
; TYPE: ERT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 776.1 heavy chain polypeptide variable region (776.1H)  
US-10-687-035-34

Query Match 100.0%; Score 758; DB 5; Length 139;  
Best Local Similarity 100.0%; Pred. No. 4.4e-59;  
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60  
Db 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60  
  
Qy 61 GKLEWIGIYYPYNGVDYQNFKSKATLIVDNSSNTAYMELRLSLTSEDSAVYYCARWDF 120  
Db 61 GKLEWIGIYYPYNGVDYQNFKSKATLIVDNSSNTAYMELRLSLTSEDSAVYYCARWDF 120  
  
Qy 121 GSGYFDYWGQGTTLTVSS 139  
Db 121 GSGYFDYWGQGTTLTVSS 139

RESULT 2  
US-10-389-155-60  
; Sequence 60, Application US/10389155  
; Publication No. US20030229208A1  
; GENERAL INFORMATION:  
; APPLICANT: Queen, Cary L.  
; Co, Man Sung  
; Schneider, William P.  
; Landolfi, Nicholas F.  
; Coelingh, Kathleen L.  
; Selick, Harold E.  
; TITLE OF INVENTION: Improved Humanized Immunoglobulins  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/389,155  
FILING DATE: 13-Mar-2003  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/325,000  
FILING DATE: 01-JUN-1999  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 08/484,537  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-002650US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 60:  
US-10-389-155-60  
  
Query Match 82.5%; Score 625; DB 4; Length 135;  
Best Local Similarity 84.9%; Pred. No. 2.3e-47;  
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;  
  
Qy 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60  
Db 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60  
  
Qy 61 GKLEWIGIYYPYNGVDYQNFKSKATLIVDNSSNTAYMELRLSLTSEDSAVYYCARWDF 120  
Db 61 GKLEWIGIYYPYNGVDYQNFKSKATLIVDNSSNTAYMELRLSLTSEDSAVYYCARWDF 120  
  
Qy 121 GSGYFDYWGQGTTLTVSS 139  
Db 118 -GRPMDYWGQGTTLTVSS 135

RESULT 3  
US-10-389-417-60  
; Sequence 60, Application US/10389417  
; Publication No. US20040049014A1  
; GENERAL INFORMATION:  
; APPLICANT: Queen, Cary L.  
; Co, Man Sung  
; Schneider, William P.  
; Landolfi, Nicholas F.  
; Coelingh, Kathleen L.  
; Selick, Harold E.  
; TITLE OF INVENTION: Improved Humanized Immunoglobulins  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/389,417  
FILING DATE: 13-Mar-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/325,000  
FILING DATE: 01-JUN-1999  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 08/484,537  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-002650US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 60:  
US-10-389-417-60

Query Match 82.58; Score 625; DB 4; Length 135;  
Best Local Similarity 84.9%; Pred. No. 2.3e-47;  
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;  
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHMKQSH 60  
DB 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHMKQSH 60  
QY 61 GKLEWIGIYYPNGVSDYNQPKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120  
DB 61 GKSLEWIGIYYPNGVSDYNQPKSKATLIVDNSSNTAYMELSLTSEDSAVYYCAR--- 117  
QY 121 GSGYYPDYWGQGTTLTVSS 139  
DB 118 -GRPAMDYWGQGTSTVTVSS 135

RESULT 4  
US-10-452-357-69  
Sequence 69, Application US/10452357  
Publication No. US20040058414A1  
GENERAL INFORMATION:  
APPLICANT: Queen, Cathy  
APPLICANT: Co. Man Sung  
APPLICANT: Schneider, William  
APPLICANT: Landolfi, Nicholas  
APPLICANT: Coelingh, Kathleen  
APPLICANT: Selick, Harold  
TITLE OF INVENTION: Improved Humanized Immunoglobulins  
FILE REFERENCE: 05882.0078.CNUS01  
CURRENT APPLICATION NUMBER: US/10/452,357  
CURRENT FILING DATE: 2003-05-30  
PRIOR FILING DATE: 09/718,993  
PRIOR FILING DATE: 2000-11-22  
PRIOR APPLICATION NUMBER: 09/487,200  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 07/634,278  
PRIOR FILING DATE: 1990-12-19  
PRIOR APPLICATION NUMBER: 07/590,275

PRIOR FILING DATE: 1990-09-28  
PRIOR APPLICATION NUMBER: 07/310,252  
PRIOR FILING DATE: 1989-02-13  
PRIOR APPLICATION NUMBER: 07/290,975  
PRIOR FILING DATE: 1988-12-28  
NUMBER OF SEQ ID NOS: 113  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 69  
LENGTH: 135  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Heavy chain M195 antibody  
US-10-452-357-69

Query Match 82.5%; Score 625; DB 4; Length 135;  
Best Local Similarity 84.9%; Pred. No. 2.3e-47;  
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;  
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHMKQSH 60  
DB 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHMKQSH 60  
QY 61 GKLEWIGIYYPNGVSDYNQPKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120  
DB 61 GKSLEWIGIYYPNGVSDYNQPKSKATLIVDNSSNTAYMELSLTSEDSAVYYCAR--- 117  
QY 121 GSGYYPDYWGQGTTLTVSS 139  
DB 118 -GRPAMDYWGQGTSTVTVSS 135

RESULT 5  
US-10-462-062-153  
Sequence 153, Application US/10462062  
Publication No. US20040044187A1  
GENERAL INFORMATION:  
APPLICANT: SATO, KOH  
APPLICANT: ADACHI, HIDEKI  
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)  
TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES  
FILE REFERENCE: 053466-0360  
CURRENT APPLICATION NUMBER: US/10/462,062  
CURRENT FILING DATE: 2003-06-16  
PRIOR APPLICATION NUMBER: PCT/JP99/01768  
PRIOR FILING DATE: 1999-04-02  
PRIOR APPLICATION NUMBER: JP 10-91850  
NUMBER OF SEQ ID NOS: 183  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 153  
LENGTH: 137  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid  
OTHER INFORMATION: sequence for H chain V region of anti-TF mouse monoclonal  
OTHER INFORMATION: antibody ATR-2  
US-10-462-062-153

Query Match 81.3%; Score 616; DB 4; Length 137;  
Best Local Similarity 82.7%; Pred. No. 1.4e-46;  
Matches 115; Conservative 8; Mismatches 14; Indels 2; Gaps 1;  
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHMKQSH 60  
DB 1 MEWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHMKQSH 60  
QY 61 GKLEWIGIYYPNGVSDYNQPKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120  
DB 61 GKSLEWIGIYYPNGVSDYNQPKSKATLIVDNSSNTAYMELSLTSEDSAVYYCAR-- 118  
QY 121 GSGYYPDYWGQGTTLTVSS 139



SOFTWARE: PastSeq for Windows Version 4.0

SEQ ID NO 6  
LENGTH: 438  
TYPE: PRT  
ORGANISM: Mouse  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (0)...(0)  
OTHER INFORMATION: Portion of DAV-1 heavy chain used for fusion protein  
OTHER INFORMATION: bifunctional antibody  
US-09-903-327A-6

Query Match 79.2%; Score 600.5; DB 3; Length 438;  
Best Local Similarity 82.0%; Pred. No. 1.2e-44;  
Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;  
  
QY 1 MGSMWIFLLSCTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
DB 1 MGSMWIFLLSCTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
  
QY 61 GKLEWIGIYYPYNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYICARWDF 120  
DB 61 GKLEWIGIYYPYNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYICARWDF 120  
  
QY 121 GSGYYFDYMGQGTTLTVSS 139  
DB 119 -----IAYWGQGTTLTVSA 132

## RESULT 10

US-09-903-327A-2  
Sequence 2, Application US/09903327A  
Patent No. US20020164333A1  
GENERAL INFORMATION:  
APPLICANT: Nemerow, Glen R.  
APPLICANT: Li, Erguang  
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET  
TITLE OF INVENTION: GENE  
FILE REFERENCE: 22908-1228  
CURRENT APPLICATION NUMBER: US/09/903,327A  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 09/613,017  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 456  
TYPE: PRT  
ORGANISM: Mouse  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (0)...(0)  
OTHER INFORMATION: DAV-1 heavy chain, penton base monoclonal antibody  
US-09-903-327A-2

Query Match 79.2%; Score 600.5; DB 3; Length 456;  
Best Local Similarity 82.0%; Pred. No. 1.2e-44;  
Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;  
  
QY 1 MGSMWIFLLSCTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
DB 1 MGSMWIFLLSCTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
  
QY 61 GKLEWIGIYYPYNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYICARWDF 120  
DB 61 GKLEWIGIYYPYNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYICARWDF 120  
  
QY 121 GSGYYFDYMGQGTTLTVSS 139  
DB 119 -----IAYWGQGTTLTVSA 132

## RESULT 11

US-09-903-327A-13  
Sequence 13, Application US/09903327A  
Patent No. US20020164333A1  
GENERAL INFORMATION:  
APPLICANT: Nemerow, Glen R.  
APPLICANT: Li, Erguang  
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET  
TITLE OF INVENTION: GENE  
FILE REFERENCE: 22908-1228  
CURRENT APPLICATION NUMBER: US/09/903,327A  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 09/613,017  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 493  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain  
OTHER INFORMATION: and EGF mature peptide  
US-09-903-327A-13

Query Match 79.2%; Score 600.5; DB 3; Length 493;  
Best Local Similarity 82.0%; Pred. No. 1.3e-44;  
Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;  
  
QY 1 MGSMWIFLLSCTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
DB 1 MGSMWIFLLSCTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
  
QY 61 GKLEWIGIYYPYNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYICARWDF 120  
DB 61 GKLEWIGIYYPYNGVDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVYICARWDF 120  
  
QY 121 GSGYYFDYMGQGTTLTVSS 139  
DB 119 -----IAYWGQGTTLTVSA 132

## RESULT 12

US-09-903-327A-12  
Sequence 12, Application US/09903327A  
Patent No. US20020164333A1  
GENERAL INFORMATION:  
APPLICANT: Nemerow, Glen R.  
APPLICANT: Li, Erguang  
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET  
TITLE OF INVENTION: GENE  
FILE REFERENCE: 22908-1228  
CURRENT APPLICATION NUMBER: US/09/903,327A  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 09/613,017  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 510  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain  
OTHER INFORMATION: and IGF-1 mature peptide  
US-09-903-327A-12

Query Match 79.2%; Score 600.5; DB 3; Length 510;  
Best Local Similarity 82.0%; Pred. No. 1.4e-44;  
Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

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QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
QY 61 GKILEWIGIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
Db 61 GKILEWIGIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 118
QY 121 GSGYFDYWGQGTTLTVSS 139
Db 119 -----IAYWGQGTTLTVSA 132

RESULT 13
US-09-903-327A-11
; Sequence 11, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
; OTHER INFORMATION: and TNF alpha mature peptide
US-09-903-327A-11

Query Match 79.2%; Score 600.5; DB 3; Length 597;
Best Local Similarity 82.0%; Pred. No. 1.6e-44;
Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
QY 61 GKILEWIGIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
Db 61 GKILEWIGIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 118
QY 121 GSGYFDYWGQGTTLTVSS 139
Db 119 -----IAYWGQGTTLTVSA 132

RESULT 14
US-09-903-327A-14
; Sequence 14, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 14
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
; OTHER INFORMATION: and SCF mature peptide
US-09-903-327A-14

Query Match 79.2%; Score 600.5; DB 3; Length 613;
Best Local Similarity 82.0%; Pred. No. 1.7e-44;
Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
QY 61 GKILEWIGIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
Db 61 GKILEWIGIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 118
QY 121 GSGYFDYWGQGTTLTVSS 139
Db 119 -----IAYWGQGTTLTVSA 132

RESULT 15
US-10-768-193-7
; Sequence 7, Application US/10768193
; Publication No. US20040181042A1
; GENERAL INFORMATION:
; APPLICANT: MEDICAL & BIOLOGICAL LABORATORIES CO., LTD.
; APPLICANT: The director of Chubu National Hospital
; APPLICANT: SHIBATA, Masao
; TITLE OF INVENTION: Antibody recognizing GM1 ganglioside-bound
; TITLE OF INVENTION: amyloid b-protein and DNA encoding the antibody
; FILE REFERENCE: P0102402
; CURRENT APPLICATION NUMBER: US/10/768,193
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: JP P2001-235700
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: PCT/JP02/07874
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 7
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-768-193-7

Query Match 77.2%; Score 585.5; DB 4; Length 136;
Best Local Similarity 79.9%; Pred. No. 6.9e-44;
Matches 111; Conservative 7; Mismatches 18; Indels 3; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60
QY 61 GKILEWIGIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
Db 61 GKILEWIGIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 117
QY 121 GSGYFDYWGQGTTLTVSS 139
Db 118 GANVFDYWGQGTTLTVSS 136

RESULT 16
US-10-774-076-9
; Sequence 9, Application US/10774076
; Publication No. US20040210040A1
```



GENERAL INFORMATION:  
; APPLICANT: Protein Design Labs, Inc.  
; APPLICANT: Landolfi, et al.  
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and  
; TITLE OF INVENTION: Psoriasis  
; FILE REFERENCE: 05882.0064.NFUS01  
; CURRENT APPLICATION NUMBER: US/10/774.076  
; CURRENT FILING DATE: 2004-02-06  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: mus sp.  
US-10-774-076-9

Query Match 76.3%; Score 578.5; DB 4; Length 138;  
Best Local Similarity 79.1%; Pred. No. 2.9e-43;  
Matches 110; Conservative 7; Mismatches 21; Indels 1; Gaps 1;  
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60  
Db 1 MEWRWIFLLSGTTGVHSDIQLQSGPELVKPGASVKVSKASGYFTFDYNIHWKQSH 60  
QY 61 GKLEWIGYIYPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120  
Db 61 GKSLEWIGYIDPYVDGPGYQKFKGKATLVKSSSTAYMHLNSLTSEDSAVYYCARRG- 119  
QY 121 GSGYYFDYWGQGTTLTVSS 139  
Db 120 NFPYFDYWGQGTTLTVSS 138

## RESULT 17

US-10-365-123-28  
; Sequence 28, Application US/10365123  
; Publication No. US20040053365A1  
; GENERAL INFORMATION:  
; APPLICANT: Renner, Christoph  
; APPLICANT: Scott, Andrew  
; APPLICANT: Burgess, Antony  
; TITLE OF INVENTION: HUMANIZED GM-CSF ANTIBODIES  
; FILE REFERENCE: LUD 5729.1  
; CURRENT APPLICATION NUMBER: US/10/365,123  
; CURRENT FILING DATE: 2003-02-12  
; NUMBER OF SEQ ID NOS: 56  
; SEQ ID NO 28  
; LENGTH: 139  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; OTHER INFORMATION: amino acid sequence for murine 19/2 heavy chain variable region  
US-10-365-123-28

Query Match 76.1%; Score 577; DB 4; Length 139;  
Best Local Similarity 83.6%; Pred. No. 4e-43;  
Matches 112; Conservative 7; Mismatches 13; Indels 2; Gaps 1;  
QY 6 IFLFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSHKILE 65  
Db 4 IMLFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSHGKSLD 63  
QY 66 WIGYIYPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDFGSGY 125  
Db 64 WIGYIAPYSGGTGYNEBPKRATLVKSSSTAYMELSLTSEDSAVYYCARRD--RFPY 121  
QY 126 FDYWGQGTTLTVSS 139  
Db 122 FDYWGQGTTLTVSS 135

## RESULT 18

US-10-462-062-158

; Sequence 158, Application US/10462062  
; Publication No. US20040044187A1  
; GENERAL INFORMATION:  
; APPLICANT: SATO, KOH  
; APPLICANT: ADACHI, HIDEKI  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)  
; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES  
; FILE REFERENCE: 053466-0360  
; CURRENT APPLICATION NUMBER: US/10/462,062  
; CURRENT FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: PCT/JP99/01768  
; PRIOR FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: JP 10-91850  
; PRIOR FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 183  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 158  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid  
; OTHER INFORMATION: sequence for H chain V region of anti-TF mouse monoclonal  
; OTHER INFORMATION: antibody ATR-8  
US-10-462-062-158

Query Match 74.9%; Score 568; DB 4; Length 137;  
Best Local Similarity 75.4%; Pred. No. 2.4e-42;  
Matches 107; Conservative 11; Mismatches 16; Indels 8; Gaps 2;  
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYFTFDYNIHWKQSH 60  
Db 1 MEWSWIFLLSGTTGVHSDIQLQSGPELVKPGASVKVSKASGYFTFDYNIHWKQSH 60  
QY 61 GKLEWIGYIYPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120  
Db 61 GKSLEWIGYIDPYTGTGYNQKFNKATLVKSSSTAFMHLNSLTSEDSAVYYCAR--- 117  
QY 121 GSGYYFD---YWGQGTTLTVSS 139  
Db 118 --GYFDYDCYWGQGTTLTVSA 137

## RESULT 19

US-10-837-904-27  
; Sequence 27, Application US/10837904  
; Publication No. US20050142635A1  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENDIG, Mary Margaret  
; APPLICANT: JONES, Steven Tarran  
; APPLICANT: SALDANHA, Jose William  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; INTERLEUKIN-6 RECEPTOR  
; NUMBER OF SEQUENCES: 134  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/10/837,904  
; FILING DATE: 04-May-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/114,285  
FILING DATE: 13-Jul-1998  
APPLICATION NUMBER: US 08/436,717  
FILING DATE: 08-MAY-1995  
APPLICATION NUMBER: US 08/137,117  
FILING DATE: 20-DEC-1993  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Wegner, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/234  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-10-837-904-27

Query Match 74.8%; Score 567; DB 5; Length 135;  
Best Local Similarity 78.4%; Pred. No. 2.9e-42;  
Matches 109; Conservative 8; Mismatches 18; Indels 4; Gaps 1;

Qy 1 MGMSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYFTTDTYNIHWVKQSH 60  
Db 1 MGMSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYFTTDTYNIHWVKQSH 60

Qy 61 GKILEWIGYIPYNGVDYNDNQFSEKATLIVDSSNTAYMELSLTSEDGSAVYYCARWDF 120  
Db 61 GKILEWIGYIPYNGVDYNDNQFSEKATLIVDSSNTAYMELSLTSEDGSAVYYCARWDF 120

Qy 121 GSGYFDYWGQGTTLTVSS 139  
Db 118 -GGNRFAYWGQGTTLTVSA 135

RESULT 20  
US-10-389-155-72  
Sequence 72, Application US/10389155  
Publication No. US20030229208A1  
GENERAL INFORMATION:  
APPLICANT: Queen, Cary L.  
Co, Man Sung  
Schneider, William P.  
Landolfi, Nicholas F.  
Coelingh, Kathleen L.  
Scllick, Harold E.  
TITLE OF INVENTION: Improved Humanized Immunoglobulins  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/389,155  
FILING DATE: 13-Mar-2003

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/325,000  
FILING DATE: 01-JUN-1999  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 08/484,537  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-002650US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 138 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 72:  
US-10-389-155-72

Query Match 74.6%; Score 565.5; DB 4; Length 138;  
Best Local Similarity 78.4%; Pred. No. 4.1e-42;  
Matches 109; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

Qy 1 MGMSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYFTTDTYNIHWVKQSH 60  
Db 1 MGMSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYFTTDTYNIHWVKQSH 60

Qy 61 GKILEWIGYIPYNGVDYNDNQFSEKATLIVDSSNTAYMELSLTSEDGSAVYYCARWDF 120  
Db 61 GKILEWIGYIPYNGVDYNDNQFSEKATLIVDSSNTAYMELSLTSEDGSAVYYCARWDF 120

Qy 121 GSGYFDYWGQGTTLTVSS 139  
Db 121 -RDYSMDYWGQGTTLTVSS 138

Search completed: March 20, 2006, 07:35:11  
Job time : 26.6746 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:30:27 ; Search time 7.40237 Seconds  
(without alignments)  
1552.466 Million cell updates/sec

Title: US-10-687-035-34

Perfect score: 758

Sequence: 1 MGWSWIFLLSCTAGVHSE.....FGSGYYFDYWGQGTTLTVSS 139

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.\*

1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	625	82.5	135	1	US-07-634-278-69
2	625	82.5	135	1	US-08-477-728-69
3	625	82.5	135	1	US-08-474-040-69
4	625	82.5	135	1	US-08-487-200-69
5	625	82.5	135	2	US-08-484-537-69
6	616	81.3	137	2	US-09-647-468-153
7	616	81.3	137	2	US-09-647-468-154
8	613.5	80.9	132	2	US-08-434-000A-14
9	613.5	80.9	132	2	US-09-312-157-14
10	613.5	80.9	132	2	US-09-717-888-14
11	604	79.7	139	1	US-08-116-778B-1
12	604	79.7	139	1	US-08-438-562-1
13	604	79.7	139	1	US-08-483-528B-91
14	586	77.3	137	1	US-08-116-778B-3
15	586	77.3	137	1	US-08-438-562-3
16	586	77.3	137	1	US-08-483-528B-93
17	568	74.9	137	2	US-09-647-468-158
18	567	74.8	135	1	US-08-137-117D-27
19	567	74.8	135	1	US-08-436-717-27
20	566.5	74.7	140	4	PCT-US93-11612-4
21	565.5	74.6	138	1	US-07-634-278-85
22	565.5	74.6	138	1	US-08-477-728-85
23	565.5	74.6	138	1	US-08-474-040-85
24	565.5	74.6	138	1	US-08-487-200-85
25	565.5	74.6	138	2	US-08-484-537-85
26	564	74.4	143	2	US-09-301-593-26
27	564	74.4	472	2	US-09-301-593-30
28	560	73.9	233	2	US-08-444-644-33
29	560	73.9	233	2	US-08-232-246A-33
30	560	73.9	235	2	US-08-444-644-19
31	560	73.9	235	2	US-08-444-644-28
32	560	73.9	235	2	US-08-444-644-42
33	560	73.9	235	2	US-08-232-246A-19
34	560	73.9	235	2	US-08-232-246A-28
35	560	73.9	235	2	US-08-232-246A-42
36	559	73.7	137	2	US-09-647-468-157
37	556.5	73.4	140	2	US-08-579-378A-4
38	553	73.0	137	2	US-08-444-644-17
39	553	73.0	137	2	US-08-232-246A-17
40	545.5	72.0	142	1	US-08-678-194-8
41	545.5	72.0	142	2	US-08-890-011-8
42	545.5	72.0	142	2	US-09-262-72A-8
43	545	71.9	144	2	US-09-393-385B-112
44	545	71.9	144	2	US-10-195-752-112
45	544	71.8	137	1	US-08-379-057-18
46	539	71.1	137	1	US-08-392-419-2
47	537.5	70.9	136	2	US-08-525-539A-47
48	537.5	70.9	140	2	US-08-836-561-27
49	537.5	70.9	140	2	US-09-434-122-27
50	531	70.1	135	1	US-07-634-278-19
51	531	70.1	135	1	US-08-477-728-19
52	531	70.1	135	1	US-08-474-040-19
53	531	70.1	135	1	US-08-487-200-19
54	531	70.1	135	1	US-08-303-569B-31
55	531	70.1	135	2	US-08-484-537-19
56	525.5	69.3	130	2	US-08-838-682-4
57	525.5	69.3	130	2	US-08-895-914-4
58	525.5	69.3	130	2	US-09-357-710A-4
59	525.5	69.3	130	2	US-09-357-707-4
60	525.5	69.3	130	2	US-09-357-708-4
61	524	69.1	139	1	US-08-202-047-3
62	524	69.1	139	2	US-08-564-690-3
63	522.5	68.9	136	4	PCT-US93-11611-11
64	522	68.9	118	2	US-09-647-468-139
65	522	68.9	118	2	US-09-647-468-140
66	521.5	68.8	147	1	US-08-579-940-4
67	521.5	68.8	147	2	US-08-838-692-6
68	519	68.5	116	1	US-07-634-278-56
69	519	68.5	116	1	US-08-477-728-56
70	519	68.5	116	1	US-08-474-040-56
71	519	68.5	116	1	US-08-487-200-56
72	519	68.5	116	2	US-08-484-537-56
73	517.5	68.3	163	4	PCT-US91-02942-5
74	513.5	67.7	468	1	US-08-303-569B-7
75	513.5	67.7	468	2	US-08-116-247-7
76	513.5	67.7	468	2	US-09-795-515-7
77	513.5	67.7	468	2	US-09-348-224-7
78	510.5	67.3	140	1	US-07-946-421-24
79	510	67.3	139	1	US-08-253-877C-8
80	510	67.3	139	1	US-08-656-586-8
81	510	67.3	139	1	US-08-452-164A-8
82	509	67.2	138	2	US-08-603-024-2
83	506.5	66.8	138	1	US-08-482-882-78
84	506.5	66.8	138	1	US-08-483-389-78
85	506.5	66.8	138	1	US-08-487-113D-78
86	506.5	66.8	138	1	US-08-473-503-78
87	506.5	66.8	138	1	US-08-483-932-78
88	506.5	66.8	138	1	US-08-720-420A-78
89	506.5	66.8	138	2	US-08-714-017-78
90	506.5	66.8	138	2	US-08-475-680-78
91	505.5	66.7	140	2	US-08-836-561-63
92	505.5	66.7	140	2	US-09-434-122-63
93	504	66.5	141	1	US-08-461-284-4
94	504	66.5	141	1	US-08-462-939-4
95	504	66.5	141	1	US-08-253-877C-4
96	504	66.5	141	1	US-08-452-164A-4
97	502	66.2	139	1	US-08-137-117D-35
98	502	66.2	139	1	US-08-436-717-35
99	501.5	66.2	143	1	US-08-236-520-7
100	501.5	66.2	143	4	PCT-US95-05262-7

## ALIGNMENTS

## RESULT 1

US-07-634-278-69  
; Sequence 69, Application US/07634278  
; Patent No. 5530101  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO. Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; NAME: Smith, William M  
; ATTORNEY/AGENT INFORMATION:  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 69:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 135 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-07-634-278-69

Query Match 82.5%; Score 625; DB 1; Length 135;

Best Local Similarity 84.9%; Pred. No. 2e-57;  
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;

Qy	1	MGWSWIFLLSGTAGVHSEVQLQSGPGLVKPGASVKISCKASGYTFTDYNHVKQSH	60
Db	1	MGWSWIFLLSGTAGVHSEVQLQSGPGLVKPGASVKISCKASGYTFTDYNHVKQSH	60
Qy	61	GKILEWIGYIYPNGVDYQNFKSKATLIYDSSNTAYMELRSITSDSAVYYCARWDF	120
Db	61	GKILEWIGYIYPNGVDYQNFKSKATLIYDSSNTAYMELRSITSDSAVYYCARWDF	120
Qy	121	GSYYFDYWGQGTTLTVSS	139
Db	118	-GRPAMDYWGQGTSTVTVSS	135

## RESULT 2

US-08-477-728-69  
; Sequence 69, Application US/08477728  
; Patent No. 5585089  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,728  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; NAME: Smith, William M  
; ATTORNEY/AGENT INFORMATION:  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 69:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 135 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-477-728-69

Query Match 82.5%; Score 625; DB 1; Length 135;

Best Local Similarity 84.9%; Pred. No. 2e-57;  
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;

Qy	1	MGWSWIFLLSGTAGVHSEVQLQSGPGLVKPGASVKISCKASGYTFTDYNHVKQSH	60
Db	1	MGWSWIFLLSGTAGVHSEVQLQSGPGLVKPGASVKISCKASGYTFTDYNHVKQSH	60
Qy	61	GKILEWIGYIYPNGVDYQNFKSKATLIYDSSNTAYMELRSITSDSAVYYCARWDF	120
Db	61	GKILEWIGYIYPNGVDYQNFKSKATLIYDSSNTAYMELRSITSDSAVYYCARWDF	120
Qy	121	GSYYFDYWGQGTTLTVSS	139
Db	118	-GRPAMDYWGQGTSTVTVSS	135

## RESULT 3

US-08-474-040-69

; Sequence 69, Application US/08474040  
; Patent No. 5693761  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO. Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,040  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 69:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 135 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

; US-08-474-040-69  
Query Match 82.5%; Score 625; DB 1; Length 135;  
Best Local Similarity 84.9%; Pred. No. 2e-57;  
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;

Qy	1	MGWSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNHVKQSH	60
Db	1	MGWSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNHVKQSH	60
Qy	61	GKLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELRSLTSEDSAVYYCARWDF	120
Db	61	GKLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELRSLTSEDSAVYYCARWDF	117
Qy	121	GSGYFDYWGQGTTLTVSS	139
Db	118	-GRPAMDYWGQGTSLTVSS	135

RESULT 4  
US-08-487-200-69

; Sequence 69, Application US/08487200  
; Patent No. 5693762  
; GENERAL INFORMATION:

; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO. Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,200  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002610  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 69:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 135 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

; US-08-487-200-69  
Query Match 82.5%; Score 625; DB 1; Length 135;  
Best Local Similarity 84.9%; Pred. No. 2e-57;  
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;

Qy	1	MGWSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNHVKQSH	60
Db	1	MGWSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNHVKQSH	60
Qy	61	GKLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELRSLTSEDSAVYYCARWDF	120
Db	61	GKLEWIGIYYPNGVDYQNFKSKATLIVDSSNTAYMELRSLTSEDSAVYYCARWDF	117
Qy	121	GSGYFDYWGQGTTLTVSS	139
Db	118	-GRPAMDYWGQGTSLTVSS	135

RESULT 5  
US-08-484-537-69

Sequence 69, Application US/08484537  
Patent No. 6180370  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO. Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08484,537  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-484-537-69

Query Match 82.5%; Score 625; DB 2; Length 135;  
Best Local Similarity 84.9%; Pred. NO. 2e-57;  
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;  
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
DB 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
QY 61 GKLEWIGYIYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120  
DB 61 GKLEWIGYIYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120  
QY 121 GSGYFDYWGQGTTLTVSS 139  
DB 119 GEGYFDYWGQGTTLTVSS 137

RESULT 7  
US-09-647-468-154  
Sequence 154, Application US/09647468  
Patent No. 6677436  
GENERAL INFORMATION:  
APPLICANT: SATO, KOH  
APPLICANT: ADACHI, HIDEKI  
APPLICANT: YABUTA, NAOKIRO  
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND  
FILE REFERENCE: 053466/0289  
CURRENT APPLICATION NUMBER: US/09/647,468  
CURRENT FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: PCT/JP99/01768  
PRIOR FILING DATE: 1999-04-02  
PRIOR APPLICATION NUMBER: JP 10-91850  
PRIOR FILING DATE: 1998-04-03  
NUMBER OF SEQ ID NOS: 183  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 154  
LENGTH: 137  
TYPE: PRT  
ORGANISM: Mus sp.  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
OTHER INFORMATION: sequence coding for H chain V region of ant-TF  
OTHER INFORMATION: mouse monoclonal antibody ATR-3  
US-09-647-468-154

Query Match 81.3%; Score 616; DB 2; Length 137;  
Best Local Similarity 82.7%; Pred. NO. 1.7e-56;  
Matches 115; Conservative 8; Mismatches 14; Indels 2; Gaps 1;  
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
DB 1 MEWSWIFLLSGTTGVHSEIQLQSGPELVKPGASVKYSCASGYSFDTNNYWKQSH 60  
QY 61 GKLEWIGYIYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120  
DB 61 GKLEWIGYIYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120  
QY 121 GSGYFDYWGQGTTLTVSS 139  
DB 119 GEGYFDYWGQGTTLTVSS 137

Query Match 81.3%; Score 616; DB 2; Length 137;  
Best Local Similarity 82.7%; Pred. NO. 1.7e-56;  
Matches 115; Conservative 8; Mismatches 14; Indels 2; Gaps 1;  
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
DB 1 MEWSWIFLLSGTTGVHSEIQLQSGPELVKPGASVKYSCASGYSFDTNNYWKQSH 60  
QY 61 GKLEWIGYIYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120  
DB 61 GKLEWIGYIYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120  
QY 121 GSGYFDYWGQGTTLTVSS 139  
DB 119 GEGYFDYWGQGTTLTVSS 137

Sequence 69, Application US/08484537  
Patent No. 6180370  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO. Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08484,537  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-484-537-69

Query Match 82.5%; Score 625; DB 2; Length 135;  
Best Local Similarity 84.9%; Pred. NO. 2e-57;  
Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;  
QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
DB 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
QY 61 GKLEWIGYIYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120  
DB 61 GKLEWIGYIYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120  
QY 121 GSGYFDYWGQGTTLTVSS 139  
DB 119 GEGYFDYWGQGTTLTVSS 135

RESULT 6  
US-09-647-468-153  
Sequence 153, Application US/09647468

Best Local Similarity 82.7%; Pred. No. 1.7e-56;  
Matches 115; Conservative 8; Mismatches 14; Indels 2; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHMKQSH 60

Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHMKQSH 60

QY 61 GKILEWIGIYYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120

Db 61 GKILEWIGIYYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120

QY 121 GSGYFDYWGQGTTLTVSS 139

Db 119 GEGYFDYWGQGTTLTVSS 137

## RESULT 8

US-08-434-000A-14

; Sequence 14, Application US/08434000A

; Patent No. 6046037

; GENERAL INFORMATION:

; APPLICANT: ANDREW C. HIATT, JULIAN

; APPLICANT: K.-C. MA, THOMAS LEHNER

; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION

; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA: US/08/434,000A

; FILING DATE:

; FILING DATE: 12/30/94

; NAME: Guise, Jeffrey W.

; REGISTRATION NUMBER: 34,613

; REFERENCE/DOCKET NUMBER: 212/127

; TELEPHONE: (619) 552-8400

; TELEFAX: (619) 552-0159

; TELEX: 67-3510

; SEQUENCE LISTING

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 132 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; TOPOLOGY: DESCRIPTION: Guy's 13 Gamma 1

; US-08-434-000A-14

Query Match 80.9%; Score 613.5; DB 2; Length 132;

Best Local Similarity 83.5%; Pred. No. 3e-56;

Matches 116; Conservative 6; Mismatches 10; Indels 7; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHMKQSH 60

Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHMKQSH 60

QY 61 GKILEWIGIYYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120

Db 61 GKILEWIGIYYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120

Db 1 MEWTWVFLFLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHMKQSR 60

QY 61 GKILEWIGIYYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120

Db 61 GKILEWIGIYYPNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120

QY 121 GSGYFDYWGQGTTLTVSS 139

Db 118 ---YFDYWGQGTTLTVSS 132

## RESULT 9

US-09-312-157-14

; Sequence 14, Application US/09312157

; Patent No. 6303341

; GENERAL INFORMATION:

; APPLICANT: ANDREW C. HIATT, JULIAN

; APPLICANT: K.-C. MA, THOMAS LEHNER

; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION

; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA: US/09/312,157

; FILING DATE: 14-May-1999

; CLASSIFICATION: <Unknown>

; APPLICATION DATA:

; APPLICATION NUMBER: 08/434,000

; FILING DATE: <Unknown>

; NAME: Guise, Jeffrey W.

; REGISTRATION NUMBER: 34,613

; REFERENCE/DOCKET NUMBER: 212/127

; TELEPHONE: (619) 552-8400

; TELEFAX: (619) 552-0159

; TELEX: 67-351

; SEQUENCE LISTING

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 132 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; TOPOLOGY: DESCRIPTION: Guy's 13 Gamma 1

; US-09-312-157-14

Query Match 80.9%; Score 613.5; DB 2; Length 132;

Best Local Similarity 83.5%; Pred. No. 3e-56;

Matches 116; Conservative 6; Mismatches 10; Indels 7; Gaps 1;

Qy 121 GSGYFDYWGQGTTLTVSS 139  
Db 118 ----YFDYWGQGTTLTVSS 132

RESULT 10  
US-09-717-888-14  
; Sequence 14, Application US/09717888  
; Patent No. 6808709  
; GENERAL INFORMATION:  
; APPLICANT: ANDREW C. HIATT, JULIAN  
; K.-C. MA, THOMAS LEHNER  
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION  
; PROTEINS IN PLANTS AND THEIR USES  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible  
storage  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/717.888  
FILING DATE: 20-No. 6808709-2000  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/434.000  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/367.395  
FILING DATE: 30-Dec-94  
ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.  
REGISTRATION NUMBER: 34,613  
REFERENCE/DOCKET NUMBER: 212/127  
TELEPHONE: (619) 552-8400  
TELEFAX: (619) 552-0159  
TELEX: 67-3510

SEQUENCE LISTING  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 132 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
DESCRIPTION: Guy's 13 Gamma 1  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Query Match 80.9%; Score 613.5; DB 2; Length 132;  
Best Local Similarity 83.5%; Pred. No. 3e-56;  
Matches 116; Conservative 6; Mismatches 10; Indels 7; Gaps 1;

Qy 1 MGWNIPLFLISGTAGVHSEVLOQSGPDLVKPGASVKISCKASGYTFTDYNHIVKQSH 60  
Db 1 MEWTVFLFLISGTAGVHSEVLOQSGPDLVKPGASVKISCKASGYTFTDYNHIVKQSR 60

Qy 61 GKILEWIGIYIPYNGVSDYNQFNKSKATLIIVDNSNTAYMELRSITSDSAVYYCARWDF 120  
Db 61 GKLEWIGIYIPYNGVSDYNQFNKSKATLIIVDNSNTAYMELRSITSDSAVYYCAT--- 117

Qy 121 GSGYFDYWGQGTTLTVSS 139  
Db 118 ----YFDYWGQGTTLTVSS 132

RESULT 11  
US-08-116-778E-1  
; Sequence 1, Application US/08116778E  
; Patent No. 5830470  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KAWANA, YOSHIHISA  
; APPLICANT: HASEGAWA, MAMORU  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/116,778E  
; FILING DATE: 07-SEP-93  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILSON, MARY J.  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 249-59  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4000  
; TELEFAX: (703)816-4100  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 139 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: -19...-1  
; IDENTIFICATION METHOD: BY SIMILARITY  
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN  
; IDENTIFICATION METHOD: ESTABLISHED CONSENSUS  
; FEATURE:  
; NAME/KEY: domain  
; LOCATION: 31..35  
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; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"  
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; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"  
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; IDENTIFICATION METHOD: CONSENSUS  
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"  
; US-08-116-778E-1  
Query Match 79.7%; Score 604; DB 1; Length 139;



Best Local Similarity 82.7%; Pred. No. 3.2e-55;  
Matches 115; Conservative 6; Mismatches 18; Indels 0; Gaps 0;  
Qy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNIHWKQSH 60  
Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNDMDVQKSH 60  
Qy 61 GKLEWIGYIYPYNGVSDYNQNFKSKATLIYDSSNTAYMELSLTSEDSAVYYCARWDF 120  
Db 61 GKLEWIGYIYPYNGVSDYNQNFKSKATLIYDSSNTAYMELSLTSEDSAVYYCATYGH 120  
Qy 121 GSGYFDPYWGQGTTLTVSS 139  
Db 121 YGYMFAYWGQGTTLTVSA 139

## RESULT 12

US-08-438-562-1  
; Sequence 1, Application US/08438562  
; Patent No. 5874255  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KUWANA, YOSHIHISA  
; APPLICANT: HASEGAWA, MAMORU  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/438,562  
; FILING DATE: 10-MAY-95  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/116,778  
; FILING DATE: 07-SEP-93  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILSON, MARY J.  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 249-76  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4000  
; TELEFAX: (703)816-4100  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 139 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: -19..-1  
; IDENTIFICATION METHOD: BY SIMILARITY  
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN  
; IDENTIFICATION METHOD: ESTABLISHED CONSENSUS  
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; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"  
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; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"  
; US-08-438-562-1

Query Match 79.7%; Score 604; DB 1; Length 139;  
Best Local Similarity 82.7%; Pred. No. 3.2e-55;  
Matches 115; Conservative 6; Mismatches 18; Indels 0; Gaps 0;  
Qy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNIHWKQSH 60  
Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDTYNDMDVQKSH 60  
Qy 61 GKLEWIGYIYPYNGVSDYNQNFKSKATLIYDSSNTAYMELSLTSEDSAVYYCARWDF 120  
Db 61 GKLEWIGYIYPYNGVSDYNQNFKSKATLIYDSSNTAYMELSLTSEDSAVYYCATYGH 120  
Qy 121 GSGYFDPYWGQGTTLTVSS 139  
Db 121 YGYMFAYWGQGTTLTVSA 139

## RESULT 13

US-08-483-528B-91  
; Sequence 91, Application US/08483528B  
; Patent No. 5939532  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: KOIKE, MASAMICHI  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: KUWANA, YOSHIHISA  
; APPLICANT: HASEGAWA, MAMORU  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHUYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,528B  
; FILING DATE: 07-JUN-95  
; CLASSIFICATION: 536  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)816-4000  
; TELEFAX: (703)816-4100  
; INFORMATION FOR SEQ ID NO: 91:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 139 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

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/ NAME/KEY: sig_peptide
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/ IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN
/ IDENTIFICATION METHOD: ESTABLISHED CONSENSUS
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/ IDENTIFICATION METHOD: CONSENSUS
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/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
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/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
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/ IDENTIFICATION METHOD: BY SIMILARITY
/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
/ IDENTIFICATION METHOD: CONSENSUS
/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
/
/ US-08-483-528B-91
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/ Query Match 79.7%; Score 604; DB 1; Length 139;
/ Best Local Similarity 82.7%; Pred. No. 3.2e-55;
/ Matches 115; Conservative 6; Mismatches 18; Indels 0; Gaps 0;
/
/ Qy 1 MGWSWIFLLISGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
/ Db 1 MGWSWIFLLISGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
/
/ Qy 61 GKLEWIGYIYPNGVDYQNFKSKATLIVDNSNTAYMELRLTSDSVAVYCARWDF 120
/ Db 61 GKLEWIGYIYPNGVDYQNFKSKATLIVDNSNTAYMELRLTSDSVAVYCARWDF 120
/
/ Qy 121 GSGYFYDYGQGTTLTVSS 139
/ Db 121 YGYMFAYWGQGTTLTVTSA 139
/
/ RESULT 14
/ US-08-116-778E-3
/ Sequence 3, Application US/08116778E
/ Patent No. 5830470
/ GENERAL INFORMATION:
/ APPLICANT: NAKAMURA, KAZUYASU
/ APPLICANT: KOIKE, MASAMICHI
/ APPLICANT: SHITARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: KAWANA, YOSHIHISA
/ APPLICANT: HASEGAWA, NAMORU
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES
/ NUMBER OF SEQUENCES: 49
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: NIXON & VANDERHYE P.C.
/ STREET: 1100 NORTH GLEBE ROAD
/ CITY: ARLINGTON
/ STATE: VIRGINIA
/ COUNTRY: U.S.A.
/ ZIP: 22201-4714
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/116,778E
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/ FILING DATE: 07-SEP-93
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: WILSON, MARY J.
/ REGISTRATION NUMBER: 32,955
/ REFERENCE/DOCKET NUMBER: 249-59
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)816-4000
/ TELEFAX: (703)816-4100
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 137 amino acids
/ TYPE: amino acids
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/
/ NAME/KEY: sig_peptide
/ LOCATION: -19..-1
/ IDENTIFICATION METHOD: BY SIMILARITY
/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
/ IDENTIFICATION METHOD: CONSENSUS
/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
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/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
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/ IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
/ IDENTIFICATION METHOD: CONSENSUS
/ OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
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/ US-08-116-778E-3
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/ Query Match 77.3%; Score 586; DB 1; Length 137;
/ Best Local Similarity 82.7%; Pred. No. 2.3e-53;
/ Matches 115; Conservative 5; Mismatches 17; Indels 2; Gaps 1;
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/ Qy 1 MGWSWIFLLISGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
/ Db 1 MGWSWIFLLISGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHVKQSH 60
/
/ Qy 61 GKLEWIGYIYPNGVDYQNFKSKATLIVDNSNTAYMELRLTSDSVAVYCARWDF 120
/ Db 61 GKLEWIGYIYPNGVDYQNFKSKATLIVDNSNTAYMELRLTSDSVAVYCARWDF 120
/
/ Qy 121 GSGYFYDYGQGTTLTVSS 139
/ Db 119 GRYTAWDYGQGTTLTVTSA 137
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/ RESULT 15
/ US-08-438-562-3
/ Sequence 3, Application US/08438562
/ Patent No. 5874255
/ GENERAL INFORMATION:
/ APPLICANT: NAKAMURA, KAZUYASU
/ APPLICANT: KOIKE, MASAMICHI
/ APPLICANT: SHITARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: KAWANA, YOSHIHISA
/ APPLICANT: HASEGAWA, NAMORU
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES
```

NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,562  
FILING DATE: 10-MAY-95  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/116,778  
FILING DATE: 07-SEP-93  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 249-76  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acids  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: -19..-1  
IDENTIFICATION METHOD: BY SIMILARITY  
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED  
IDENTIFICATION METHOD: CONSENSUS  
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"  
FEATURE:  
NAME/KEY: domain  
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IDENTIFICATION METHOD: CONSENSUS  
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"  
FEATURE:  
NAME/KEY: domain  
LOCATION: 99..107  
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IDENTIFICATION METHOD: CONSENSUS  
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"  
US-08-438-562-3  
Query Match 77.1%; Score 586; DB 1; Length 137;  
Best Local Similarity 82.7%; Pred. No. 2.3e-53;  
Matches 115; Conservative 5; Mismatches 17; Indels 2; Gaps 1;  
QY 1 MGMSWIFLLSCTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFDYNLHWKQSH 60  
DB 1 MGMSWIFLLSCTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFDYNLHWKQSH 60  
QY 61 GKLEWIGYIYPNNGGTGYNQKFKSKATLTVDKSSSTAYMELSLTSEDSAVYCAR--A 118  
DB 61 GKLEWIGYIYPNNGGTGYNQKFKSKATLTVDKSSSTAYMELSLTSEDSAVYCAR--A 118  
QY 121 GSGYFYFDYWGQGTTLTVSS 139  
DB 119 GRYYYANDWGQGTTLTVSA 137  
RESULT 16  
US-08-483-528B-93  
Sequence 93, Application US/08483528B  
Patent No. 5939532  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, KAZUYASU  
APPLICANT: KOIKE, MASAMICHI  
APPLICANT: SHITARA, KENYA  
APPLICANT: HANAI, NOBUO  
APPLICANT: KAWANA, YOSHIHISA  
APPLICANT: HASEGAWA, MAMORU  
TITLE OF INVENTION: HUMANIZED ANTIBODIES  
NUMBER OF SEQUENCES: 103  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,528B  
FILING DATE: 07-JUN-95  
CLASSIFICATION: 536  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acids  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: -19..-1  
IDENTIFICATION METHOD: BY SIMILARITY  
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US-08-483-528B-93

Query Match 77.3%; Score 586; DB 1; Length 137;  
Best Local Similarity 82.7%; Pred. No. 2.3e-53;  
Matches 115; Conservative 5; Mismatches 17; Indels 2; Gaps 1;  
  
Qy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60  
Db 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60  
  
Qy 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRSLTSEDSAVYYCARWDF 120  
Db 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRSLTSEDSAVYYCARWDF 120  
  
Qy 121 GSGYFDYWGQGTTLTVSS 139  
Db 119 GRYIYAWDWGQGTTLTVSA 137

## RESULT 17

US-09-647-468-158  
; Sequence 158, Application US/09647468  
; Patent No. 6677436  
; GENERAL INFORMATION:  
; APPLICANT: SATO, KOH  
; APPLICANT: ADACHI, HIDEKI  
; APPLICANT: YABUCHI, NAOKI  
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND  
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY  
; FILE REFERENCE: 053466/0289  
; CURRENT APPLICATION NUMBER: US/09/647,468  
; CURRENT FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: PCT/JP99/01768  
; PRIOR FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: JP 10-91850  
; PRIOR FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 183  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 158  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide  
; OTHER INFORMATION: sequence coding for H chain V region of ant-TF  
; OTHER INFORMATION: mouse monoclonal antibody ATR-8  
US-09-647-468-158

Query Match 74.9%; Score 568; DB 2; Length 137;  
Best Local Similarity 75.4%; Pred. No. 1.7e-51;  
Matches 107; Conservative 11; Mismatches 16; Indels 8; Gaps 2;  
  
Qy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60  
Db 1 MEWSWIFLLSGTAGVHSDIQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60  
  
Qy 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRSLTSEDSAVYYCARWDF 120  
Db 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRSLTSEDSAVYYCARWDF 120  
  
Qy 121 GSGYFDYWGQGTTLTVSS 139  
Db 118 --GFYIDYDCYWGQGTTLTVSA 137

## RESULT 18

US-08-137-117D-27  
; Sequence 27, Application US/08137117D  
; Patent No. 5795965  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, KOH  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANHA, Jose

; APPLICANT: SALDANHA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
; NUMBER OF SEQUENCES: 158  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,117D  
; FILING DATE: 20-DEC-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP92/00544  
; FILING DATE: 24-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-32084  
; FILING DATE: 19-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 3-95476  
; FILING DATE: 25-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 135 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-137-117D-27

Query Match 74.8%; Score 567; DB 1; Length 135;  
Best Local Similarity 78.4%; Pred. No. 2.2e-51;  
Matches 109; Conservative 8; Mismatches 18; Indels 4; Gaps 1;  
  
Qy 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60  
Db 1 MGWSGIFLLSGTAGVHSEIQLQSGPELVKPGASVKISCKASGYFTSYIHWKQSH 60  
  
Qy 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRSLTSEDSAVYYCARWDF 120  
Db 61 GKLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSNTAYMELRSLTSEDSAVYYCARWDF 120  
  
Qy 121 GSGYFDYWGQGTTLTVSS 139  
Db 118 -GGRFAYWGQGTTLTVSA 135

## RESULT 19

US-08-436-717-27  
; Sequence 27, Application US/08436717  
; Patent No. 5817790  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, KOH  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANHA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,717  
FILING DATE:  
CLASSIFICATION: 536  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117  
FILING DATE: 20-DEC-1993  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-436-717-27

Query Match 74.8%; Score 567; DB 1; Length 135;  
Best Local Similarity 78.4%; Pred. No. 2.2e-51;  
Matches 109; Conservative 8; Mismatches 18; Indels 4; Gaps 1;

Qy 1 MGWSWIFLLSGLTAGVHSEVQLQQSGPELVKPGASVKISCKASGYFTDYNHVKQSH 60  
Db 1 MGWSGIFLLSGLTAGVHSEVQLQQSGPELVKPGASVKISCKASGYFTSYIHVKQSH 60

Qy 61 GKLEWIGYIYPNGVDYQNGFNKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120  
Db 61 GKLEWIGYIDPENGGSYQNGKPKATLVKSSSTAYMHLSSLTSEDSAVVYCARWDF 120

Qy 121 GSGYFDYWGQGTTLTVSS 139  
Db 118 -GGRFAYWGQGTTLTVSSA 135

RESULT 20  
PCT-US93-11612-4  
Sequence 4, Application PC/TUS9311612  
GENERAL INFORMATION:  
APPLICANT: Co, Man Sung  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
TITLE OF INVENTION: L-Selectin  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11612  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,946  
FILING DATE: 01-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 140 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-11612-4

Query Match 74.7%; Score 566.5; DB 4; Length 140;  
Best Local Similarity 77.1%; Pred. No. 2.6e-51;  
Matches 108; Conservative 11; Mismatches 20; Indels 1; Gaps 1;

Qy 1 MGWSWIFLLSGLTAGVHSEVQLQQSGPELVKPGASVKISCKASGYFTDYNHVKQSH 60  
Db 1 MGWSWIFLLSGLTAGVHSEVQLQQSGPELVKPGASVKISCKASGYFTSYIHVKQKP 60

Qy 61 GKLEWIGYIYPNGVDYQNGFNKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120  
Db 61 GQGLEWIGYIYPNGDTKYNKPKATLTSKSSSTAYMELSLTSEDSAVVYCARWDF 120

Qy 121 GSGY-YFDYWGQGTTLTVSS 139  
Db 121 GNYVRYFDVWGAGTTTVSS 140

Search completed: March 20, 2006, 07:31:35  
Job time : 8.40237 secs

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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:28:19 ; Search time 50.3087 Seconds

(without alignments)  
1213.978 Million cell updates/sec

Title: US-10-687-035-34

Perfect score: 758

Sequence: 1 MGWSWIFLLSCTAGVHSE.....FGSGYFYDVGQQTTLTVSS 139

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003s.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	758	100.0	139	ADS94335	Ads94335 Antibody
2	644	85.0	135	AAW60866	AAW60866 Variable
3	644	85.0	135	AAW80293	AAW80293 IGM chime
4	644	85.0	590	AAW31751	AAW31751 H chain s
5	644	85.0	590	AAW1888	AAW1888 Anti-huma
6	644	85.0	590	AAW12908	AAW12908 Anti-huma
7	625	82.5	135	AAW68548	AAW68548 Anti-CD33
8	625	82.5	135	AAW69682	AAW69682 Murine M1
9	625	82.5	135	ADO47773	ADO47773 Murine M19
10	623	82.2	137	AAW05090	AAW05090 Heavy cha
11	613.5	80.9	132	AAW03183	AAW03183 Guy's 13
12	604	79.7	139	AAW33328	AAW33328 KM-796 he
13	604	79.7	139	AAW28356	AAW28356 Antibody
14	604	79.7	139	AAW28384	AAW28384 Anti-OM2
15	600.5	79.2	438	AAE18372	AAE18372 Human pen
16	600.5	79.2	438	ABG76347	ABG76347 Portion o
17	600.5	79.2	456	AAE18370	AAE18370 Human pen
18	600.5	79.2	456	ABG76345	ABG76345 Mouse DAV
19	600.5	79.2	456	ABG76354	ABG76354 DAV-1 ant
20	600.5	79.2	493	AAE18379	AAE18379 Human N-t
21	600.5	79.2	493	ABG76354	ABG76354 Mouse DAV
22	600.5	79.2	510	AAE18378	AAE18378 Human N-t
23	600.5	79.2	510	ABG76353	ABG76353 Mouse DAV
24	600.5	79.2	597	AAE18377	AAE18377 Human N-t

25	600.5	79.2	597	5	ABG76352	ABG76352 Mouse DAV
26	600.5	79.2	613	5	AAE18380	AAE18380 Human N-t
27	600.5	79.2	613	5	ABG76355	ABG76355 Mouse DAV
28	593	78.2	588	3	AAW1881	AAW1881 Anti-huma
29	593	78.2	588	3	AAW12918	AAW12918 Anti-huma
30	587	77.4	130	2	AAW71886	AAW71886 Anti-Pas
31	586	77.3	137	2	AAW53330	AAW53330 KM-750 he
32	586	77.3	137	2	AAW28386	AAW28386 Anti-OM2
33	586	77.3	137	2	AAW28358	AAW28358 Antibody
34	585.5	77.2	136	6	ABU08927	ABU08927 Mouse amy
35	585.5	77.2	140	7	ADC24943	ADC24943 Mouse 19/
36	585.5	77.2	140	7	ADK51711	ADK51711 Murine 19
37	578.5	76.3	138	8	ADR73595	ADR73595 Anti-AR a
38	574	75.7	588	2	AAW71880	AAW71880 Anti-huma
39	574	75.7	588	2	AAW12917	AAW12917 Anti-huma
40	573.5	75.7	151	9	AAE31602	AAE31602 Murine in
41	566.5	74.7	140	2	AAW55554	AAW55554 DREG-200
42	565.5	74.6	138	4	AAW69688	AAW69688 Murine CM
43	565.5	74.6	138	4	ADO47789	ADO47789 Mouse CMV
44	564	74.4	135	2	AAW28669	AAW28669 p12-h2. 3
45	564	74.4	143	2	AAW50155	AAW50155 Murine mo
46	564	74.4	472	2	AAW50157	AAW50157 ChimERIC
47	562	74.1	137	2	AAW03724	AAW03724 Anti-huma
48	560	73.9	139	2	AAW38259	AAW38259 ChimERIC
49	560	73.9	141	2	AAW12356	AAW12356 Heavy cha
50	560	73.9	233	2	AAW41710	AAW41710 Murine 12
51	560	73.9	235	2	AAW41707	AAW41707 Murine 12
52	560	73.9	235	2	AAW41682	AAW41682 ChimERIC a
53	560	73.9	235	2	AAW41715	AAW41715 Murine 12
54	559	73.7	140	2	AAW12234	AAW12234 Mouse MAB
55	559	73.7	167	9	ADY94496	ADY94496 Human/mou
56	559	73.7	469	2	AAW40384	AAW40384 Monoclonal
57	557.5	73.5	140	2	AAW06213	AAW06213 MAB Co-1
58	557.5	73.5	140	2	AAW85061	AAW85061 Mouse Co-
59	557.5	73.5	140	6	ABU58895	ABU58895 Mouse ant
60	557	73.5	133	8	ADO00820	ADO00820 Antibody
61	557	73.5	133	8	ADO43850	ADO43850 Heavy cha
62	557	73.5	133	8	ADO43846	ADO43846 Heavy cha
63	557	73.5	133	9	ADO08854	ADO08854 Mammalian
64	557	73.5	144	2	AAW73188	AAW73188 Fragment
65	556.5	73.4	278	6	ABJ19277	ABJ19277 Anti-huma
66	555.5	73.3	140	2	AAW09425	AAW09425 Co-1 Heav
67	555.5	73.3	462	9	ADU70079	ADU70079 Mouse/hum
68	552	72.8	467	6	AAE38408	AAE38408 Mouse vir
69	551.5	72.8	136	3	AAW23815	AAW23815 Plasmid p
70	551.5	72.8	136	4	AAW67491	AAW67491 Amino aci
71	551.5	72.8	136	5	AAW47629	AAW47629 Murine MA
72	551.5	72.8	136	5	ABG97806	ABG97806 Mouse MAB
73	551.5	72.8	136	5	ABG35309	ABG35309 Thrombopo
74	551	72.7	144	2	AAW73189	AAW73189 Fragment
75	551	72.7	144	2	AAW73186	AAW73186 Fragment
76	550	72.6	152	8	ADJ57084	ADJ57084 3G4 antib
77	550	72.6	159	8	ADJ57088	ADJ57088 3G4-2BVH-
78	546	72.0	137	3	AAW99845	AAW99845 Mouse par
79	545.5	72.0	142	4	AAW48249	AAW48249 A77 anti-
80	545.5	72.0	142	4	AAW74622	AAW74622 A77 anti-
81	545.5	72.0	142	4	AAW74622	AAW74622 A77 anti-
82	545.5	72.0	460	9	ADM97108	ADM97108 Murine A7
83	545	71.9	144	2	AAW73187	AAW73187 Fragment
84	545	71.9	144	2	AAW73175	AAW73175 Heavy cha
85	544	71.8	135	3	AAW80288	AAW80288 Humanised
86	541.5	71.4	459	9	ADM97104	ADM97104 Murine MA
87	541.5	71.4	460	9	ADM97139	ADM97139 Murine MA
88	540.5	71.3	136	3	AAW23813	AAW23813 Plasmid p
89	540.5	71.3	136	4	AAW67489	AAW67489 Amino aci
90	540.5	71.3	136	5	AAW47627	AAW47627 Murine MA
91	540.5	71.3	136	5	ABG97804	ABG97804 Mouse MAB
92	540.5	71.3	136	5	ABG35307	ABG35307 Thrombopo
93	539.5	71.2	138	9	ADV92464	ADV92464 Mouse SM5
94	539.5	71.2	138	9	ADV98527	ADV98527 Novel ch1
95	539.5	71.2	468	9	ADV92458	ADV92458 SM5-1 ch1
96	539.5	71.2	468	9	ADV98531	ADV98531 Novel ch1
97	539.5	71.2	624	9	ADV92486	ADV92486 chSMVH/FC

98 539.5 71.2 624 9 ADV98549  
99 539.5 71.2 639 9 ADV92488  
100 539.5 71.2 639 9 ADV98551

# ALIGNMENTS

RESULT 1  
ADS94335  
ID ADS94335 standard; protein; 139 AA.  
AC ADS94335;  
XX  
XX 02-DEC-2004 (first entry)  
XX  
XX Antibody 776.1 heavy chain variable region (776.1H) SEQ ID NO:34.  
XX  
XX antibody; antigen-binding antibody fragment;  
XX cell-associated CA 125/O772P; monoclonal antibody; cytostatic;  
XX immunostimulant; mediator of lysis; tumour; cell proliferative disorder;  
XX cancer; cervical cancer; uterine cancer; breast cancer; lung cancer;  
XX ovarian cancer.  
XX  
XX Synthetic.  
XX WO2004035537-A2.  
XX  
XX 29-APR-2004.  
XX  
XX 15-OCT-2003; 2003WO-US032945.  
XX  
XX 16-OCT-2002; 2002US-0418828P.  
XX 10-JUL-2003; 2003US-0485986P.  
XX  
XX (EURO-) EUROCELTIQUE SA.  
XX  
XX Albone EF, Soltis DA;  
XX  
XX WPI; 2004-357171/33.  
XX N-PSDB; ADS94342.  
XX  
XX Novel isolated antibody, or antigen-binding antibody fragment binding  
XX with cell-associated CA 125/O772P polypeptide relative to shed CA  
XX 125/O772P polypeptide, useful for ameliorating cervical or ovarian cancer.  
XX  
XX Claim 38; SEQ ID NO 34; 153pp; English.  
XX  
XX The present invention describes an isolated antibody, or an antigen-  
XX binding antibody fragment (I), that preferentially binds cell-associated  
XX CA 125/O772P polypeptide relative to shed CA 125/O772P polypeptide. Also  
XX described: (1) a monoclonal antibody (II) produced by hybridoma 4E7; (2)  
XX as a monoclonal antibody that competes with binding of (II); (3) a hybridoma  
XX as deposited in (II); (4) an isolated nucleic acid molecule (III)  
XX comprising a nucleotide sequence that encodes a variable chain region of  
XX (I); (5) a pharmaceutical composition comprising an antibody or an  
XX antigen-binding antibody fragment that preferentially binds cell-  
XX associated CA 125/O772P polypeptide relative to shed CA 125/O772P  
XX polypeptide, and a carrier; (6) a pharmaceutical composition comprising a  
XX monoclonal antibody or an antigen-binding monoclonal antibody fragment  
XX that preferentially binds cell-associated CA 125/O772P polypeptide  
XX relative to shed CA 125/O772P polypeptide, and a carrier; (7) an article  
XX of manufacture (IV) comprising packaging material and a composition  
XX comprising an antibody, or an antigen-binding antibody fragment that  
XX preferentially binds cell-associated CA 125/O772P relative to shed CA  
XX 125/O772P, and a carrier contained within the packaging material, and  
XX composition in a form suitable for administration to a subject; (8) a  
XX fusion polypeptide (V) comprising an antibody, or an antigen-binding  
XX antibody fragment, which preferentially binds cell-associated CA  
XX 125/O772P relative to shed CA 125/O772P operably linked to a heterologous  
XX agent; (9) ameliorating (M1) a symptom of a CA 125/O772P-related disorder  
XX; (10) a monoclonal antibody (VI) chosen from 325.1, 621.1, 633.1, 654.1,  
XX 725.1, 8G9, 7F10, 8A1, 8AC3, 15C9, 8E3, 8B5, 7G10, 16C7, 7H1, 16H9,

7A11, 4E7, 117.1, 368.1, 446.1, 501.1, and 776.1 or its antigen-binding  
antibody fragment; (11) an antibody or antigen binding antibody fragment  
that competes with (VI); and (12) a pharmaceutical composition comprising  
(VI) and a carrier. (1) has cytostatic activity, and can be used as an  
immunostimulant and a mediator of lysis of positive tumour cell. (II) is  
useful for ameliorating a symptom of a CA 125/O772P-related disorder which  
is a cell proliferative disorder such as cancer, cervical or uterine  
cancer, breast or lung cancer or ovarian cancer. (V) is useful  
diagnostically for monitoring the development or progression of cancer or  
tumour as part of clinical testing procedure. The present sequence  
represents an antibody heavy chain variable region amino acid sequence,  
which is used in the exemplification of the present invention.  
XX  
XX Sequence 139 AA;  
SQ  
Query Match 100.0%; Score 758; DB 8; Length 139;  
Best Local Similarity 100.0%; Pred. No. 6.9e-56;  
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGMSWIFLFLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60  
DB 1 MGMSWIFLFLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60  
QY 61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYCARWDF 120  
DB 61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDSSNTAYMELSLTSEDSAVYCARWDF 120  
QY 121 GSGYFDYWGQGTTLTVSS 139  
DB 121 GSGYFDYWGQGTTLTVSS 139  
RESULT 2  
AAW60866  
ID AAW60866 standard; protein; 135 AA.  
XX  
XX AAW60866;  
XX  
XX 10-SEP-1998 (first entry)  
XX  
XX Variable region of an anti-Fas antibody heavy chain.  
XX  
XX Variable region; heavy chain; anti-Fas antibody; human; mouse;  
XX immunoglobulin G; IgG; light chain; treatment; diagnosis;  
XX autoimmune disease.  
XX  
XX Mus sp.  
XX  
XX JF10165178-A.  
XX  
XX 23-JUN-1998.  
XX  
XX 01-JUL-1997; 97JP-00191769.  
XX  
XX 02-JUL-1996; 96JP-00172228.  
XX 09-OCT-1996; 96JP-00268737.  
XX  
XX (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.  
XX  
XX WPI; 1998-406105/35.  
XX N-PSDB; AAV37264.  
XX  
XX DNA encoding, e.g. variable region of anti-Fas antibody - useful for,  
XX e.g. diagnosis and treatment of auto-immune diseases.  
XX  
XX Claim 7; Page 13; 16pp; Japanese.  
XX  
XX The present sequence represents a variable region of the heavy chain of  
XX an anti-Fas antibody. The constant region of the heavy chain is derived  
XX from human immunoglobulin G (19G). The anti-Fas antibody can be used for  
XX the treatment and diagnosis of autoimmune diseases  
XX  
XX Sequence 135 AA;



Query Match 85.0%; Score 644; DB 2; Length 135;  
 Best Local Similarity 87.8%; Pred. No. 2.5e-46;  
 Matches 122; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 1 MGMSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60  
 DB 1 MGMSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60

QY 61 GKLEWIGYIYPNGVDYQNFKSKATLVDNNSNTAYMELSLTSEDSAVYYCARWDF 120  
 DB 61 GKLEWIGYIYPNGGTGYNQKPKSKATLVDNNSSTAYMELSLTSEDSAVYYCAR--- 117

QY 121 GSGYFDYWGQGTTLTVSS 139  
 DB 118 -SYANDYWGQGTSTVTVSS 135

RESULT 4  
 AAW31751  
 ID AAW31751 standard; protein; 590 AA.  
 AC AAW31751;  
 XX  
 XX 15-APR-1998 (first entry)  
 DT  
 DE H chain subunit of Fas specific antibody.  
 XX  
 KW Fas; antibody; human; immunoglobulin; variable region; rheumatism;  
 KW autoimmune disease; rheumatoid arthritis; therapy; CDR; heavy chain;  
 KW complementarity determining region.  
 XX  
 OS Mus musculus.  
 XX  
 XX Key Location/Qualifiers  
 FT Peptide 1-19  
 FT Protein /note= "signal peptide"  
 FT /note= "mature protein"  
 XX EP799891-A1.  
 XX  
 XX 08-OCT-1997.  
 PD  
 PF 27-MAR-1997; 97EP-00302415.  
 XX  
 PR 01-APR-1996; 96JP-00078570.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 PA  
 PI Serizawa N, Ichikawa K, Nakahara K, Yonehara S;  
 XX  
 XX WPI: 1997-482673/45.  
 DR N-PSDB; AAT88869.  
 XX  
 XX Anti-Fas recombinant antibodies - useful for treating auto-immune  
 PT diseases, especially rheumatoid arthritis.  
 PT  
 PS Claim 11; Page 29-31; 72pp; English.  
 XX  
 CC This sequence represents the heavy chain of the protein of the invention.  
 CC The protein of the invention is a recombinant protein (A), that comprises  
 CC at least one region corresponding to an immunoglobulin (Ig) variable  
 CC region which enables the protein to recognise and specifically bind to an  
 CC antigen, preferably human Fas, and has substantially no more  
 CC immunogenicity in a human patient than a human antibody. The proteins are  
 CC useful for treating autoimmune diseases, especially rheumatism  
 CC (rheumatoid arthritis). (A) is based on a murine monoclonal antibody. As  
 CC the protein lacks the constant region, it has substantially no more  
 CC immunogenicity in the human patient than a human antibody  
 XX  
 SQ Sequence 590 AA;

Query Match 85.0%; Score 644; DB 2; Length 590;  
 Best Local Similarity 87.8%; Pred. No. 1.2e-45;  
 Matches 122; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 1 MGMSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60  
 DB 1 MGMSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60

QY 61 GKLEWIGYIYPNGVDYQNFKSKATLVDNNSNTAYMELSLTSEDSAVYYCARWDF 120  
 DB 61 GKLEWIGYIYPNGGTGYNQKPKSKATLVDNNSSTAYMELSLTSEDSAVYYCAR--- 117

QY 121 GSGYFDYWGQGTTLTVSS 139  
 DB 118 -SYANDYWGQGTSTVTVSS 135

RESULT 3  
 AAY80293  
 ID AAY80293 standard; protein; 135 AA.  
 AC AAY80293;  
 XX  
 XX 30-MAY-2000 (first entry)  
 DT  
 DE IGM chimeric antibody heavy chain variable region SEQ ID NO:1.  
 XX  
 KW Humanised; anti-Fas antibody; mouse hybridoma; autoimmune disease;  
 KW diagnosis; CDR; complementarity determining region; apoptosis;  
 KW immunosuppressive.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 XX JP2000014383-A.  
 XX  
 XX 18-JAN-2000.  
 PD  
 PF 03-JUL-1998; 98JP-00204318.  
 XX  
 PR 03-JUL-1998; 98JP-00204318.  
 XX  
 XX (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.  
 PA  
 PI WPI: 2000-199626/18.  
 DR N-PSDB; AAZ95282.  
 XX  
 XX Novel recombinant antibody used for treating and diagnosing autoimmune  
 PT diseases - is humanized anti-Fas antibody which controls and induces  
 PT apoptosis in cells expressing fas antigen.  
 PT  
 PS Example 1; Page 9-10; 25pp; Japanese.  
 XX  
 CC The present invention describes a recombinant antibody (A) which binds to  
 CC fas antigen, and controls and induces apoptosis in cells which expressed  
 CC fas antigen. The complementarity determining regions (CDR) of (A) contain  
 CC amino acid sequences obtained from a mammal other than human, other  
 CC regions contain amino acid sequences from human and they partly contain  
 CC modified amino acids. (A) has immunosuppressive activity. (A) is used for  
 CC treating and/or diagnosing autoimmune diseases. The present sequence  
 CC represents an immunoglobulin M chimeric antibody heavy chain variable  
 CC region from an example from the present invention  
 XX  
 SQ Sequence 135 AA;

Query Match 85.0%; Score 644; DB 3; Length 135;  
 Best Local Similarity 87.8%; Pred. No. 2.5e-46;  
 Matches 122; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 1 MGMSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60  
 DB 1 MGMSWIFLLSAGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60

QY 61 GKLEWIGYIYPYNGVDYQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120  
 DB 61 GKLEWIGYIYPYNGVDYQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120  
 QY 121 GSGYFYDYGQGTTLTVSS 139  
 DB 118 -SYAMDYWGQGTSTVTVSS 135

RESULT 5  
 AAW71888  
 ID AAW71888 standard; protein; 590 AA.  
 XX  
 AC AAW71888;  
 XX  
 DT 18-JAN-1999 (first entry)  
 XX  
 DE Anti-human Fas monoclonal antibody CH11 heavy chain.  
 XX  
 KW Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;  
 KW autoimmune disease; rheumatoid arthritis; therapy; human; mouse;  
 KW antibody engineering.  
 XX  
 OS Synthetic.  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= Sig\_peptide  
 FT Protein 20..590  
 FT /label= Mat\_protein  
 FT Region 50..54  
 FT /label= CDR1  
 FT Region 69..84  
 FT /label= CDR2  
 FT Region 118..124  
 FT /label= CDR3  
 XX  
 FN EP866131-A2.  
 XX  
 PD 23-SEP-1998.  
 XX  
 DF 20-MAR-1998; 98EP-00302113.  
 XX  
 PR 21-MAR-1997; 97JP-00067938.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 PI Serizawa N, Haryuyama H, Takahashi T, Nakahara K, Yonehara S;  
 XX  
 DR WPI; 1998-482965/42.  
 DR N-PSDB; AAV66735.  
 XX  
 PT Production of anti-Fas protein humanised antibodies - for use in inducing  
 PT apoptosis on Fas expressing cells in the treatment of auto-immune  
 PT diseases, especially rheumatoid arthritis.  
 XX  
 PS Example 4; Page 58-60; 187pp; English.  
 XX  
 CC This is the amino acid sequence of the heavy chain of the mouse anti-  
 CC human Fas monoclonal antibody CH11, as deduced from an amplified cDNA  
 CC clone (see AAV66735). The invention relates to novel humanised antibodies  
 CC comprising humanised light and heavy chains (see AAW71876-81) of CH11.  
 CC These humanised anti-human Fas antibodies are capable of inducing  
 CC apoptosis in cells expressing Fas (e.g. synovocytes) and are useful in  
 CC the treatment of autoimmune disease and chronic rheumatoid arthritis  
 XX  
 SQ Sequence 590 AA;

Query Match 85.0%; Score 644; DB 2; Length 590;  
 Best Local Similarity 87.8%; Pred. No. 1.2e-45;  
 Matches 122; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60  
 DB 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHVKQSH 60  
 QY 61 GKLEWIGYIYPYNGVDYQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120  
 DB 61 GKLEWIGYIYPYNGVDYQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120  
 QY 121 GSGYFYDYGQGTTLTVSS 139  
 DB 118 -SYAMDYWGQGTSTVTVSS 135

RESULT 6  
 AAB12908  
 ID AAB12908 standard; protein; 590 AA.  
 XX  
 AC AAB12908;  
 XX  
 DT 16-NOV-2000 (first entry)  
 XX  
 DE Anti-human Fas antibody CH11 H chain protein sequence SEQ ID #8.  
 XX  
 KW Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;  
 KW immunosuppression; autoimmune disease; treatment; rheumatism;  
 KW anti-Fas antibody.  
 XX  
 OS Synthetic.  
 XX  
 PN JP2000154149-A.  
 XX  
 PD 06-JUN-2000.  
 XX  
 PF 17-SEP-1999; 99JP-00263984.  
 XX  
 PR 18-SEP-1998; 98JP-00264598.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 DR WPI; 2000-454476/40.  
 DR N-PSDB; AAB78202.  
 XX  
 PT Anti-human Fas humanizing antibody-containing antirheumatic agents.  
 PS Disclosure; Page 47-48; 109pp; Japanese.

The present invention relates to antirheumatic agents which comprise as active ingredients an immunoglobulin M (IgM) protein. The IgM protein does not include a J segment, has apoptosis inducing activity, and consists of a light and heavy chain polypeptide produced synthetically. The agents of the invention exhibit antirheumatic and immunosuppressive activity and can be used to treat autoimmune diseases, especially rheumatism. The IgM molecule used in the invention has human Fas-antigen binding properties. Included in the invention are nucleotide sequences of the IgM light and heavy chains (see AAB78267-A78272) and the corresponding protein sequences (see AAB12913-B12918 and AAB12919), and nucleotide sequences of the humanised anti-human Fas Ig CH11 (see AAB78202-A78206) and protein sequences (see AAB12908-B12910). Also included are anti-human Fas antibody CDR peptides (AAB12902-B12907). Primers specific for the anti-human Fas antibody, light, heavy and kappa chains used in the invention are represented by sequences AAB78213-A78266. Primers used for sequencing the human Ig DNA used in the invention are represented by sequences AAB78277-A78318 and AAB78335-A78337, while humanised anti-Fas Ig DNA sequencing primers are represented by sequences AAB78321-A78334 and AAB78338-A78367. Primer sequences AAB78207-A78212 are specific for murine Ig DNA, and are used in the production of the agent of the invention

Sequence 590 AA;

Query Match 85.0%; Score 644; DB 3; Length 590;  
 Best Local Similarity 87.8%; Pred. No. 1.2e-45;  
 Matches 122; Conservative 5; Mismatches 8; Indels 4; Gaps 1;



Query Match 82.5%; Score 625; DB 4; Length 135;  
 Best Local Similarity 84.9%; Pred. No. 9.7e-45;  
 Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHWKQSH 60  
 DB 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHWKQSH 60

QY 61 GKLEWIGYIYPYNGVSDYQNFKSKATLIVDSSNTAYMELRSLTSEDSAVYYCARWDF 120  
 DB 61 GKLEWIGYIYPYNGVSDYQNFKSKATLIVDSSNTAYMELRSLTSEDSAVYYCARWDF 120

QY 121 GSGYFDYWGQGTTLTVSS 139  
 DB 118 -GRPAMDYWGQGTSTVTVSS 135

RESULT 9  
 ADO47773  
 ID ADO47773 standard; protein; 135 AA.  
 AC ADO47773;  
 DT 15-JUN-2004 (first entry)  
 DE Mouse M195 antibody heavy chain variable region #2.  
 KW humanised immunoglobulin; Ig; immunoglobulin; framework; acceptor Ig;  
 KW donor Ig; CDR; complementarity determining region; interleukin-2; IL-2;  
 KW IL-2 receptor; T-cell mediated disorder; mouse; M195 antibody;  
 KW heavy chain variable region.  
 OS Mus sp.  
 XX US2004058414-A1.  
 XX 25-MAR-2004.  
 XX 30-MAY-2003; 2003US-00452357.  
 XX 28-DEC-1988; 88US-00290975.  
 XX 13-FEB-1989; 89US-00310252.  
 XX 28-SEP-1990; 90US-00590274.  
 XX 07-JUN-1995; 95US-00484537.  
 XX 22-NOV-2000; 2000US-00718993.  
 XX (QUEE/) QUEEN C L.  
 XX (COMS/) CO M S.  
 XX (SCHN/) SCHNEIDER W P.  
 XX (LAND/) LANDOLFI N P.  
 XX (COEL/) COELINGH K L.  
 XX (SELI/) SELICK H E.  
 XX Queen CL, Co MS, Schneider WP, Landolfi NF, Coelingh KL;  
 XX Selick HE;  
 XX WPI; 2004-304235/28.  
 XX N-PSDB; ADO47772.  
 XX Designing humanized immunoglobulin chain comprises substituting human  
 XX framework amino acids of acceptor immunoglobulin with corresponding amino  
 XX acid from donor immunoglobulin at position in immunoglobulin.  
 XX Disclosure; Fig 41; 130pp; English.  
 XX The invention describes a method of designing a humanised immunoglobulin  
 XX (Ig) chain. The method comprises substituting human framework amino acids  
 XX of the acceptor Ig with a corresponding amino acid from the donor Ig at a  
 XX position in the Ig, where the amino acid is immediately adjacent to one  
 XX of the CDR's or the amino acid is predicted to have a side chain atom  
 XX whose Van der Waals surface is 3 angstroms from the CDR's in three-  
 XX dimensional Ig model and is capable of interacting with the antigen or

CC with the CDR's of the humanised Ig that when the chain is a heavy chain,  
 CC substituted amino acid(s) is capable of interacting with CDR's 2 or 3.  
 CC Also described are: an Ig comprising two light/heavy chains; a DNA  
 CC sequence which upon expression encodes a humanised Ig chain; a  
 CC polynucleotide composition comprising a DNA sequence coding for a  
 CC humanised Ig; a composition comprising a pure humanised immunoglobulin  
 CC capable of inhibiting binding of human interleukin-2 (IL-2) to a human IL  
 CC -2 receptor; treating T-cell mediated disorders in a human patient  
 CC comprising administering to the patient a therapeutic dose of an Ig; and  
 CC a composition comprising a pure humanised Ig reactive with the p75 chain  
 CC of the human IL-2 receptor. The method is used for designing a humanised  
 CC immunoglobulin chain, useful for treating T-cell mediated disorders in a  
 CC human patient. The invented method produces an Ig chain that is easily  
 CC and economically produced. This is the amino acid sequence of mouse M195  
 CC antibody heavy chain variable region. Residues in the human antibody  
 CC framework can be replaced with residues from the mouse antibody to create  
 CC a humanised antibody.  
 XX Sequence 135 AA;  
 SQ

Query Match 82.5%; Score 625; DB 8; Length 135;  
 Best Local Similarity 84.9%; Pred. No. 9.7e-45;  
 Matches 118; Conservative 7; Mismatches 10; Indels 4; Gaps 1;

QY 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHWKQSH 60  
 DB 1 MGWSWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHWKQSH 60

QY 61 GKLEWIGYIYPYNGVSDYQNFKSKATLIVDSSNTAYMELRSLTSEDSAVYYCARWDF 120  
 DB 61 GKLEWIGYIYPYNGVSDYQNFKSKATLIVDSSNTAYMELRSLTSEDSAVYYCARWDF 120

QY 121 GSGYFDYWGQGTTLTVSS 139  
 DB 118 -GRPAMDYWGQGTSTVTVSS 135

RESULT 10  
 AAR05090  
 ID AAR05090 standard; protein; 137 AA.  
 AC AAR05090;  
 DT 25-MAR-2003 (revised)  
 DT 04-OCT-1990 (first entry)  
 XX Heavy chain variable domain of human chorion gonadotropin-binding pptde.  
 XX Human chorionic gonadotropin; antibodies; heavy chain; choriocarcinoma;  
 XX abortion; tumour detection; complementary determining regions;  
 XX pregnancy prevention.  
 XX Mus musculus.  
 XX Key Location/Qualifiers  
 XX Binding-site 50..54  
 XX /label= CDR 1  
 XX Binding-site 70..85  
 XX /label= CDR 2  
 XX Binding-site 118..126  
 XX /label= CDR 3  
 XX EP370581-A.  
 XX 30-MAY-1990.  
 XX 21-NOV-1989; 89EP-00202951.  
 XX 25-NOV-1988; 88NL-00002902.  
 XX (ALKU) AKZO NV.  
 XX Vanwezenb PM, Bos ES;

XX WPI; 1990-165307/22.  
 DR N-PSDB; AAQ04694.  
 XX  
 XX Polypeptide(s) which specifically bind human chorionic gonadotropin -  
 PT contg. antigen-binding domains comprising complementary determining  
 PT regions.  
 XX  
 XX Disclosure; Page ?; -pp; English.  
 XX  
 CC Together with the light chain variable domain (AAR05089) the sequence  
 CC forms a hCH-binding antibody fragment (PhCG). For the production of Abs  
 CC the variable region was fused to a constant region of human origin. The  
 CC product can be used to prevent pregnancy or for combatting  
 CC choriocarcinomas or other hCG-producing tumours. They also have  
 CC diagnostic applications as immune reagents for in vivo diagnosis, eg for  
 CC localisation of tumours and for in vitro diagnosis for detection of hCG  
 CC in body fluids. (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 137 AA;  
 Query Match 82.2%; Score 623; DB 2; Length 137;  
 Best Local Similarity 84.2%; Pred. No. 1.5e-44;  
 Matches 117; Conservative 9; Mismatches 11; Indels 2; Gaps 1;  
 QY 1 MGWSWIFLFLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHMKQSH 60  
 DB 1 MGWSWIFLFLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHMKQSH 60  
 QY 61 GKILEWIGIYIPYNGVSDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120  
 DB 61 GRLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCAR--E 118  
 QY 121 GSGYFDYWGQGTTLTVSS 139  
 DB 119 GIFYTDYWGQGTSTVTVSS 137  
 RESULT 11  
 AA03183  
 ID AA03183 standard; protein; 132 AA.  
 XX  
 AC AA03183;  
 XX  
 DT 24-FEB-1997 (first entry)  
 XX  
 DE Guy's 13 anti-Streptococcus mutans antibody gamma chain.  
 XX  
 KW Rabbit; immunoglobulin; receptor; protection protein; mutans;  
 KW heavy chain; antigen binding domain; protection; pathogen; mucosal;  
 KW environment; gastrointestinal; passive; immunisation; Guy's 13 antibody;  
 KW prevention; dental caries; Streptococcus; poly; gamma chain.  
 XX  
 OS Mus musculus.  
 PH  
 FT Key Location/Qualifiers  
 FT Peptide 1..19 /label= sig\_peptide  
 FT Region 50..54 /label= CDR1  
 FT FT /note= "claim 8"  
 FT Region 69..85 /label= CDR2  
 FT FT /note= "claim 8"  
 FT Region 118..128 /label= CDR3  
 FT FT /note= "claim 8"  
 XX  
 PN AU9346181-A.  
 XX  
 PD 17-MAR-1994.  
 XX  
 PP 07-SEP-1993; 93AU-00046181.  
 XX  
 PR 07-SEP-1992; 92JP-00238452.  
 XX

useful for passive immunisation against mucosal antigens, esp. against S.  
 mutans and S. sorbinus to prevent dental caries.  
 Claim 23; Page 131; 152pp; English.  
 The present sequence is the Guy's 13 anti-Streptococcus mutans antibody,  
 gamma chain. The immunoglobulin (Ig) of the invention comprises a  
 protection protein (PP), pref. a portion of the rabbit poly-Ig receptor,  
 in association with an Ig derived light or heavy chain, having at least a  
 portion of an antigen (Ag) binding domain, specifically the Guy's 13  
 kappa or gamma chain. The Ig can be used to prevent dental caries by  
 binding S. mutans serotypes c, e and f, while the PP protects the Ig in  
 harsh mucosal, e.g. gastrointestinal, environments, therefore enhancing  
 its effectiveness in passively immunising animals against mucosal  
 pathogens  
 Sequence 132 AA;  
 Query Match 80.9%; Score 613.5; DB 2; Length 132;  
 Best Local Similarity 83.5%; Pred. No. 8.8e-44;  
 Matches 116; Conservative 6; Mismatches 10; Indels 7; Gaps 1;  
 QY 1 MGWSWIFLFLSLGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHMKQSH 60  
 DB 1 MEWTWVFLFLSLGTAGVHSGVQLQSGPDLVLPFGASVKISKASGYTFTDYNHMKQSR 60  
 QY 61 GKILEWIGIYIPYNGVSDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120  
 DB 61 GKSLEWIGIYIPYNGVSDYNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCAT--- 117  
 QY 121 GSGYFDYWGQGTTLTVSS 139  
 DB 118 ---YFDYWGQGTTLTVSS 132  
 RESULT 12  
 AAR53328  
 ID AAR53328 standard; protein; 139 AA.  
 XX  
 AC AAR53328;  
 XX  
 DT 17-NOV-1994 (first entry)  
 XX  
 DE KM-796 heavy chain.  
 XX  
 KW Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;  
 KW expression vector; heavy; light; chain; hypervariable region; CDR; KM-603;  
 KW constant region; hybridoma; Ig; immunoglobulin; KM-796; KM-750;  
 XX  
 OS Mus musculus.  
 PH  
 FT Key Location/Qualifiers  
 FT Peptide 1..19 /label= sig\_peptide  
 FT Region 50..54 /label= CDR1  
 FT FT /note= "claim 8"  
 FT Region 69..85 /label= CDR2  
 FT FT /note= "claim 8"  
 FT Region 118..128 /label= CDR3  
 FT FT /note= "claim 8"  
 XX  
 PN AU9346181-A.  
 XX  
 PD 17-MAR-1994.  
 XX  
 PP 07-SEP-1993; 93AU-00046181.  
 XX  
 PR 07-SEP-1992; 92JP-00238452.  
 XX

Immunoglobulin and protection protein complex and its prodn. in plants -

PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;  
 XX WPI; 1994-126857/16.  
 DR N-PSDB; AAQ45426.  
 XX Humanised antibody specific for ganglioside GM2 - used for producing a  
 FT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.  
 XX Claim 5; Page 104-105; 19ipp; English.  
 XX Chimeric human Ab expression vectors are constructed by inserting the Ab  
 CC heavy and light chain variable region-encoding cDNA isolated from  
 CC hybridomas producing a mouse or rat monoclonal Ab reacting with the  
 CC ganglioside GM2 respectively into an expression vector for use in animal  
 CC cells which contains the human Ab heavy and light chain constant region-  
 CC encoding cDNA. The expression vectors are introduced into animal cells  
 CC and the transformant thus obtained is cultured for the prodn. of a  
 CC chimeric human Ab reacting with the ganglioside GM2. In contrast to mouse  
 CC monoclonal Abs, the chimeric human Abs will not cause anti-mouse Ig Ab  
 CC prodn. in the patient's body but show a prolonged blood half-life, with a  
 CC reduced frequency of adverse effects, so that it can be expected to be  
 CC superior to mouse monoclonal Abs in the efficacy in the treatment of  
 CC human cancer, for instance. Mouse anti-GM2 monoclonal Ab KM-796 and KM-  
 CC 750 and rat KM-603 heavy and light chain sequences are given in AAQ45426-  
 CC 30. CDR regions for use in chimeric Abs are indicated in the Features  
 CC Table  
 XX SQ Sequence 139 AA;

Query Match 79.7%; Score 604; DB 2; Length 139;  
 Best Local Similarity 82.7%; Pred. No. 5.8e-43;  
 Matches 115; Conservative 6; Mismatches 18; Indels 0; Gaps 0;  
 QY 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISKASGYFTDYNHIVKQSH 60  
 DB 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISKASGYFTDYNHIVKQSH 60  
 QY 61 GKILEWIGIYPYNGVSDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120  
 DB 61 GKILEWIGIYPYNGVSDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120  
 QY 121 GSGYFYDWGQGTTLTVSS 139  
 DB 121 YGYMFAYWGQGTTLTVTSA 139

RESULT 13  
 AAY28356  
 ID AAY28356 standard; protein; 139 AA.  
 XX AAY28356;

XX AC AAY28356;  
 XX 27-AUG-2003 (revised)  
 DT 04-NOV-1999 (first entry)  
 XX Antibody chain used to produce Human chimeric antibodies.  
 DE antibody; nucleotide; genomic; hypervariable region; chimeric;  
 KW light chain; heavy chain; amino acid.  
 XX Mammalia.

XX Key Location/Qualifiers  
 FH Peptide 1..19  
 FT /label= Signal peptide  
 FT Protein 20..139  
 FT /label= Mature antibody chain  
 FT Domain 50..55  
 FT /label= CDR1  
 FT /note= "Complementarity determining region"  
 FT Domain 69..86

FT /label= CDR2  
 FT /note= "Complementarity determining region"  
 FT 118..129  
 FT /label= CDR3  
 FT /note= "Complementarity determining region"  
 PN US5939532-A.  
 XX 17-AUG-1999.  
 PD 07-JUN-1995; 95US-00483528.  
 XX 07-SEP-1993; 93US-00116778.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;  
 XX WPI; 1999-468416/39.  
 XX N-PSDB; AAX99474.  
 DR Chimeric human antibody expression vectors.  
 XX Disclosure; Col 81-83; 188pp; English.  
 CC This antibody chain is used in the production of Human chimeric  
 CC antibodies. The chimeric human antibodies are useful in the treatment of  
 CC cancer, especially that which is of neural ectodermal origin. In contrast  
 CC to prior art constructs based on mouse monoclonal antibodies, the  
 CC chimeric human antibodies do not cause anti-mouse immunoglobulin  
 CC production. The chimeric human antibodies have a prolonged half-life and  
 CC a reduced frequency of adverse effects when compared to mouse monoclonal  
 CC antibodies. (Updated on 27-AUG-2003 to correct OS field.)  
 XX SQ Sequence 139 AA;  
 Query Match 79.7%; Score 604; DB 2; Length 139;  
 Best Local Similarity 82.7%; Pred. No. 5.8e-43;  
 Matches 115; Conservative 6; Mismatches 18; Indels 0; Gaps 0;  
 QY 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISKASGYFTDYNHIVKQSH 60  
 DB 1 MGWSWIFLLSLGAGVHSEVQLQSGPELVKPGASVKISKASGYFTDYNHIVKQSH 60  
 QY 61 GKILEWIGIYPYNGVSDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120  
 DB 61 GKILEWIGIYPYNGVSDYQNFKSKATLIVDSSNTAYMELSLTSEDSAVVYCARWDF 120  
 QY 121 GSGYFYDWGQGTTLTVSS 139  
 DB 121 YGYMFAYWGQGTTLTVTSA 139  
 RESULT 14  
 AAY28384  
 ID AAY28384 standard; protein; 139 AA.  
 XX AAY28384;  
 XX 04-NOV-1999 (first entry)  
 DT Anti-GM2 heavy chain from KM796 mouse hybridoma cell line.  
 DE antibody; nucleotide; genomic; hypervariable region; chimeric;  
 KW light chain; heavy chain; plasmid; hypervariable.  
 XX Mus sp.  
 XX Key Location/Qualifiers  
 FH Peptide 1..19  
 FT /label= Signal peptide  
 FT Protein 20..139  
 FT /label= Mature mouse heavy chain

FT Domain 50..54  
 FT /label= Hypervariable region 1  
 FT Domain 69..85  
 FT /label= Hypervariable region 2  
 FT Domain 118..128  
 FT /label= Hypervariable region 3  
 XX US5939532-A.  
 XX 17-AUG-1999.  
 XX 07-JUN-1995; 95US-00483528.  
 XX 07-SEP-1993; 93US-00116778.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;  
 XX WPI; 1999-468416/39.  
 XX Chimeric human antibody expression vectors.  
 XX Example 1; Col 151-153; 188pp; English.  
 XX This amino acid sequence was isolated from mouse hybridoma cell line KM-  
 CC 796, and encodes for the anti-GM2 heavy chain. Chimeric human antibodies  
 CC of the invention are useful in the treatment of cancer, especially that  
 CC which is of neural ectodermal origin. In contrast to prior art constructs  
 CC based on mouse monoclonal antibodies, the chimeric human antibodies do  
 CC not cause anti-mouse immunoglobulin production. The chimeric human  
 CC antibodies have a prolonged half-life and a reduced frequency of adverse  
 CC effects when compared to mouse monoclonal antibodies  
 XX Sequence 139 AA;  
 SQ  
 Query Match 79.7%; Score 604; DB 2; Length 139;  
 Best Local Similarity 82.7%; Pred. No. 5.8e-43;  
 Matches 115; Conservative 6; Mismatches 18; Indels 0; Gaps 0;  
 QY 1 MGMSWIFLLSCTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60  
 DB 1 MGMSWIFLLSCTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60  
 QY 61 GKLEWIGIYYPNGVSDYNQNPFSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120  
 DB 61 GKLEWIGIYYPNGVSDYNQNPFSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120  
 QY 121 GSGYFDYWGQGTTLTVSS 139  
 DB 121 YGYMPEYWGQGTTLTVSA 139  
 RESULT 15  
 AAE18372  
 ID AAE18372 standard; protein; 438 AA.  
 XX AAE18372;  
 XX 07-MAY-2002 (first entry)  
 XX Human penton base monoclonal antibody, DAV-1 heavy chain fragment.  
 XX Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;  
 KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;  
 KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;  
 KW cytostatic; vasotropic; ophthalmological.  
 XX Homo sapiens.  
 XX WO200204522-A2.  
 XX 17-JAN-2002.  
 PD  
 09-JUL-2001; 2001WO-EP007878.  
 XX PF  
 XX 10-JUL-2000; 2000US-00613017.  
 PR  
 XX (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 PA (SCRI ) SCRIPPS RES INST.  
 XX PI  
 XX Nemerow GR, Li E;  
 XX WPI; 2002-171707/22.  
 DR N-PSDB; AAE18372.  
 XX New bifunctional molecules comprising an antibody or its antigen-binding  
 PT portion, and a targeting agent, useful for e.g. gene therapy, or for  
 PT promoting Adenoviral vector-mediated gene delivery to cells lacking av  
 PT integrins.  
 XX Claim 10; Page 96; 106pp; English.  
 XX The present invention relates to a bifunctional molecule comprising an  
 CC antibody or its antigen-binding portion, and a targeting agent where the  
 CC antibody specifically binds to an antigen in a protein that binds to av  
 CC integrin, and the targeting agent specifically binds to a cell surface  
 CC protein that activates the phosphatidylinositol 3 (PI3K) signalling  
 CC pathway. The bifunctional molecules are useful for gene therapy, for  
 CC promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking  
 CC av integrins, for enhancing Ad binding and internalisation, and in gene  
 CC delivery of by fibroless adenovirus particles. The bifunctional molecules  
 CC permit targeting of viral and bacterial vectors to cells that express  
 CC targeted receptors. Diseases that can be targeted include cancers,  
 CC vascular disorders, diabetic retinopathies, restenosis, ophthalmic  
 CC disorders, hyperproliferative disorders, and hormonal disorders. The  
 CC present sequence is human penton base monoclonal antibody, DAV-1 heavy  
 CC chain fragment  
 XX SQ Sequence 438 AA;  
 Query Match 79.2%; Score 600.5; DB 5; Length 438;  
 Best Local Similarity 82.0%; Pred. No. 3.9e-42;  
 Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;  
 QY 1 MGMSWIFLLSCTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60  
 DB 1 MGMSWIFLLSCTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNHWKQSH 60  
 QY 61 GKLEWIGIYYPNGVSDYNQNPFSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120  
 DB 61 GKLEWIGIYYPNGVSDYNQNPFSKATLIVDSSNTAYMELSLTSEDSAVYYCARWDF 120  
 QY 121 GSGYFDYWGQGTTLTVSS 139  
 DB 119 -----IAYWGQGTTLTVSA 132  
 RESULT 16  
 ABG76347  
 ID ABG76347 standard; protein; 438 AA.  
 XX ABG76347;  
 XX 10-MAY-2003 (first entry)  
 XX Portion of mouse DAV-1 heavy chain monoclonal antibody.  
 XX Mouse; bifunctional molecule; antigen-binding portion; alpha integrin;  
 KW cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;  
 KW signalling pathway; targeted gene therapy; delivery vector;  
 KW adenoviral gene delivery particle; viral infection; cancer;  
 KW rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;  
 KW restenosis; ophthalmic disorder; hyperproliferative disorder;  
 KW hormonal disorder; virucide; antiinflammatory; antirheumatic;

KW antiarthritic; ophthalmological; DAV-1 heavy chain;  
 KW penton base monoclonal antibody.

XX Mus sp.  
 XX US2002164333-A1.  
 XX 07-NOV-2002.  
 XX 10-JUL-2001; 2001US-00903327.  
 XX 10-JUL-2000; 2000US-00613017.  
 PR 10-JUL-2000; 2000US-0325781P.  
 XX (SCRI ) SCRIPPS RES INST.

XX Nemerow GR, Li E;  
 XX WPI; 2002-171707/22.  
 DR N-PSDB; ABX12746.

XX New bifunctional molecules comprising an antibody or its antigen-binding  
 PT portion, and a targeting agent, useful for e.g. gene therapy, or for  
 PT promoting Adenoviral vector-mediated gene delivery to cells lacking av  
 PT integrins.

XX Claim 10; Page 35-36; 49pp; English.

XX The present invention relates to a bifunctional molecule comprising an  
 PS antibody or its antigen-binding portion, and a targeting agent. The  
 CC antibody specifically binds to an antigen in a protein that binds to  
 CC alpha integrin, and the targeting agent specifically binds to a cell  
 CC surface protein that activates the phosphatidylinositol-3-OH kinase  
 CC (PI3K) signalling pathway. The bifunctional molecules are useful for  
 CC targeted gene therapy using targeting delivery vectors, such as  
 CC adenoviral gene delivery particles. The bifunctional molecules are useful  
 CC for treating viral infections, rheumatoid arthritis, cancers, ophthalmic  
 CC cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic  
 CC disorders, hyperproliferative disorders, and hormonal disorders. The  
 CC present sequence represents a portion of the mouse DAV-1 heavy chain that  
 CC is used for a fusion protein bifunctional antibody

XX Sequence 438 AA;

Query Match 79.2%; Score 600.5; DB 5; Length 438;  
 Best Local Similarity 82.0%; Pred. No. 3.9e-42;  
 Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
 Db 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
 Qy 61 GKILEWIGYIYPYNGVDYNGVSNQNFKSKATLIVDNSNTAYMELRLSITSDSAVYICARWDF 120  
 Db 61 GKILEWIGYIYPYNGVSNQNFKSKATLIVDNSNTAYMELRLSITSDSAVYICARWDF 120  
 Qy 121 GSGYFDYWGQGTTLTVSS 139  
 Db 119 -----IAYWGQGTTLTVSA 132

RESULT 17  
 AAEL18370  
 ID AAEL18370 standard; protein; 456 AA.

XX AC AAEL18370;

XX 07-MAY-2002 (first entry)

XX Human penton base monoclonal antibody, DAV-1 heavy chain.

XX Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;  
 KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;

KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;  
 KW cystostatic; vasotropic; ophthalmological.

XX Homo sapiens.

XX Key Location/Qualifiers  
 XX OS 230..242  
 XX Region /note= "Hinge region"

XX WO200204522-A2.

XX 17-JAN-2002.

XX 09-JUL-2001; 2001WO-EP007878.

XX 10-JUL-2000; 2000US-00613017.

XX (NOVS ) NOVARTIS AG.

XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX (SCRI ) SCRIPPS RES INST.

XX Nemerow GR, Li E;

XX WPI; 2002-171707/22.

XX N-PSDB; AAD29308.

XX New bifunctional molecules comprising an antibody or its antigen-binding  
 PT portion, and a targeting agent, useful for e.g. gene therapy, or for  
 PT promoting Adenoviral vector-mediated gene delivery to cells lacking av  
 PT integrins.

XX Claim 10; Page 91-92; 106pp; English.

XX The present invention relates to a bifunctional molecule comprising an  
 CC antibody or its antigen-binding portion, and a targeting agent where the  
 CC antibody specifically binds to an antigen in a protein that binds to av  
 CC integrin, and the targeting agent specifically binds to a cell surface  
 CC protein that activates the phosphatidylinositol 3 (PI3K) signalling  
 CC pathway. The bifunctional molecules are useful for gene therapy, for  
 CC promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking  
 CC av integrins, for enhancing Ad binding and internalisation, and in gene  
 CC delivery of by fibreless adenovirus particles. The bifunctional molecules  
 CC permit targeting of viral and bacterial vectors to cells that express  
 CC targeted receptors. Diseases that can be targeted include cancers,  
 CC vascular disorders, diabetic retinopathies, restenosis, ophthalmic  
 CC disorders, hyperproliferative disorders, and hormonal disorders. The  
 CC present sequence is human penton base monoclonal antibody, DAV-1 heavy  
 CC chain

XX Sequence 456 AA;

Query Match 79.2%; Score 600.5; DB 5; Length 456;  
 Best Local Similarity 82.0%; Pred. No. 4.1e-42;  
 Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

Qy 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
 Db 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISCKASGYTFDYNHVKQSH 60  
 Qy 61 GKILEWIGYIYPYNGVDYNGVSNQNFKSKATLIVDNSNTAYMELRLSITSDSAVYICARWDF 120  
 Db 61 GKILEWIGYIYPYNGVSNQNFKSKATLIVDNSNTAYMELRLSITSDSAVYICARWDF 120  
 Qy 121 GSGYFDYWGQGTTLTVSS 139  
 Db 119 -----IAYWGQGTTLTVSA 132

RESULT 18  
 ABG76345  
 ID ABG76345 standard; protein; 456 AA.  
 XX AC ABG76345;



```
XX 10-MAY-2003 (first entry)
XX Mouse DAV-1 heavy chain monoclonal antibody.
XX
XX Mouse; bifunctional molecule; antigen-binding portion; alpha integrin;
XX cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;
XX signalling pathway; targeted gene therapy; delivery vector;
XX adenoviral gene delivery particle; viral infection; cancer;
XX rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;
XX restenosis; ophthalmic disorder; hyperproliferative disorder;
XX hormonal disorder; virucide; antiinflammatory; antirheumatic;
XX antiarthritic; ophthalmological; DAV-1 heavy chain;
XX penton base monoclonal antibody.
XX
XX Mus sp.
XX
XX US2002164333-A1.
XX
XX 07-NOV-2002.
XX
XX 10-JUL-2001; 2001US-00903327.
XX
XX 10-JUL-2000; 2000US-00613017.
XX
XX 10-JUL-2000; 2000US-0325781P.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Nemerow GR, Li E;
XX
XX WPI; 2002-171707/22.
XX
XX N-PSDB; ABX12744.
XX
XX New bifunctional molecules comprising an antibody or its antigen-binding
XX portion, and a targeting agent, useful for e.g. gene therapy, or for
XX promoting Adenoviral vector-mediated gene delivery to cells lacking av
XX integrins.
XX
XX Claim 10; Page 30-31; 49pp; English.
XX
XX The present invention relates to a bifunctional molecule comprising an
XX antibody or its antigen-binding portion, and a targeting agent. The
XX antibody specifically binds to an antigen in a protein that binds to
XX alpha integrin, and the targeting agent specifically binds to a cell
XX surface protein that activates the phosphatidylinositol-3-OH kinase
XX (PI3K) signalling pathway. The bifunctional molecules are useful for
XX targeted gene therapy using targeting delivery vectors, such as
XX adenoviral gene delivery particles. The bifunctional molecules are useful
XX for treating viral infections, rheumatoid arthritis, cancers,
XX cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic
XX disorders, hyperproliferative disorders, and hormonal disorders. The
XX present sequence represents mouse DAV-1 heavy chain, penton base
XX monoclonal antibody
XX
XX Sequence 456 AA;
XX
XX Query Match 79.2%; Score 600.5; DB 5; Length 456;
XX Best Local Similarity 82.0%; Pred. No. 4.1e-42;
XX Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;
XX
XX 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHWKQSH 60
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHWKQSH 60
XX
XX 61 GKLEWIGIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELSLTSDSAVYCARWDF 120
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 61 GKLEWIGIYPYNGVSDYNQNFKSKATLITDSSNTAYMELSLTSDSAVYCARWDF 118
XX
XX 121 GSGYYPDYWGQGTTLTVSS 139
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 119 -----TAYWGQGLTVTVA 132
XX
XX RESULT 19
XX AEB96754
XX ID AEB96754 standard; protein; 456 AA.
XX
XX AC AEB96754;
XX
XX XX 20-OCT-2005 (first entry)
XX
XX DAV-1 antibody heavy chain.
XX
XX Gene therapy; cancer; vascular disease; diabetic retinopathy; restenosis;
XX ocular disease; hyperproliferation; hormone metabolism disorder;
XX cytostatic; vasotropic; antidiabetic; ophthalmological; metabolic-gen.;
XX DAV-1; heavy chain; antibody.
XX
XX OS Synthetic.
XX
XX WO2005075506-A1.
XX
XX 18-AUG-2005.
XX
XX 29-DEC-2004; 2004WO-IB004324.
XX
XX 09-JAN-2004; 2004US-0535199P.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Nemerow GR, Li E;
XX
XX WPI; 2005-555928/56.
XX
XX New modified adenovirus fiber protein comprising a fiber shaft and a
XX modified knob, useful for treating cancer, vascular disorders, diabetic
XX retinopathies, restenosis and vascular, ophthalmic, hyperproliferative or
XX hormonal disorders.
XX
XX Example 1; SEQ ID NO 28; 250pp; English.
XX
XX The invention relates to a modified adenovirus fiber protein comprising a
XX fiber shaft that contains a sufficient number of shaft repeats to permit
XX trimerization in the absence of a fiber knob or in the absence of an
XX extrinsic trimerization domain, and optionally a modified knob, where, if
XX the knob is included, it is modified to remove or disable the
XX trimerization domain of the knob. The invention also relates to a
XX modified adenovirus fiber protein comprising a modified knob, where the
XX modification of the knob removes or disables a trimerization domain of
XX the knob, and the modified fiber trimerizes a nucleic acid molecule
XX comprising a sequence of nucleotides that encodes the modified adenovirus
XX fiber protein, a cell comprising the nucleic acid, an adenovirus particle
XX comprising the modified fiber, a composition formulated for
XX administration to a subject, comprising the adenovirus particle,
XX detargeting an adenoviral vector particle comprising producing the
XX adenoviral particle, where the binding of the particle to a native
XX receptor is reduced or eliminated as compared to binding of a particle
XX containing the unmodified fiber, introducing the adenoviral particle into
XX cells, introducing the cells into a subject and administering the
XX composition to the subject. The modified adenovirus fiber protein is
XX useful for treating cancer, vascular disease, diabetic retinopathy,
XX restenosis, ocular diseases, hyperproliferative disorders and hormonal
XX disorders. This sequence represents a DAV-1 antibody heavy chain used in
XX the scope of the invention.
XX
XX Sequence 456 AA;
XX
XX Query Match 79.2%; Score 600.5; DB 9; Length 456;
XX Best Local Similarity 82.0%; Pred. No. 4.1e-42;
XX Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;
XX
XX 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHWKQSH 60
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 1 MGWSWIFLLSCTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFDYNHWKQSH 60
XX
XX 61 GKLEWIGIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELSLTSDSAVYCARWDF 120
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 61 GKLEWIGIYPYNGVSDYNQNFKSKATLITDSSNTAYMELSLTSDSAVYCARWDF 120
```

Db 61 GKLEWIGYIPYKGGTGYNQKPKSKATLTDTSSNTAYMELSLTSDASAVYYCARG-- 118  
QY 121 GSGYFDYWGQGTTLTVSS 139  
Db 119 -----IAYWGQGTTLTVSA 132

RESULT 20  
AAE18379  
ID AAE18379 standard; protein; 493 AA.  
AC AAE18379;  
XX 07-MAY-2002 (first entry)  
DT XX  
DE Human N-terminal DAV-1 heavy chain-mature EGF fusion protein.  
XX Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;  
KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;  
KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;  
KW cytostatic; vasotropic; ophthalmological; epidermal growth factor; EGF;  
KW fusion protein.  
XX Homo sapiens.  
OS Synthetic.  
OS Chimeric.  
XX  
XX  
FH Key Location/Qualifiers  
FT Region 1..439  
FT /note= "N-terminal portion of DAV-1 heavy chain"  
FT Region 441..493  
FT /note= "Human mature EGF"  
XX  
XX WO200204522-A2.  
XX  
XX 17-JAN-2002.  
XX  
XX 09-JUL-2001; 2001WO-EP007878.  
XX  
XX 10-JUL-2000; 2000US-00613017.  
XX (NOVS ) NOVARTIS AG.  
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GRS MBH.  
XX (SCRI ) SCRIPPS RES INST.  
XX  
XX Nemerow GR, Li E;  
XX WPI; 2002-171707/22.  
XX  
XX New bifunctional molecules comprising an antibody or its antigen-binding  
PT portion, and a targeting agent, useful for e.g. gene therapy, or for  
PT promoting Adenoviral vector-mediated gene delivery to cells lacking av  
PT integrins.  
XX  
XX Claim 15; Page 101-102; 106pp; English.  
XX  
XX The present invention relates to a bifunctional molecule comprising an  
CC antibody or its antigen-binding portion, and a targeting agent where the  
CC antibody specifically binds to an antigen in a protein that binds to av  
CC integrin, and the targeting agent specifically binds to a cell surface  
CC protein that activates the phosphatidylinositol 3 (PI3K) signalling  
CC pathway. The bifunctional molecules are useful for gene therapy, for  
CC promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking  
CC av integrins, for enhancing Ad binding and internalisation, and in gene  
CC delivery of by fibreless adenovirus particles. The bifunctional molecules  
CC permit targeting of viral and bacterial vectors to cells that express  
CC targeted receptors. Diseases that can be targeted include cancers,  
CC vascular disorders, diabetic retinopathies, restenosis, ophthalmic  
CC disorders, hyperproliferative disorders, and hormonal disorders. The  
CC present sequence is human N-terminal DAV-1 heavy chain-mature epidermal  
CC growth factor (EGF) fusion protein which is used in the invention  
XX

SQ Sequence 493 AA;  
Query Match 79.2%; Score 600.5; DB 5; Length 493;  
Best Local Similarity 82.0%; Pred. No. 4.5e-42;  
Matches 114; Conservative 6; Mismatches 12; Indels 7; Gaps 1;  
QY 1 MGWSWIFLFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHMKQSH 60  
Db 1 MGWSWIFLFLLSGTAGVHSEVQLQSGPELVKPGASVKISKASGYTFTDYNHMKQSH 60  
QY 61 GKILEWIGYIYPYNGVSDYNNQNFKSKATLIVDNSSNTAYMELSLTSEDSAVYYCARWDF 120  
Db 61 GKLEWIGYIYPYKGGTGYNQKPKSKATLTDTSSNTAYMELSLTSDASAVYYCARG-- 118  
QY 121 GSGYFDYWGQGTTLTVSS 139  
Db 119 -----IAYWGQGTTLTVSA 132

Search completed: March 20, 2006, 07:35:44  
Job time : 54.3087 secs

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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:28:38 ; Search time 23.7968 Seconds  
(without alignments)  
3765.293 Million cell updates/sec

Title: US-10-687-035-33  
Perfect score: 656  
Sequence: 1 MDPQVQIFSLISASVMS.....YCOQWSSNPTFGSGTKLEI 127

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Uniprot\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	574	87.5	235	2	Q5XFY8_MOUSE
2	533	81.2	235	2	Q58EV6_MOUSE
3	526	80.2	134	2	Q8VDD0_MOUSE
4	511.5	78.0	131	2	Q811C3_MOUSE
5	473	72.1	237	2	Q569Y8_MOUSE
6	452	68.9	129	1	KV4A_MOUSE
7	434	66.2	112	2	Q8KIF3_MOUSE
8	429	65.4	107	1	KV6F_MOUSE
9	428	65.2	112	2	Q8KIF2_MOUSE
10	424	64.6	107	1	KV6I_MOUSE
11	423	64.5	107	1	KV6I_MOUSE
12	423	64.5	107	1	KV6J_MOUSE
13	422	64.3	112	2	Q8KIF0_MOUSE
14	421	64.2	106	2	Q9U410_MOUSE
15	420	64.0	107	1	KV6G_MOUSE
16	419.5	63.9	97	2	Q9JL76_MOUSE
17	409	62.3	108	1	KV6K_MOUSE
18	408	62.2	114	2	Q8KIF1_MOUSE
19	395	60.2	107	1	KV6B_MOUSE
20	392	59.8	107	1	KV6A_MOUSE
21	391	59.6	107	1	KV6D_MOUSE
22	390	59.5	107	1	KV6C_MOUSE
23	375	57.2	107	1	KV6E_MOUSE
24	350	53.4	109	2	Q9UL78_HUMAN
25	349	53.2	129	1	KV3M_HUMAN
26	348	53.0	129	1	KV3L_HUMAN
27	345.5	52.7	240	2	Q52L64_MOUSE
28	341.5	52.1	101	2	Q9JL78_MOUSE
29	341.5	52.1	236	2	Q7Z3Y4_HUMAN
30	338.5	51.6	237	2	Q7S236_XENLA
31	338	51.5	109	1	KV3B_HUMAN

ALIGNMENTS

32	335.5	51.1	236	2	Q6PIH7_HUMAN
33	334	50.9	108	1	KV3A_HUMAN
34	334	50.9	235	2	Q6GMV9_HUMAN
35	333.5	50.8	236	2	Q6PIL8_HUMAN
36	333	50.8	129	1	KV3H_HUMAN
37	332.5	50.7	111	1	KV3M_MOUSE
38	332	50.6	235	2	Q6RUF2_HUMAN
39	331.5	50.5	108	1	KV1V_HUMAN
40	331.5	50.5	108	2	Q9UL70_HUMAN
41	331	50.5	109	1	KV3D_HUMAN
42	331	50.5	109	2	Q9UL86_HUMAN
43	330	50.3	109	1	KV3G_HUMAN
44	329	50.2	109	1	KV3E_HUMAN
45	328.5	50.1	134	1	KV4C_HUMAN
46	327.5	49.9	131	1	KV3I_MOUSE
47	327	49.8	109	1	KV3F_HUMAN
48	326.5	49.8	128	1	KV3K_HUMAN
49	325.5	49.6	108	2	Q9UL79_HUMAN
50	325.5	49.6	111	1	KV3L_MOUSE
51	325.5	49.6	111	1	KV3O_MOUSE
52	325.5	49.6	236	2	Q6GMX9_HUMAN
53	325.5	49.6	236	2	Q6GMX8_HUMAN
54	325.5	49.6	244	2	Q65ZC8_HUMAN
55	325.5	49.6	255	2	Q6XB05_MOUSE
56	324.5	49.5	111	1	KV3Q_MOUSE
57	323.5	49.3	239	2	Q5HZC6_XENLA
58	322.5	49.2	243	2	Q6NTU5_XENLA
59	321.5	49.0	111	1	KV3N_MOUSE
60	321.5	49.0	238	2	Q58EU4_MOUSE
61	320.5	48.9	108	1	KV1O_HUMAN
62	320.5	48.9	109	2	Q920E6_MOUSE
63	320.5	48.9	111	1	KV3J_MOUSE
64	320.5	48.9	236	2	Q6P5S8_HUMAN
65	320.5	48.9	236	2	Q6P5S8_HUMAN
66	319.5	48.7	111	1	KV3H_MOUSE
67	318.5	48.6	108	2	Q9UL83_HUMAN
68	318.5	48.6	114	1	KV4A_HUMAN
69	318.5	48.6	234	2	Q7Z473_HUMAN
70	318.5	48.6	236	2	Q6PIT5_HUMAN
71	318.5	48.6	240	2	Q65ZC9_HUMAN
72	317.5	48.4	108	1	KV1R_HUMAN
73	317.5	48.4	129	1	KV1N_HUMAN
74	316.5	48.2	111	1	KV3K_MOUSE
75	316.5	48.2	132	1	KV3F_MOUSE
76	315.5	48.1	108	1	KV1L_HUMAN
77	315.5	48.1	108	1	KV1Y_HUMAN
78	315.5	48.1	136	1	KV5B_MOUSE
79	315.5	48.1	149	1	KV5A_MOUSE
80	315	48.0	110	1	KV3P_MOUSE
81	314.5	47.9	108	2	Q9UL77_HUMAN
82	314.5	47.9	111	2	Q920E9_MOUSE
83	314.5	47.9	189	2	Q569I7_HUMAN
84	313	47.7	109	2	Q9UL85_HUMAN
85	312.5	47.6	111	2	Q811U6_MOUSE
86	312	47.6	107	2	Q96A89_HUMAN
87	311.5	47.5	234	2	Q58FE6_HUMAN
88	310.5	47.3	111	1	KV3S_MOUSE
89	309.5	47.2	108	1	KV1E_HUMAN
90	309.5	47.2	108	1	KV1H_HUMAN
91	309.5	47.2	108	1	KV1M_HUMAN
92	309.5	47.2	236	2	Q502W4_HUMAN
93	308.5	47.0	108	1	KV5D_MOUSE
94	308.5	47.0	111	1	KV3R_MOUSE
95	307.5	46.9	236	2	Q7TS98_MOUSE
96	307.5	46.9	240	2	Q6PIH6_HUMAN
97	307	46.8	107	2	Q9UL81_HUMAN
98	306.5	46.7	111	1	KV3U_MOUSE
99	306.5	46.7	127	2	Q925S9_MOUSE
100	306.5	46.7	130	1	KV5G_MOUSE

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RESULT 1
Q5XFY8_MOUSE
ID ID Q5XFY8_MOUSE PRELIMINARY; PRT; 235 AA.
AC Q5XFY8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bobak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallation D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield A.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Director MGC Project;
RA Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC084663; AAB84663.1; -, mRNA.
DR SKR; Q5XFY8; 23-235.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPRO03599; IG.
DR InterPro; IPRO07110; IG-like.
DR InterPro; IPRO03597; IG CI.
DR InterPro; IPRO03006; IG MHC.
DR InterPro; IPRO03596; IG v.
DR Pfam; PF07654; CI-set; I.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 828E9ED277FDC667 CRC64;

Query Match 87.5%; Score 574; DB 2; Length 235;
Best Local Similarity 89.0%; Pred. No. 4.4e-47;
Matches 113; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQPAILFASPGETVTWTCRASSSVIYCNWQOK 60
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQPAILSGFFPGCKVTWTCRASSSVYNMHWYQOK 60
Qy 61 PGSSPKWIKYGTSLASGVPTFSGSGTGSYSITISRVEADAATYYCQOWSSNPFTFG 120
Db 61 PGSSPKWIKYATSKLASGVPARFSGSGSGTGSYSITISRVEADAATYYCQOWSSNPFTFG 120
Qy 121 SGTGLEI 127

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Db 61 SGTSPKRWIYDTSKLASGVPARFSGSGTYSYSLTSSMEAEADAATYYCQWTSNPLTFG 120
Qy 121 SGTKLEI 127
   :||||:
Db 121 AGTKLDL 127

RESULT 3
ID Q8VDDO MOUSE PRELIMINARY; PRT; 134 AA.
AC Q8VDDO;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Anti-MOG 212 variable light chain (Fragment).
GN Name=Gm1502; Synonyms=anti-MOG kappa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MRL/lpr/lpr; TISSUE=Spleen;
RX MEDLINE=93156722; PubMed=8429833; DOI=10.1016/0161-5890(93)90089-T;
RA Takahashi S., Itoh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;
RT "Cloning and cDNA sequence analysis of nephritogenic monoclonal
RT antibodies derived from an MRL/lpr lupus mouse.";
RL Mol. Immunol. 30:177-182(1993)
DR EMBL; D14625; BAA03482.1; -; mRNA.
DR HSP; P01679; 2FBJ.
DR SMR; Q811C3; 23-131.
DR Ensembl; ENSMUSG00000058987; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT SIGNAL. 1 22 Potential.
FT CHAIN 23 >131 immunoglobulin gamma-3 kappa chain.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14083 MW; 5E83656954666B9E CRC64;

Query Match 78.0%; Score 511.5; DB 2; Length 131;
Best Local Similarity 81.5%; Pred. No. 2.4e-41;
Matches 106; Conservative 7; Mismatches 14; Indels 3; Gaps 2;

Qy 1 MDPQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVWTTCRASSV--IYMCWNQ 58
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MDSQVQIFSFLLISALVIMSRGQIVLTQSPAINASPGKVTWTCRASSVRSYLHWYQ 60
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 59 QKPGSSPKWIYGTSTLASGVPTRFSGSGTYSYSLTISRVEAEADAATYYCQWSSNP-F 117
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 QKPGSSPKLWIYSTNLASGVPVRFSGSGTYSYSLTISRVEAEADAATYYCQYDSSPSI 120
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 118 TFGSGTKLEI 127
   :||||:
Db 121 TFGAGTKLEL 130

RESULT 5
ID Q569Y8 MOUSE PRELIMINARY; PRT; 237 AA.
AC Q569Y8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Igk-C protein.
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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Db 61 SGTSPKRWIYDTSKLASGVPARFSGSGTYSYSLTSSMEAEADAATYYCQWTSNPLTFG 120
Qy 121 SGTKLEI 127
   :||||:
Db 121 AGTKLDL 127

RESULT 3
ID Q8VDDO MOUSE PRELIMINARY; PRT; 134 AA.
AC Q8VDDO;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Anti-MOG 212 variable light chain (Fragment).
GN Name=Gm1502; Synonyms=anti-MOG kappa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RA Chernajovsky Y.;
RT Structural and functional implications of a restricted antibody
RT response to a defined antigenic region on the influenza virus
RT hemagglutinin.";
RL EMBO J. 5:1577-1587(1986).
DR EMBL; AJ416331; CAC94866.1; -; mRNA.
DR PIR; G27887; G27887.
DR HSP; P01834; 1M1M.
DR SMR; Q8VDDO; 23-134.
DR Ensembl; ENSMUSG00000062047; Mus musculus.
DR MGI; MGI:2686348; Gm1502.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14525 MW; CDF68E2236E2D0CF CRC64;

Query Match 80.28; Score 526; DB 2; Length 134;
Best Local Similarity 82.74; Pred. No. 1e-42;
Matches 105; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MDPQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVWTTCRASSVIVYMCWNOQ 60
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MDPQVQIFSFLLISASVILSRGQIVLTQSPAINASPGKVTWTCRASSSISTMHWYQK 60
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 61 PGSSPKWIYGTSTLASGVPTRFSGSGTYSYSLTISRVEAEADAATYYCQWSSNPFTFG 120
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 PGTSPKRWIYDTSKLASGVPARFSGSGTYSYSLTISRVEAEADAATYYCHQRSSYPWTFG 120
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 121 SGTKLEI 127
   :||||:
Db 121 GGTKLEI 127

RESULT 4
Q811C3 MOUSE
ID Q811C3 MOUSE PRELIMINARY; PRT; 131 AA.
AC Q811C3;

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[3] NUCLEOTIDE SEQUENCE.  
 MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;  
 Tillman D.M., Jou N.T., Hill R.J., Marion T.N.;  
 "Both IgM and IgG anti-DNA antibodies are the products of clonally  
 selective B cell stimulation in (NZB x NZW)F1 mice.";  
 J. Exp. Med. 176:761-779(1992).  
 EMBL; AF516282; AAM64200.1; -; Genomic\_DNA.  
 DR PIR; A33933; A33933.  
 DR PIR; PH1085; PH1085.  
 DR HSSP; P01837; 25C8.  
 DR SMR; O8K1P2; 2-112.  
 DR Ensembl; ENSMUSG0000063156; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR NON\_TER 1  
 DR NON\_TER 112  
 DR NON\_TER 112  
 SQ SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;  
 Query Match 66.2%; Score 434; DB 2; Length 112;  
 Best Local Similarity 80.8%; Pred. No. 6e-34;  
 Matches 84; Conservative 7; Mismatches 13; Indels 0; Gaps 0;  
 QY 24 IVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWYGTSTLASGVPTRF 83  
 Db 2 IVLTQSPAIMSASPGKVTITCSASSSVYMYWYQKPGSSPKPWYRTSNLASGVPARF 61  
 QY 84 SGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFGSGTKLEI 127  
 Db 62 SGSGSGTSYSLTISRMEADAATYCCQVHSYPYTFGGTKLEI 105  
 RESULT 8  
 KV6F MOUSE STANDARD; PRT; 107 AA.  
 ID KV6F MOUSE  
 AC P04940;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ig kappa chain V-J region NQ2-17.4.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=83271467; PubMed=6877353;  
 Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;  
 "mRNA sequences define an unusually restricted IgG response to 2-  
 phenylloxazalone and its early diversification.";  
 Nature 304:320-324(1983).  
 CC -!- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
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 removed.  
 CC EMBL; K00735; AAA38680.1; -; mRNA.  
 DR HSSP; P01679; 2FBJ.  
 DR SMR; P04940; 1-107.  
 DR Ensembl; ENSMUSG0000062047; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; IGV.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Hybridoma; Immunoglobulin domain; Immunoglobulin V region.  
 KW Framework-1.  
 FT REGION 24 33  
 Complementarity-determining-1.

FT REGION 34 48 Framework-2.  
 FT REGION 49 55 Complementarity-determining-2.  
 FT REGION 56 87 Framework-3.  
 FT REGION 88 96 Complementarity-determining-3.  
 FT REGION 97 106 Framework-4.  
 FT DISULFID 23 87 By similarity.  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA; 11561 MW; 6F694284CEFA68B6 CRC64;  
 Query Match 65.4%; Score 429; DB 1; Length 107;  
 Best Local Similarity 78.1%; Pred. No. 1.7e-33;  
 Matches 82; Conservative 9; Mismatches 14; Indels 0; Gaps 0;  
 QY 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWYGTSTLASGVPTRF 82  
 Db 1 QIVLTQSPAIMSASPGKVTITCSASSSVYMYWYQKPGSSPKPWYGTSTLASGVPAR 60  
 QY 83 FGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFGSGTKLEI 127  
 Db 61 FGSGSGTSYSLTISRMEADAATYCCQWSSNPFTFGAGTKLEI 105

RESULT 9  
 Q8K1F2 MOUSE PRELIMINARY; PRT; 112 AA.  
 ID Q8K1F2 MOUSE  
 AC Q8K1P2;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Anti-VIPase light chain variable region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BALE/c; TISSUE=Hyperimmunized spleen;  
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=2499887;  
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;  
 RT "Two murine natural polyreactive autoantibodies are encoded by  
 nonmutated germ-line genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).  
 DR EMBL; AF516283; AAM64201.1; -; Genomic\_DNA.  
 DR PIR; H33932; H33932.  
 DR HSSP; P01837; 25C8.  
 DR SMR; O8K1P2; 2-112.  
 DR Ensembl; ENSMUSG0000064150; Mus musculus.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; IGV.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR NON\_TER 1  
 DR NON\_TER 112  
 DR NON\_TER 112  
 SQ SEQUENCE 112 AA; 11953 MW; 4716B87FADB543ED CRC64;

Query Match 65.2%; Score 428; DB 2; Length 112;  
 Best Local Similarity 80.8%; Pred. No. 2.3e-33;  
 Matches 84; Conservative 7; Mismatches 13; Indels 0; Gaps 0;  
 QY 24 IVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWYGTSTLASGVPTRF 83  
 Db 2 IVLTQSPAIMSASPGKVTITCSASSSVYMYWYQKPGSSPKPWYGTSTLASGVPAR 61  
 QY 84 SGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFGSGTKLEI 127  
 Db 62 SGSGSGTSYSLTISRMEADAATYCCQWSSNPFTFGAGTKLEI 105

Mon Mar 20 08:49:45 2006

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RESULT 10
KV6I_MOUSE
ID KV6I_MOUSE STANDARD; PRT; 107 AA.
AC P04943;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NQ6-8.3.1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
phenyloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC
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removed.
CC
CC EMBL; K00739; AAA38684.1; -; mRNA.
DR HSSP; P01679; 2FBJ.
DR SMR; P04943; 1-107.
DR Ensembl; ENSMUSG00000062047; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 33 Complementarity-determining-1.
FT REGION 34 48 Framework-2.
FT REGION 49 55 Complementarity-determining-2.
FT REGION 56 87 Framework-3.
FT REGION 88 96 Complementarity-determining-3.
FT REGION 97 106 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 107 107
FT SEQUENCE 107 AA; 11573 MW; 6F694824ECF0C8E6 CRC64;
Query Match 64.6%; Score 424; DB 1; Length 107;
Best Local Similarity 77.1%; Pred. No. 5.2e-33;
Matches 81; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

OY 23 QIVLSQSPAILPASPGTWTTCRASSSVIYMCNQKPGSSPKPWYGTSTLASGVPT 82
DB 1 QIVLTQSPAIMASPGQKVTWTCSSASSVSYMHYQKSGTSPKRWYDTSKLSGXPAR 60
OY 83 FSGSGSGTSYSLTISRVEAEDAATYCCQWSSNPFPGSGTKLEI 127
DB 61 FSGSGSATSYSLTITSMQAEADAATYCCQWSSNPLTFGAGTKLEL 105

RESULT 11
KV6H_MOUSE
ID KV6H_MOUSE STANDARD; PRT; 107 AA.
AC P04942;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NQ5-6.1.2.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
phenyloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC
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removed.
CC
CC EMBL; K00740; AAA38685.1; -; mRNA.
DR HSSP; P01679; 2FBJ.
DR SMR; P04943; 1-107.
DR Ensembl; ENSMUSG00000062047; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 33 Complementarity-determining-1.
FT REGION 34 48 Framework-2.
FT REGION 49 55 Complementarity-determining-2.
FT REGION 56 87 Framework-3.
FT REGION 88 96 Complementarity-determining-3.
FT REGION 97 106 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 107 107
FT SEQUENCE 107 AA; 11573 MW; 6F694824ECF0C8E6 CRC64;
Query Match 64.6%; Score 424; DB 1; Length 107;
Best Local Similarity 77.1%; Pred. No. 5.2e-33;
Matches 81; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

OY 23 QIVLSQSPAILPASPGTWTTCRASSSVIYMCNQKPGSSPKPWYGTSTLASGVPT 82
DB 1 QIVLTQSPAIMASPGQKVTWTCSSASSVSYMHYQKSGTSPKRWYDTSKLSGXPAR 60
OY 83 FSGSGSGTSYSLTISRVEAEDAATYCCQWSSNPFPGSGTKLEI 127
DB 61 FSGSGSATSYSLTITSMQAEADAATYCCQWSSNPLTFGAGTKLEL 105

RESULT 12
KV6J_MOUSE
ID KV6J_MOUSE STANDARD; PRT; 107 AA.
AC P04944;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NQ5-78.2.6.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
phenyloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC
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removed.
CC
CC EMBL; K00739; AAA38684.1; -; mRNA.
DR HSSP; P01679; 2FBJ.
DR SMR; P04942; 1-107.
DR Ensembl; ENSMUSG00000062047; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 33 Complementarity-determining-1.
FT REGION 34 48 Framework-2.
FT REGION 49 55 Complementarity-determining-2.
FT REGION 56 87 Framework-3.
FT REGION 88 96 Complementarity-determining-3.
FT REGION 97 106 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 107 107
FT SEQUENCE 107 AA; 11605 MW; CA6C4284ECFCB550 CRC64;
Query Match 64.5%; Score 423; DB 1; Length 107;
Best Local Similarity 77.1%; Pred. No. 6.5e-33;
Matches 81; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

OY 23 QIVLSQSPAILPASPGTWTTCRASSSVIYMCNQKPGSSPKPWYGTSTLASGVPT 82
DB 1 QIVLTQSPAIMASPGQKVTWTCSSASSVSYMHYQKSGTSPKRWYDTSKLSGXPAR 60
OY 83 FSGSGSGTSYSLTISRVEAEDAATYCCQWSSNPFPGSGTKLEI 127
DB 61 FSGSGSATSYSLTITSMQAEADAATYCCQWSSNPLTFGAGTKLEL 105

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
RL phenylloxazalone and its early diversification.";
CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.
CC
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CC removed.
CC -----
CC EMBL; K00737; AAA38682.1; -; mRNA.
DR HSSP; Q91W12; IAY1.
DR SMR; P04941; 1-103.
DR Ensembl; ENSMUSG00000062047; Mus musculus.
DR InterPro; IPR003596; Iq-like.
DR InterPro; IPR003596; Iq_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; Iq Like; 1.
DR Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
KW REGION 1 23
FT REGION 24 33
FT REGION 34 48
FT REGION 49 55
FT REGION 56 87
FT REGION 88 96
FT REGION 97 106
FT DISULFID 23 87
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11557 MW; 72488DA9EF354934 CRC64;
Query Match 64.0%; Score 420; DB 1; Length 107;
Best Local Similarity 76.2%; Pred. No. 1.3e-32;
Matches 80; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
Qy 23 QIVLSQSPALFASPGETVTTCRASSSVIYMCNQKPGSSPKPWIYGTSTLASGVPT 82
Db 1 QILLTQSPAINMSFGQKVTTCRASSSVSYMHYQQKSGTSPKRWIYDTSKLASGV 60
Qy 83 FSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127
Db 61 FSGSGSATSYSLTITSMQAEADAATYYCQWSSNPFTFGAGTKLXL 105
RESULT 16
Q9JL76_MOUSE PRELIMINARY; PRT; 97 AA.
AC Q9JL76_MOUSE
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=DBA/2;
RX MEDLINE=20448942; PubMed=10992488;
RX DOI=10.1128/TAI.68.10.5803-5808.2000;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
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RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206030; AAF69328.1; -; mRNA.
DR HSSP; P01679; 2FBJ.
DR SMR; Q9JL76; 1-97.
DR Ensembl; ENSMUSG00000057015; Mus musculus.
DR InterPro; IPR007110; Iq-like.
DR InterPro; IPR003596; Iq_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; Iq Like; 1.
DR NON_TER 1 1
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10542 MW; C9EE1FFELF49DA1C CRC64;
Query Match 63.9%; Score 419.5; DB 2; Length 97;
Best Local Similarity 86.5%; Pred. No. 1.3e-32;
Matches 83; Conservative 1; Mismatches 11; Indels 1; Gaps 1;
Qy 33 LFASPGETVTTCRASSSVIYMCNQKPGSSPKPWIYGTSTLASGVPTFRFSGSGTSY 92
Db 1 LSASPGKVTTCRASSSVSYMHYQQKPGSSPKPWIYATSNLASGVPTFRFSGSGTSY 60
Qy 93 SLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127
Db 61 SLTISRVEADAATYYCQWSSKVTMTFGGTKLEI 96
RESULT 17
KV6K_MOUSE STANDARD; PRT; 108 AA.
AC KV6K_MOUSE
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-MAY-2005 (Rel. 47, Last annotation update)
DE Iq kappa chain V-VI region NQ2-6.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
RL phenylloxazalone and its early diversification.";
CC -----
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CC removed.
CC -----
CC EMBL; K00746; AAA38691.1; -; mRNA.
DR HSSP; Q91W12; IAY1.
DR SMR; P04945; 1-108.
DR Ensembl; ENSMUSG00000062686; Mus musculus.
DR InterPro; IPR007110; Iq-like.
DR InterPro; IPR003596; Iq_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; Iq Like; 1.
DR Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
KW REGION 1 23
FT REGION 24 33
FT REGION 34 48
FT REGION 49 55
FT REGION 56 87
FT REGION 88 98
FT REGION 99 108
FT DISULFID 23 87
FT NON_TER 108 108
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SQ SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;
Query Match 62.3%; Score 409; DB 1; Length 108;
Best Local Similarity 75.7%; Pred. No. 1.5e-31;
Matches 81; Conservative 10; Mismatches 14; Indels 2; Gaps 1;

QY 23 QIVLSQSPAILFASPGETVTMTTCRASSSVIYMCWNQKPGSSPKPMIYGTSTLASGVPT 82
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QILLTQSPAIMSAPGKVTMTCSASSSVSYMYWYQKPGSPRLLIYDTSNLSASGVPR 60

QY 83 FSGSGSGTSYSLTISRVEADAATYYCQWSSNP--FTFGSGTKLEI 127
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FSGSGSATSYSLTITRQAEADAATYYCQWSSYPPMLTFGAGTKLEI 107

RESULT 18
Q8K1F1_MOUSE
ID Q8K1F1_MOUSE PRELIMINARY; PRT; 114 AA.
AC Q8K1F1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed2499887;
RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT "Two murine natural polyreactive autoantibodies are encoded by
RT nonmutated germ-line genes.";
RN Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).
[3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
RA Tillman D.M., Jou N.T., Hill R.J., Marion T.N.;
RT "Both IgM and IgG anti-DNA antibodies are the products of clonally
RT selective B cell stimulation in (NZB x NZW)F1 mice.";
RL J. Exp. Med. 176:761-779 (1992).
DR EMBL; AF516284; AAM64202.1; -; Genomic_DNA.
DR PIR; A33933; A33933.
DR PIR; PH1058; PH1058.
DR HSSP; P01837; 25C8.
DR SMR; Q8K1F1; 2-114.
DR Ensembl; ENSMUSG0000059896; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12163 MW; 8BD9833DBF3EEFD1 CRC64;

Query Match 62.2%; Score 408; DB 2; Length 114;
Best Local Similarity 78.3%; Pred. No. 1.9e-31;
Matches 83; Conservative 6; Mismatches 15; Indels 2; Gaps 1;

QY 24 IVLSQSPAILFASPGETVTMTTCRASSSV--IYMCWNQKPGSSPKPMIYGTSTLASGVPT 81
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 IVLTQSPAIMSAPGKVTMTTCRASSSVSSYLHWYQKPGSPKLMYIYSTNLSASGVA 61

QY 82 FSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 FSGSGSGTSYSLTISMEADAATYYCQWYHSYPRFTFGGTKLEI 107

RESULT 19
KV6B_MOUSE
ID KV6B_MOUSE STANDARD; PRT; 107 AA.
AC P01676;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region XRPC 24.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP PROTEIN SEQUENCE.
RX MEDLINE=79082830; PubMed=1035573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
RT proteins.";
RL Biochemistry 17:5555-5559 (1978).
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC bind galactan.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC HSSP; P01679; 2FBJ.
DR SMR; P01676; 1-107.
DR Ensembl; ENSMUSG0000062047; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 33
FT REGION 34 48
FT REGION 49 55
FT REGION 56 87
FT REGION 88 96
FT REGION 97 106
FT REGION 107 107
FT DISULFID 23 87
FT NON_TER 107
SQ SEQUENCE 107 AA; 11584 MW; 36E6D022A5EC34D7 CRC64;

Query Match 60.2%; Score 395; DB 1; Length 107;
Best Local Similarity 75.2%; Pred. No. 3.2e-30;
Matches 79; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 23 QIVLSQSPAILFASPGETVTMTTCRASSSVIYMCWNQKPGSSPKPMIYGTSTLASGVPT 82
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EIVLTQSPAITAASLGQKVTITCSASSSVSYNHWYQKSGTSPKPMIYEISKLASGVPR 60

QY 83 FSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FSGSGSGTSYSLTISMEADAATYYCQWNYPLITFGSGTKLEI 105

RESULT 20
KV6A_MOUSE
ID KV6A_MOUSE STANDARD; PRT; 107 AA.
AC P01675;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region XRPC 44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP PROTEIN SEQUENCE.
RX MEDLINE=79082830; PubMed=1035573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
RT proteins.";
RL Biochemistry 17:5555-5559 (1978).
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC bind galactan.
CC
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CC removed.
CC
CC HSSP; P01679; 2FBJ.
DR SMR; P01676; 1-107.
DR Ensembl; ENSMUSG0000062047; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 33
FT REGION 34 48
FT REGION 49 55
FT REGION 56 87
FT REGION 88 96
FT REGION 97 106
FT REGION 107 107
FT DISULFID 23 87
FT NON_TER 107
SQ SEQUENCE 107 AA; 11584 MW; 36E6D022A5EC34D7 CRC64;

Query Match 60.2%; Score 395; DB 1; Length 107;
Best Local Similarity 75.2%; Pred. No. 3.2e-30;
Matches 79; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 23 QIVLSQSPAILFASPGETVTMTTCRASSSVIYMCWNQKPGSSPKPMIYGTSTLASGVPT 82
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EIVLTQSPAITAASLGQKVTITCSASSSVSYNHWYQKSGTSPKPMIYEISKLASGVPR 60

QY 83 FSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 FSGSGSGTSYSLTISMEADAATYYCQWNYPLITFGSGTKLEI 105
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OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=79082830; PubMed=103573;  
RA Rao D.N., Rudikoff S., Potter M.;  
RT "k Chain variable regions from three galactan binding myeloma  
RL proteins.";  
RL Biochemistry 17:5555-5559 (1978) .  
RN [2]  
RP PROTEIN SEQUENCE.  
RX PubMed=6776525;  
RA Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;  
RT "Kappa Chain joining segments and structural diversity of antibody  
RT combining sites.";  
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274 (1980) .  
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein that  
CC bind galactan.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR PIR; A90420; KVMX4.  
DR HSSP; P01679; 2FBJ.  
DR SNR; P01675; 1-107.  
DR Ensembl; ENSMUSG00000062047; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
DR Direct protein sequencing; Immunoglobulin domain;  
KW Immunoglobulin V region.  
FT REGION 1 23 Framework-1.  
FT REGION 24 33 Complementarity-determining-1.  
FT REGION 34 48 Framework-2.  
FT REGION 49 55 Complementarity-determining-2.  
FT REGION 56 87 Framework-3.  
FT REGION 88 96 Complementarity-determining-3.  
FT REGION 97 106 Framework-4.  
FT DISULFID 23 87 By similarity.  
FT CONFLICT 95 95 W -> I (in Ref. 2).  
FT NON TER 107 107  
SQ SEQUENCE 107 AA; 11627 MW; 27A2D022BC0A34D7 CRC64;  
  
Query Match 59.8%; Score 392; DB 1; Length 107;  
Best Local Similarity 74.3%; Pred. No. 6.3e-30;  
Matches 78; Conservative 8; Mismatches 19; Indels 0; Gaps 0;  
  
Qy 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYWCNQKPGSSPKPWIYGTSTLASGVPT 82  
Db 1 EIVLTQSPAITAASLGKVTITCSASSSVYWHYQQKSGTSPKPIYIEISKLASGVPT 60  
  
Qy 83 FSGSGSGTSYSLTISRVEAEADAATYCCQWSSNPFTFGSGTKLEI 127  
Db 61 FSGSGSGTSYSLTISSEAEADAATYCCQWNYPLWTFGGTKLEI 105  
  
Search completed: March 20, 2006, 07:32:04  
Job time : 25.7968 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:29:34 ; Search time 4.63412 Seconds  
(without alignments)  
2636.859 Million cell updates/sec

Title: US-10-687-035-33

Perfect score: 656

Sequence: 1 MDPQVQIFPLLSASVMS.....YCOQWSSNPFTFGSGTKLEI 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR\_80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	536	81.7	130	1 JL0079	Ig kappa chain pre
2	533	81.2	130	2 A32513	Ig kappa chain pre
3	532	81.1	235	2 S25058	Ig kappa chain - m
4	518	79.0	130	2 S04573	Ig kappa chain pre
5	515	78.5	140	2 PL0013	Ig kappa chain pre
6	501	76.4	130	2 B32456	Ig kappa chain pre
7	469	71.5	107	2 A42848	Ig light chain v r
8	462	70.4	106	2 PL0082	Ig kappa chain v r
9	458	69.8	132	2 S05268	Ig kappa chain pre
10	452	68.9	107	2 B30562	Ig kappa chain v r
11	452	68.9	129	1 KVMS7B	Ig kappa chain pre
12	448	68.3	107	2 A30562	Ig kappa chain v r
13	440.5	67.1	108	2 G30560	Ig kappa chain v r
14	438	66.8	104	2 B49049	Ig kappa chain v r
15	437	66.6	103	2 S29591	Ig kappa chain v r
16	437	66.6	107	2 PC4405	Ig kappa chain v r
17	435.5	66.4	108	2 S38720	Ig light chain v r
18	435	66.3	106	2 PS0071	Ig kappa chain v r
19	432	65.9	105	2 S26338	Ig kappa chain v r
20	429	65.4	107	2 PT0406	Ig kappa chain v r
21	425	64.8	106	2 B54378	Ig light chain v r
22	424	64.6	107	2 S11118	Ig kappa chain v r
23	423	64.5	100	2 S29590	Ig kappa chain v r
24	422	64.3	113	2 S03410	Ig kappa chain pre
25	420	64.0	97	2 S26341	Ig light chain v r
26	420	64.0	107	2 S11119	Ig kappa chain v r
27	416	63.4	106	2 G27887	Ig kappa chain v r
28	415	63.3	107	2 PD0011	Ig kappa chain v r
29	412	62.8	107	2 S11121	Ig kappa chain v r

30	411	62.7	123	2	S05269	Ig kappa chain pre
31	410	62.5	97	2	PH1084	Ig light chain v r
32	408	62.2	108	2	S29581	Ig kappa chain v r
33	407	62.0	106	2	PS0070	Ig kappa chain v r
34	405	61.7	107	2	S11117	Ig kappa chain v r
35	404	61.6	108	2	PL0278	Ig kappa chain v r
36	402	61.3	124	2	S05267	Ig kappa chain pre
37	401	61.1	107	2	S11112	Ig kappa chain v r
38	400	61.0	99	2	S29585	Ig kappa chain v r
39	400	61.0	104	2	JC6076	anti-D-dimer monoc
40	400	61.0	108	2	PL0277	Ig kappa chain v r
41	400	61.0	108	2	PL0276	Ig kappa chain v r
42	399	60.8	109	2	PT0405	Ig light chain v r
43	398	60.7	97	2	PH1085	Ig light chain v r
44	397	60.5	107	2	S11113	Ig kappa chain v r
45	393	59.9	95	2	D33730	Ig kappa chain v r
46	392	59.8	107	1	KVMSX4	Ig kappa chain v r
47	390	59.5	107	2	S11122	Ig kappa chain v r
48	388	59.1	104	2	S29592	Ig kappa chain v r
49	387	59.0	109	2	PT0404	Ig light chain v r
50	386	58.8	102	2	S29584	Ig kappa chain v r
51	385	58.7	94	2	S26340	Ig light chain v r
52	384	58.5	108	2	PS0069	Ig kappa chain v r
53	383	58.4	91	2	S17629	Ig kappa chain v r
54	382	58.2	106	2	S11120	Ig kappa chain v r
55	381	58.1	99	2	D38601	Ig kappa chain v r
56	381	58.1	104	2	S26475	Ig kappa chain v r
57	379	57.8	91	2	S17637	Ig kappa chain v r
58	379	57.8	268	2	A56446	Ig heavy chain v r
59	378.5	57.7	106	2	S11114	Ig kappa chain v r
60	377.5	57.5	98	2	PH1061	Ig light chain v r
61	377	57.5	90	2	S26339	Ig kappa chain v r
62	376	57.3	120	2	A34871	Ig kappa chain v r
63	375	57.2	107	1	KVMSJ5	Ig kappa chain v r
64	374	57.0	91	2	S17626	Ig kappa chain v r
65	374	57.0	107	2	PT0401	Ig light chain v r
66	373	56.9	120	2	S66536	Ig light chain v r
67	372	56.7	91	2	S17639	Ig kappa chain v r
68	371	56.6	96	2	C33730	Ig kappa chain v r
69	370	56.4	107	2	S11123	Ig kappa chain v r
70	370	56.4	107	2	PT0398	Ig light chain v r
71	369	56.2	99	2	PH1059	Ig light chain v r
72	368	56.1	108	2	S11125	Ig kappa chain v r
73	367	55.9	91	2	S17627	Ig kappa chain v r
74	367	55.9	91	2	S17630	Ig kappa chain v r
75	366	55.8	98	2	S26342	Ig kappa chain v r
76	366	55.8	99	2	PH1058	Ig light chain v r
77	366	55.8	107	2	PT0402	Ig light chain v r
78	365	55.6	107	2	PT0403	Ig light chain v r
79	364	55.5	109	2	S13699	Ig kappa chain v r
80	363	55.3	91	2	S17638	Ig kappa chain v r
81	362	55.2	107	2	PT0395	Ig light chain v r
82	360	54.9	93	2	S17641	Ig kappa chain v r
83	359.5	54.8	102	2	S11115	Ig kappa chain v r
84	359	54.7	91	2	S17628	Ig kappa chain v r
85	359	54.7	93	2	S17623	Ig kappa chain v r
86	358	54.6	93	2	S17642	Ig kappa chain v r
87	358	54.6	93	2	S17640	Ig kappa chain v r
88	358	54.6	106	2	S29583	Ig kappa chain v r
89	357.5	54.5	145	2	PL0014	Ig kappa chain pre
90	357	54.4	107	2	S11116	Ig kappa chain v r
91	357	54.4	107	2	PT0397	Ig light chain v r
92	356	54.3	107	2	PT0400	Ig light chain v r
93	354	54.0	99	2	PH1060	Ig light chain v r
94	354	54.0	109	2	H30601	Ig kappa chain v r
95	354	54.0	129	2	S46369	Ig light chain var
96	354	54.0	134	2	S38643	Ig kappa chain v r
97	352	53.7	102	2	S29582	Ig kappa chain v r
98	352	53.7	106	2	PS0072	Ig kappa chain v r
99	352	53.7	108	2	C30608	Ig kappa chain v r
100	352	53.7	109	2	A30608	Ig kappa chain v r

## ALIGNMENTS

## RESULT 1

IG kappa chain precursor V region (anti-phenylloxazalone 6F6) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Dec-1991 #sequence\_revision 09-Aug-1996 #text\_change 16-Jul-1999  
C:Accession: J00079; A49044; B49044  
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.  
Mol. Immunol. 25, 859-865, 1988  
A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reacting V regions  
A:Reference number: J00076; MUID:89096973; PMID:3211160  
A:Accession: J00079  
A:Molecule type: mRNA  
A:Residues: 1-130 <KAA>  
A:Cross-references: UNIPARC:UPI000017371P; GB:M27792; NID:g197159  
A:Experimental source: mRNA clones for anti-phenylloxazalone antibody 6F6  
A>Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10 as Leu  
A>Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation  
R:Milstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.  
Eur. J. Immunol. 22, 1627-1634, 1992  
A:Title: Non-random features of the repertoire expressed by the members of one V kappa gene  
A:Reference number: A49044; MUID:92289826; PMID:1601044  
A:Accession: A49044  
A:Molecule type: DNA  
A:Residues: 1-25 <MIL>  
A:Cross-references: UNIPARC:UPI000011760C; GB:837663; NID:g250214; PIDN:AAB22331.1; PIDN:AAB22332.1; PIDN:AAB22333.1  
A:Experimental source: BALB/c germ-line  
A>Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 additional sequences extracted from NCBI backbone (NCBI:106807, NCBIP:106822)  
C:Genetics:  
A:Gene: V(kappa)Ox1  
A:Introns: 17/1  
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) and two heavy (lambda) chains. In some cases, such as IGA and IGM, the subunits associate into 1A and 1B disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1A and 1B disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1A and 1B disulfide bonds.  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-130/Product: IG kappa chain V region (6F6) #status predicted <VAT>  
F:38-111/Domain: immunoglobulin homology <IMW>  
F:45-109/Disulfide bonds: #status predicted

Query Match 81.7%; Score 536; DB 1; Length 130;  
Best Local Similarity 84.1%; Pred. No. 3.8e-37; Mismatches 6; Indels 0; Gaps 0;  
Matches 106; Conservative 6; Mismatches 14; Indels 0; Gaps 0;  
Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVYIMCNQOK 60  
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVYIMCNQOK 60  
Qy 61 PGSSPKPMWYGTSTLAGVPTFRFGSGSGTSTISRVAEADAATYYCQWSSNPFTFG 120  
Db 61 SGTSPKRWYDTSKLASGVPRFSGSGTSTISRVAEADAATYYCQWSSNPFTFG 120  
Qy 121 SGTKLEI 126  
Db 121 AGTKLEI 126

## RESULT 2

A32513  
IG kappa chain precursor V region (MRL22) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000  
C:Accession: A32513  
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; J. Clin. Invest. 92, 852-860, 1998

A:Title: Immunoglobulin kappa light chain variable region gene complex organization and  
A:Reference number: A94689; MUID:88331394; PMID:3138286  
A:Accession: A32513  
A:Molecule type: DNA  
A:Residues: 1-130 <KOF>  
A:Cross-references: UNIPARC:UPI000011499C; GB:M20834; NID:g196943; PIDN:AAA38846.1; PIDN:AAA38847.1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:38-113/Domain: immunoglobulin homology <IMW>

Query Match 81.2%; Score 533; DB 2; Length 130;  
Best Local Similarity 83.7%; Pred. No. 6.7e-37; Mismatches 6; Indels 2; Gaps 1;  
Matches 108; Conservative 6; Mismatches 13; Indels 2; Gaps 1;  
Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSV--IYMCWNQ 58  
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVSSSYLYWYQ 60  
Qy 59 QKPGSPKPMWYGTSTLAGVPTFRFGSGSGTSTISRVAEADAATYYCQWSSNPFT 118  
Db 61 QKPGSPKPMWYGTSTLAGVPTFRFGSGSGTSTISRVAEADAATYYCQWSSNPFT 120  
Qy 119 FGSGTKLEI 127  
Db 121 FGSGTKLEI 129

## RESULT 3

S25058  
IG kappa chain - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Jan-2000  
C:Accession: S25058  
R:Fischer, R.; Voos, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
submitted to the EMBL Data Library, July 1992  
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m  
A:Reference number: S25057  
A:Accession: S25058  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-235 <FIS>  
A:Cross-references: UNIPARC:UPI0000116096; EMBL:X67211; NID:g54828; PIDN:CAA47650.1; PIDN:CAA47651.1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:38-111/Domain: immunoglobulin homology <IMW>

Query Match 81.1%; Score 532; DB 2; Length 235;  
Best Local Similarity 83.5%; Pred. No. 1.4e-36; Mismatches 14; Indels 0; Gaps 0;  
Matches 106; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVYIMCNQOK 60  
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVYIMCNQOK 60  
Qy 61 PGSSPKPMWYGTSTLAGVPTFRFGSGSGTSTISRVAEADAATYYCQWSSNPFTFG 120  
Db 61 SGTSPKRWYDTSKLASGVPRFSGSGTSTISRVAEADAATYYCQWSSNPFTFG 120  
Qy 121 SGTKLEI 127  
Db 121 AGTKLEI 127

## RESULT 4

S04573  
IG kappa chain precursor V region (MRL-histone 7L) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 21-Jan-2000  
C:Accession: S04573  
R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th  
Eur. J. Immunol. 17, 91-95, 1987  
A:Title: Molecular analysis of the murine lupus-associated anti-self response: involveme  
A:Reference number: S04573; MUID:87133856; PMID:3102255  
A:Accession: S04573

A:Molecule type: mRNA  
A:Residues: 1-130 <KOF>  
A:CROSS-references: UNIPARC:UPI0000115DFE; EMBL:X14620; NID:G52031; PIDN:CAA32773.1; PII  
A>Note: the authors translated the codon AGC for residue 47 as Asn  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-130/Product: Ig kappa chain V region (fragment) #status predicted <MAT>  
F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 518; DB 2; Length 130;  
Best Local Similarity 80.6%; Pred. No. 1.1e-35;  
Matches 104; Conservative 10; Mismatches 13; Indels 2; Gaps 1;

QY 1 MDPQVQIFSLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVI--YMCWNQ 58  
DB 1 MDPQVQIFSLISASVIMTRGQIVLTQSPAINASPGKVTMTCRASSSVSSKYLNNYQ 60

QY 59 QKPGSPKPMIYGTSTLASGVPTRFSGSGSGTYSYLTISRVEAEDAATYYCQWSSNPFT 118  
DB 61 QRSQSPKLMYIYGTSTLASGVPTRFSGSGSGTYSYLTISRVEAEDAATYYCQYHSDPLT 120

QY 119 FGSSTKLEI 127  
DB 121 FGAGTKLEI 129

RESULT 5  
PL0013  
Ig kappa chain precursor V region (4C11) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jan-2000  
C:Accession: PL0013  
R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.  
Mol. Immunol. 25, 33-40, 1988  
A:Title: Structural basis of stimulatory anti-idiotypic antibodies.  
A:Reference number: PL0011; MUID:88142863; PMID:3125424  
A:Molecule type: mRNA  
A:Residues: 1-140 <CHE>  
A:CROSS-references: UNIPARC:UPI00001767A6  
A:Experimental source: cell line 4C11  
C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylch  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>  
F:38-111/Domain: immunoglobulin homology <IMM>  
F:46-55/Region: complementarity-determining 1  
F:71-77/Region: complementarity-determining 2  
F:110-118/Region: complementarity-determining 3  
F:130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 78.5%; Score 515; DB 2; Length 140;  
Best Local Similarity 82.7%; Pred. No. 2.1e-35;  
Matches 105; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 MDPQVQIFSLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQ 60  
DB 1 MDPQVQIFSLISASVIMSRGQIVLTQSPAINASPGKVTMTCRASSSVIYHWFQOK 60

QY 61 PGSSPKPMIYGTSTLASGVPTRFSGSGSGTYSYLTISRVEAEDAATYYCQWSSNPFTFG 120  
DB 61 PDSPKLMYIYGTSTLASGVPTRFSGSGSGTYSYLTISRVEAEDAATYYCQYHSDPLT 120

QY 121 SGTKLEI 127  
DB 121 GGTKLEI 127

RESULT 6  
B32456  
Ig kappa chain precursor V region - mouse

C:Species: Mus musculus (house mouse)  
C>Date: 26-Oct-1989 #sequence\_revision 26-Oct-1989 #text\_change 21-Jan-2000  
C:Accession: B32456  
R:Dombink-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.W.  
J. Biol. Chem. 264, 4513-4522, 1989  
A:Title: Variable region primary structures of a high affinity anti-fluorescein immunogl  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 501; DB 2; Length 130;  
Best Local Similarity 78.3%; Pred. No. 2.8e-34;  
Matches 101; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

QY 1 MDPQVQIFSLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSV--IYMCWNQ 58  
DB 1 MDPQVQIFSLISASVIMSRGQIVLTQSPAINASPGKVTMTCRASSSVSSYLHWYQ 60

QY 59 QKPGSPKPMIYGTSTLASGVPTRFSGSGSGTYSYLTISRVEAEDAATYYCQWSSNPFT 118  
DB 61 QKSGASPKLMYIYGTSTLASGVPTRFSGSGSGTYSYLTISRVEAEDAATYYCQYGYPLT 120

QY 119 FGSSTKLEI 127  
DB 121 FGAGTKLEI 129

RESULT 7  
A42848  
Ig light chain V region - mouse (fragment)  
N:Alternate names: L6 anti-tumor antibody  
C:Species: Mus musculus (house mouse)  
C>Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: A42848; S33902  
R:Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffo,  
J. Biol. Chem. 267, 15552-15558, 1992  
A:Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and character  
A:Reference number: A42848; MUID:92348410; PMID:1639794  
A:Accession: A42848  
A:Molecule type: DNA  
A:Residues: 1-107 <FEL>  
A:CROSS-references: UNIPARC:UPI0000115334; EMBL:M90690  
A>Note: sequence extracted from NCBI backbone (NCBIN:109958, NCBIP:109959)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 71.5%; Score 469; DB 2; Length 107;  
Best Local Similarity 85.7%; Pred. No. 9.5e-32;  
Matches 90; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOKPGSPKPMIYGTSTLASGVPTR 82  
DB 1 QIVLSQSPAILFASPGKVTMTCRASSSVIYMCWNQOKPGSPKPMIYATSNLASGVPGR 60

QY 83 FSGSGSGTYSYLTISRVEAEDAATYYCQWSSNPFTFGSGTKLEI 127  
DB 61 FSGSGSGTYSYLTISRVEAEDAATYYCQWSSNPFTFGAGTKLEI 105

RESULT 8  
PL0082  
Ig kappa chain V region (2D3) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 21-Jan-2000  
C:Accession: PL0082

R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca  
J. Exp. Med. 169, 519-533, 1989  
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are  
A;Reference number: PLO080; MUID:89094248; PMID:2492056  
A;Accession: PLO082  
A;Molecule type: mRNA  
A;Residues: 1-106 <MEE>  
A;Cross-references: UNIPARC:UPI00001767ED  
A;Experimental source: strain BALB/c  
A;Note: the sequence shown here is from the V kappa region of an antiidiotypic monoclonal  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-89/Domain: immunoglobulin homology <IMW>

Query Match 70.4%; Score 462; DB 2; Length 106;  
Best Local Similarity 87.6%; Pred. No. 3.5e-31;  
Matches 92; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 23 QIVLSQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKPWIYGTSTLASGVPTTR 82  
DB 1 QIVLSQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKPWIYGTSTLASGVPTTR 60

QY 83 FSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127  
DB 61 FSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 105

RESULT 9  
S05268  
Ig kappa chain precursor V-J region (38C13-VI) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 21-Jan-2000  
C;Accession: S05268; JLO062; S03846  
R;Levy, S.  
submitted to the EMBL Data Library, February 1989  
A;Reference number: S05267  
A;Accession: S05268  
A;Molecule type: mRNA  
A;Residues: 1-132 <LEV>  
A;Cross-references: UNIPARC:UPI000015DEC; EMBL:X14098; NID:952562; PIDN:CAA32260.1; PID  
R;Carroll, W.L.; Starnes, C.O.; Levy, R.; Levy, S.  
J. Exp. Med. 168, 1607-1620, 1988  
A;Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An explana  
A;Reference number: JLO061; MUID:89035985; PMID:3141553  
A;Accession: JLO062  
A;Molecule type: mRNA  
A;Residues: 1-120 <CAR>  
A;Cross-references: UNIPARC:UPI0000176789; EMBL:X14098  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>  
F;15-132/Product: Ig kappa chain (fragment) #status predicted <MAT>  
F;15-108/Domain: V region (V-kappa-1) <VRE>  
F;30-103/Domain: immunoglobulin homology <IMW>  
F;109-132/Domain: J region (J-kappa-4) (fragment) <JRE>

Query Match 69.8%; Score 458; DB 2; Length 132;  
Best Local Similarity 76.3%; Pred. No. 9.2e-31;  
Matches 90; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 10 FLLISAVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKPWI 69  
DB 2 FLLISVTLITNGEITFQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKIWI 61

QY 70 YGTSTLASGVPTTRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127  
DB 62 YGINSLASGVPTTRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 119

RESULT 10  
B30562  
Ig kappa chain V region (27.10.2) - mouse (fragment)  
C;Species: Mus musculus (house mouse)

C;Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000  
C;Accession: B30562  
R;Skder, S.K.; Borden, P.; Gruero, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.  
J. Immunol. 142, 888-893, 1989  
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bir  
A;Reference number: A30562; MUID:89110066; PMID:2464031  
A;Accession: B30562  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-107 <SIK>  
A;Cross-references: UNIPARC:UPI00001767BA  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-89/Domain: immunoglobulin homology <IMW>

Query Match 68.9%; Score 452; DB 2; Length 107;  
Best Local Similarity 82.9%; Pred. No. 2.3e-30;  
Matches 87; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 23 QIVLSQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKPWIYGTSTLASGVPTTR 82  
DB 1 QIVLSQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKPWIYGTSTLASGVPTTR 60

QY 83 FSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 127  
DB 61 FSGSGSGTSYSLTISRVEADAATYYCQWSSNPFTFGSGTKLEI 105

RESULT 11  
KVMS7B  
Ig kappa chain precursor V region (S107B) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Dec-1982 #sequence\_revision 17-Dec-1982 #text\_change 09-Jul-2004  
C;Accession: A01943  
R;Kwan, S.P.; Max, E.E.; Seidman, J.G.; Leder, P.; Scharff, M.D.  
Cell 26, 57-66, 1981  
A;Title: Two kappa immunoglobulin genes are expressed in the myeloma S107.  
A;Reference number: A01943; MUID:82115300; PMID:6799208  
A;Accession: A01943  
A;Molecule type: mRNA  
A;Residues: 1-129 <KWA>  
A;Cross-references: UNIPROT:P01680; UNIPARC:UPI000002A119; GB:V00780; NID:951676; PIDN:CA  
A;Note: the sequence was determined from the differentiated gene  
C;Comment: This protein, in which there is a deletion of two amino acids at the V-J recomb  
al kappa chain S107.  
C;Genetics: 17/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp  
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-129/Product: Ig kappa chain V region (S107B) #status predicted <MAT>  
F;38-113/Domain: immunoglobulin homology <IMW>  
F;45-111/Disulfide bonds: #status predicted

Query Match 68.9%; Score 452; DB 1; Length 129;  
Best Local Similarity 74.4%; Pred. No. 2.8e-30;  
Matches 96; Conservative 8; Mismatches 21; Indels 4; Gaps 2;

QY 1 MDFQVQFFSFLILISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSV--IYMCWNQ 58  
DB 1 MDLQVQIIXFLILISVIMSRGENVLTQSPALMAASLGQKVTMTCSASSSVSSSYLHWYQ 60

QY 59 QKPGSSPKPWIYGTSTLASGVPTTRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPFT 118  
DB 61 QKSGASPKPLIHRSTNLASGVPTTRFSGSGSGTSYSLTISRVEADAATYYCQWSSNPFT 118

QY 119 FSGTKLEI 127  
DB 119 FSGTKLEI 127



## RESULT 12

A30562  
Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000  
C;Accession: A30562  
R;Skidder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.  
J. Immunol. 142, 888-893, 1989  
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site  
A;Reference number: A30562; MUID:89110066; PMID:2464031  
A;Accession: A30562  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-107 <SIK>  
A;Cross-references: UNIPARC:UPI00001767B0  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 68.3%; Score 448; DB 2; Length 107;  
Best Local Similarity 82.9%; Pred. No. 4.9e-30;  
Matches 87; Conservative 5; Mismatches 13; Indels 0; Gaps 0;  
QY 23 QIVLSQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKPWIYGTSTLASGVPTTR 82  
DB 1 QIVLTQSPALMSASPGKVTMTCSASSSVYMHYQKSGTSPKRWIYDTSKLASGVPAR 60  
QY 83 FSGSGGTSLTISRVEADAATYCCQWSSNPFTFGSGTKLEI 127  
DB 61 FSGSGGTSLTISRVEADAATYCCQWSSNPFTFGSGTKLEI 105

## RESULT 13

G30560  
Ig kappa chain V region (35.8.2H) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000  
C;Accession: G30560  
R;Matsuda, T.; Kabat, E.A.  
J. Immunol. 142, 863-870, 1989  
A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibody  
A;Reference number: A30560; MUID:89110062; PMID:2464028  
A;Accession: G30560  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-108 <MAT>  
A;Cross-references: UNIPARC:UPI00001767B8  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 67.1%; Score 440.5; DB 2; Length 108;  
Best Local Similarity 83.0%; Pred. No. 2e-29;  
Matches 88; Conservative 4; Mismatches 13; Indels 1; Gaps 1;  
QY 23 QIVLSQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKPWIYGTSTLASGVPTTR 82  
DB 1 QIVLTQSPALMSASPGKVTMTCSASSSVYMHYQKSGTSPKRWIYDTSKLASGVPAR 60  
QY 83 FSGSGGTSLTISRVEADAATYCCQWSSNPFTFGSGTKLEI 127  
DB 61 FSGSGGTSLTISRVEADAATYCCQWTRNPPFTFGSGTKLEI 106

## RESULT 14

B49049  
Ig kappa chain V region (anti-idiotypic) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C;Accession: B49049  
R;Arandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.  
Eur. J. Immunol. 22, 2893-2899, 1992

A;Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antigen  
A;Reference number: A49049; MUID:93049629; PMID:1425914  
A;Accession: B49049  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-104 <ARM>  
A;Cross-references: UNIPARC:UPI00001767AD  
A;Experimental source: BALB/c  
A;Note: sequence extracted from NCBI backbone (NCBI:118298, NCBIP:118299)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 66.8%; Score 438; DB 2; Length 104;  
Best Local Similarity 81.7%; Pred. No. 3.2e-29;  
Matches 85; Conservative 5; Mismatches 14; Indels 0; Gaps 0;  
QY 23 QIVLSQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKPWIYGTSTLASGVPTTR 82  
DB 1 QIVLTQSPALMSASPGKVTMTCSASSSVYMHYQKSGTSPKRWIYDTSKLASGVPAR 60  
QY 83 FSGSGGTSLTISRVEADAATYCCQWSSNPFTFGSGTKLE 126  
DB 61 FSGSGGTSLTISRVEADAATYCCQWSSNPFTFGAGTKLE 104

## RESULT 15

S29591  
Ig kappa chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C;Accession: S29591  
R;Kavaler, J.  
Submitted to the EMBL Data Library, April 1991  
A;Reference number: S26459  
A;Accession: S29591  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-103 <KAV>  
A;Cross-references: UNIPARC:UPI0000115F57; EMBL:X59094; NID:952227; PIDN:CAA41820.1; PID  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-88/Domain: immunoglobulin homology <IMM>

Query Match 66.6%; Score 437; DB 2; Length 103;  
Best Local Similarity 82.5%; Pred. No. 3.8e-29;  
Matches 85; Conservative 5; Mismatches 13; Indels 0; Gaps 0;  
QY 24 IVLSQSPAILFASPGETVMTTCRASSSVIYMCWQKPGSSPKPWIYGTSTLASGVPTTR 83  
DB 1 IVLTQSPALMSASPGKVTMTCSASSSVYMHYQKSGTSPKRWIYDTSKLASGVPAR 60

QY 84 SSGSGGTSLTISRVEADAATYCCQWSSNPFTFGSGTKLE 126  
DB 61 SSGSGGTSLTISRVEADAATYCCQWSSNPFTFGAGTKLE 103

## RESULT 16

PC4405  
Ig kappa chain V region (F3, anti-AFP) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Nov-1997 #sequence\_revision 23-Jan-1998 #text\_change 09-Jul-2004  
C;Accession: PC4405  
R;Peng, J.B.; Han, H.; Su, C.-Z.; Chen, C.Q.  
Chinese Biochem. J. 12, 648-653, 1996  
A;Title: Generation of a phage display library of the immunoglobulin repertoire from hum  
A;Reference number: PC4405  
A;Accession: PC4405  
A;Molecule type: mRNA  
A;Residues: 1-107 <DEN>  
A;Cross-references: UNIPROT:Q8K1F0; UNIPARC:UPI00001767BB  
A;Experimental source: spleen cell  
C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 66.6%; Score 437; DB 2; Length 107;  
Best Local Similarity 81.7%; Pred. No. 3.9e-29;  
Matches 85; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Qy 24 IIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPTRF 83  
Db 2 IELVTSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPTRF 61  
Qy 84 SGSGSGTSLTISRVEAEDAATYYCOQWSSNPFTFGSGTKLEI 127  
Db 62 SGSGSGTSLTISRVEAEDAATYYCOQWSSNPFTFGSGTKLEI 105

## RESULT 17

S38720  
Ig light chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Jun-2000  
C;Accession: S38720  
R;Cimanis, A.Y.  
Submitted to the EMBL Data Library, November 1993

A;Reference number: S38713  
A;Accession: S38720  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-108 <IM>  
A;Cross-references: UNIPARC:UPI0000117544; EMBL:X76023; NID:9416104; PIDN:CAA53610.1; PID  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 66.4%; Score 435.5; DB 2; Length 108;  
Best Local Similarity 80.2%; Pred. No. 5.2e-29;  
Matches 85; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

Qy 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPTTR 82  
Db 1 EIVLTQSPALMSASPGKVTMTCSASSSVSYMYWYQKPGSSPKPWIYLTSTNLASGVPLR 60  
Qy 83 FSGSGSGTSLTISRVEAEDAATYYCOQWSSNPFTFGSGTKLEI 127  
Db 61 FSGSGSGTSLTISRVEAEDAATYYCOQWSSNPFTFGAGTKLQL 106

## RESULT 18

PS0071  
Ig kappa chain V region (38C13.V8) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000  
C;Accession: PS0071  
R;Levy, S.; Campbell, M.J.; Levy, R.  
J. Exp. Med. 170, 1-13, 1989  
A;Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement  
A;Reference number: A92781; MUID:89310348; PMID:2501443  
A;Accession: PS0071  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-106 <LEV>  
A;Cross-references: UNIPARC:UPI00001767C9  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 435; DB 2; Length 106;  
Best Local Similarity 81.0%; Pred. No. 5.7e-29;  
Matches 85; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPTTR 82  
Db 1 QIVLTQSPALMSASPGKVTMTCSASSSVSYMYWYQKSGTSPKRWIYDTSKLASGVDPAR 60

Qy 83 FSGSGSGTSLTISRVEAEDAATYYCOQWSSNPFTFGSGTKLEI 127  
Db 61 FSGSGSGTSLTISRVEAEDAATYYCOQWSSNPFTFGAPTKLEL 105

## RESULT 19

S26338  
Ig kappa chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C;Accession: S26338  
R;Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e  
A;Reference number: S26309; MUID:91341421; PMID:1908510  
A;Accession: S26338  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-105 <STA>  
A;Cross-references: UNIPARC:UPI0000115F82; EMBL:X59197; NID:952328; PIDN:CAA41907.1; PID  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 65.9%; Score 432; DB 2; Length 105;  
Best Local Similarity 81.0%; Pred. No. 9.8e-29;  
Matches 85; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPTTR 82  
Db 1 QIVLTQSPALMSASPGKVTMTCSASSSVSYMYWYQKPGSSPKPWIYRTSNLASGVDPAR 60  
Qy 83 FSGSGSGTSLTISRVEAEDAATYYCOQWSSNPFTFGSGTKLEI 127  
Db 61 FSGSGSGTSLTISRMEADAATYYCQYHSYPTTFGGGTKLEI 105

## RESULT 20

PT0406  
Ig kappa chain V region (S107/VH11 group 6-26) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C;Accession: PT0406  
R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.  
J. Exp. Med. 173, 731-741, 1991  
A;Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodi  
A;Reference number: PT0376; MUID:91147903; PMID:1900082  
A;Accession: PT0406  
A;Molecule type: DNA  
A;Residues: 1-107 <BEH>  
A;Cross-references: UNIPARC:UPI00001767E8  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 429; DB 2; Length 107;  
Best Local Similarity 79.0%; Pred. No. 1.8e-28;  
Matches 83; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQKPGSSPKPWIYGTSTLASGVPTTR 82  
Db 1 QIVLTQSPALMSASPGKVTMTCSASSSVSYMYWYQKSGTSPKRWIYDTSKLASGVDPAR 60  
Qy 83 FSGSGSGTSLTISRVEAEDAATYYCOQWSSNPFTFGSGTKLEI 127  
Db 61 FSGSGSGTSLTXISMEADAATYYCOQWSSNPFTFGGGTXXEI 105

Search completed: March 20, 2006, 07:36:25  
Job time : 5.63412 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:32:13 ; Search time 2.37968 Seconds  
(without alignments)  
1527.558 Million cell updates/sec

Title: US-10-687-035-33

Perfect score: 656

Sequence: 1 MDPVQVIFSLISASVIMS.....YCOQSSNPFTFGSGTKLRI 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications\_AA\_New.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pdb.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pdb.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pdb.\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pdb.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pdb.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pdb.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pdb.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	87.2	128	7	US-11-193-205-60
2	524	79.9	128	7	US-11-250-411-87
3	494	75.3	130	7	US-11-090-331-4
4	494	75.3	138	7	US-11-090-331-8
5	493	75.2	130	7	US-11-125-837-21
6	478	72.9	126	7	US-11-250-411-89
7	475	72.4	213	7	US-11-124-620-6
8	475	72.4	236	7	US-11-106-820-19
9	475	72.4	236	7	US-11-190-364-17
10	475	72.4	236	7	US-11-147-780-17
11	470	71.6	106	7	US-11-107-028-28
12	470	71.6	107	7	US-11-120-338-1
13	470	71.6	107	7	US-11-106-820-1
14	470	71.6	107	7	US-11-143-077-1
15	470	71.6	107	7	US-11-190-364-1
16	470	71.6	107	7	US-11-147-780-1
17	470	71.6	107	7	US-11-143-386-1
18	467	71.2	106	7	US-11-193-440-89
19	462	70.4	128	7	US-11-250-411-92
20	461	70.3	106	7	US-11-107-028-34
21	457	69.7	235	7	US-11-166-994-2
22	449.5	68.5	110	7	US-11-193-512-33
23	445	67.8	126	7	US-11-250-411-96
24	444	67.7	107	7	US-11-221-900-6
25	440	67.1	126	7	US-11-250-411-94
26	437	66.6	106	6	US-10-507-662-43
27	435	66.3	106	6	US-10-507-662-42
28	434	66.2	126	7	US-11-250-411-93
29	426	64.9	108	7	US-11-097-812-39
30	425	64.8	106	7	US-11-250-411-98
31	424.5	64.7	107	7	US-11-097-812-101
32	422	64.3	106	7	US-11-174-186-1
33	421	64.2	110	7	US-11-097-812-99
34	421	64.2	110	7	US-11-097-812-100
35	421	64.2	110	7	US-11-097-812-171
36	418	63.7	110	7	US-11-097-812-207
37	417	63.6	106	7	US-11-174-186-8
38	415	63.3	110	7	US-11-097-812-174
39	414	63.1	110	7	US-11-097-812-110
40	413	63.0	110	7	US-11-097-812-104
41	411	62.7	106	7	US-11-174-186-9
42	411	62.7	213	7	US-11-174-186-42
43	409	62.3	106	7	US-11-174-186-16
44	408	62.2	108	6	US-10-507-662-44
45	404	61.6	106	7	US-11-174-186-15
46	403	61.4	241	6	US-10-902-546-6
47	400	61.0	106	7	US-11-107-028-36
48	400	61.0	110	7	US-11-097-812-97
49	400	61.0	111	7	US-11-097-812-112
50	400	61.0	248	6	US-10-512-184-36
51	400	61.0	615	6	US-10-512-184-50
52	399	60.8	241	6	US-10-902-546-5
53	398	60.7	108	6	US-10-507-662-45
54	398	60.7	110	7	US-11-097-812-96
55	398	60.7	110	7	US-11-097-812-114
56	397	60.5	111	7	US-11-097-812-180
57	396	60.4	237	6	US-10-073-301A-9
58	396	60.4	237	7	US-11-203-137-9
59	395	60.2	106	7	US-11-174-186-12
60	394	60.1	111	7	US-11-097-812-107
61	393	59.9	107	7	US-11-009-939-7
62	393	59.9	107	7	US-11-107-028-40
63	392	59.8	106	7	US-11-174-186-13
64	391	59.6	106	7	US-11-174-186-10
65	391	59.6	106	7	US-11-174-186-11
66	391	59.6	106	7	US-11-174-186-14
67	391	59.6	215	7	US-11-102-621-141
68	391	59.6	215	7	US-11-166-906-2
69	387	59.0	107	7	US-11-221-900-9
70	387	59.0	110	7	US-11-097-812-179
71	386	58.8	113	7	US-11-097-812-108
72	386	58.8	290	7	US-11-032-773-957
73	386	58.8	319	7	US-11-032-773-955
74	383	58.4	111	7	US-11-097-812-115
75	383	58.4	232	7	US-11-106-820-23
76	383	58.4	232	7	US-11-190-364-21
77	383	58.4	232	7	US-11-147-780-21
78	381	58.1	102	7	US-11-097-812-109
79	381	58.1	111	7	US-11-097-812-111
80	380	57.9	110	7	US-11-097-812-98
81	380	57.9	110	7	US-11-097-812-172
82	379	57.8	111	7	US-11-097-812-106
83	375	57.2	104	7	US-11-250-411-100
84	375	57.2	105	7	US-11-250-411-108
85	374	57.0	107	7	US-11-120-338-2
86	374	57.0	107	7	US-11-107-028-29
87	374	57.0	107	7	US-11-106-820-2
88	374	57.0	107	7	US-11-143-077-2
89	374	57.0	107	7	US-11-190-364-2
90	374	57.0	107	7	US-11-147-780-2
91	374	57.0	107	7	US-11-143-386-2
92	374	57.0	213	7	US-11-120-338-13
93	374	57.0	213	7	US-11-107-028-31
94	374	57.0	213	7	US-11-106-820-24
95	374	57.0	213	7	US-11-143-077-13
96	374	57.0	213	7	US-11-143-386-13
97	373	56.9	107	7	US-11-221-900-8
98	369	56.2	111	7	US-11-097-812-103

Sequence 43, Appl  
Sequence 42, Appl  
Sequence 93, Appl  
Sequence 39, Appl  
Sequence 98, Appl  
Sequence 101, Appl  
Sequence 1, Appl  
Sequence 99, Appl  
Sequence 100, Appl  
Sequence 171, Appl  
Sequence 207, Appl  
Sequence 8, Appl  
Sequence 174, Appl  
Sequence 104, Appl  
Sequence 110, Appl  
Sequence 9, Appl  
Sequence 42, Appl  
Sequence 15, Appl  
Sequence 48, Appl  
Sequence 15, Appl  
Sequence 6, Appl  
Sequence 36, Appl  
Sequence 97, Appl  
Sequence 112, Appl  
Sequence 36, Appl  
Sequence 50, Appl  
Sequence 5, Appl  
Sequence 45, Appl  
Sequence 96, Appl  
Sequence 114, Appl  
Sequence 180, Appl  
Sequence 9, Appl  
Sequence 12, Appl  
Sequence 10, Appl  
Sequence 11, Appl  
Sequence 14, Appl  
Sequence 14, Appl  
Sequence 141, Appl  
Sequence 2, Appl  
Sequence 9, Appl  
Sequence 179, Appl  
Sequence 108, Appl  
Sequence 957, Appl  
Sequence 955, Appl  
Sequence 115, Appl  
Sequence 23, Appl  
Sequence 21, Appl  
Sequence 21, Appl  
Sequence 109, Appl  
Sequence 111, Appl  
Sequence 98, Appl  
Sequence 172, Appl  
Sequence 106, Appl  
Sequence 100, Appl  
Sequence 108, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 13, Appl  
Sequence 31, Appl  
Sequence 24, Appl  
Sequence 13, Appl  
Sequence 8, Appl  
Sequence 103, Appl



```
; SEQ ID NO 4
; LENGTH: 130
; TYPE: PRT
; ORGANISM: mus musculus
US-11-090-331-4

Query Match      75.3%; Score 494; DB 7; Length 130;
Best Local Similarity 79.1%; Pred. No. 6.9e-32;
Matches 102; Conservative 7; Mismatches 18; Indels 2; Gaps 1;

QY 1 MDFQVQIFSPFLLSASVIMSRGQIVLSQSPAILFASPGETVTTWTCRASSSVI--YMCWNQ 58
DB 1 MDFQVQIFSPFLLSASVIMSRGQIVLTQSPAIMSALGERVTWTCRASSSVSNYLHWYQ 60

QY 59 QKPGSPKPIWYGTSTLASGVPTRFSGSGSGTSGTYSLTISRVEAEDAATYYCQWSSNPFT 118
DB 61 QKPGAPNLWIYTSNLSAGVPAFSGSGSGTSGTYSLTISMEAEADAATYYCHQYLSRPPT 120

QY 119 FGSQTKLEI 127
DB 121 FGGGTKLEI 129

RESULT 4
US-11-090-331-8
; Sequence 8, Application US/11090331
; Publication No. US20050260210A1
; GENERAL INFORMATION:
; APPLICANT: PROTEIN DESIGN LABS, INC.
; APPLICANT: RAMAKRISHNAN, Vanitha
; APPLICANT: HO, Sun
; APPLICANT: MURRAY, Richard
; APPLICANT: LAW, Debbie
; TITLE OF INVENTION: USE OF ANTI ALPHASBETAL ANTIBODIES TO INHIBIT CANCER CELL
; FILE REFERENCE: 05882.0156.NPUS11
; CURRENT APPLICATION NUMBER: US/11/090,331
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/556,421
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/556,422
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/625,049
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: 60/651,098
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: 60/657,514
; PRIOR FILING DATE: 2005-02-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: chimeric antibody
US-11-090-331-8

Query Match      75.3%; Score 494; DB 7; Length 138;
Best Local Similarity 79.1%; Pred. No. 7.3e-32;
Matches 102; Conservative 7; Mismatches 18; Indels 2; Gaps 1;

QY 1 MDFQVQIFSPFLLSASVIMSRGQIVLSQSPAILFASPGETVTTWTCRASSSVI--YMCWNQ 58
DB 1 MDFQVQIFSPFLLSASVIMSRGQIVLTQSPAIMSALGERVTWTCRASSSVSNYLHWYQ 60

QY 59 QKPGSPKPIWYGTSTLASGVPTRFSGSGSGTSGTYSLTISRVEAEDAATYYCQWSSNPFT 118
DB 61 QKPGAPNLWIYTSNLSAGVPAFSGSGSGTSGTYSLTISMEAEADAATYYCHQYLSRPPT 120

QY 119 FGSQTKLEI 127
DB 121 FGGGTKLEI 129

; SEQ ID NO 121
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-21

Query Match      75.2%; Score 493; DB 7; Length 130;
Best Local Similarity 77.5%; Pred. No. 8.3e-32;
Matches 100; Conservative 10; Mismatches 17; Indels 2; Gaps 1;

QY 1 MDFQVQIFSPFLLSASVIMSRGQIVLSQSPAILFASPGETVTTWTCRASSSV--IYMCWNQ 58
DB 1 MDFQVQIFSPFLLSASVIMSRGENVLTQSPAIMSASPGSKVTWTCRASSVTNSTYLHWQ 60

QY 59 QKPGSPKPIWYGTSTLASGVPTRFSGSGSGTSGTYSLTISRVEAEDAATYYCQWSSNPFT 118
DB 61 QKGSAPKLIWYGSNLSAGVPAFSGSGSGTSGTYSLTISVVEAEDAATYYCQYSGYPLT 120

QY 119 FGSQTKLEI 127
DB 121 FGGGTKLEI 129

RESULT 5
US-11-125-837-21
; Sequence 21, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-21

; SEQ ID NO 121
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-250-411-89

Query Match      72.9%; Score 478; DB 7; Length 126;
Best Local Similarity 78.7%; Pred. No. 1.2e-30;
Matches 100; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

Qy 1 MDFQVQIFSLISASVIMRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNOOK 60
Db 1 MDFQVQIFSLISASVIMRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNOOK 60
Qy 61 PGSPKPIWGTSTLGGVPTFRFGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120
Db 61 SGTSFKLLIYRTSNLGSVPTFRFGSGSGTSYSLTISRVEADAADYCHQWSM--YTFG 118

Qy 121 SGTKEI 127
Db 119 GGTKEI 125

RESULT 7
US-11-124-620-6
; Sequence 6, Application US/11124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Dang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Karki, Sher Bahadur
; APPLICANT: Vafa, Omid
; APPLICANT: Hayes, Robert
; TITLE OF INVENTION: OPTIMIZED FC VARIANTS
; FILE REFERENCE: A-71386-9
; CURRENT APPLICATION NUMBER: US/11/124,620
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US 60/568,440
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/589,906
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/627,026
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 60/626,991
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/627,774
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 10/822,231
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 10/672,280
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 10/379,392
; PRIOR FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 6
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-620-6

Query Match      72.4%; Score 475; DB 7; Length 213;
Best Local Similarity 88.6%; Pred. No. 3.1e-30;
Matches 93; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNOOKPGSPKPIWGTSTLGGVPT 82
Db 1 QIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQKPGSPKPIWYATSNLGSVPVR 60

Qy 83 FSGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFGSGTKLEI 127
Db 61 FSGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFGGKLEI 105

RESULT 8
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-11-106-820-19
; Sequence 19, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 19
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-820-19

Query Match      72.4%; Score 475; DB 7; Length 236;
Best Local Similarity 78.9%; Pred. No. 3.3e-30;
Matches 97; Conservative 4; Mismatches 18; Indels 4; Gaps 1;

Qy 9 SFLIISASVIM----SRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNOOKPGSS 64
Db 6 AFLASMFVFSIATNAYAQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQKPGSS 65
Qy 65 PKPIWGTSTLGGVPTFRFGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFGSGTK 124
Db 66 PKPIWYAPSNLGSVPTFRFGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFGAGTK 125

Qy 125 LEI 127
Db 126 LEL 128

RESULT 9
US-11-190-364-17
; Sequence 17, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams Et Al.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is chimeric
US-11-190-364-17

Query Match      72.4%; Score 475; DB 7; Length 236;
Best Local Similarity 78.9%; Pred. No. 3.3e-30;
Matches 97; Conservative 4; Mismatches 18; Indels 4; Gaps 1;

Qy 9 SFLIISASVIM----SRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNOOKPGSS 64
Db 6 AFLASMFVFSIATNAYAQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQKPGSS 65
```

Db 6 AFLASMFVSIATNAVAQIVLSQSPAILASPGKVTMTCRASSSVSYMHYQKQPGSS 65  
Qy 65 PKWIYGTSTLASGVPTRFSGSGTYSYLTISRVEADAATYCCQWSSNPFTFGSGTK 124  
Db 66 PKWIYAPSNLASGVPARFSGSGTYSYLTISRVEADAATYCCQWSSNPFTFGAGTK 125  
Qy 125 LEI 127  
Db 126 LEL 128

## RESULT 10

## US-11-147-780-17

; Sequence 17, Application US/11147780  
; Publication No. US20060034835A1  
; GENERAL INFORMATION:  
; APPLICANT: Adams ET AL.  
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof  
; FILE REFERENCE: PI990R3CI  
; CURRENT APPLICATION NUMBER: US/11/147,780  
; PRIOR FILING DATE: 2005-06-07  
; PRIOR APPLICATION NUMBER: US 60/434,115  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: US 60/526,163  
; PRIOR FILING DATE: 2003-12-01  
; PRIOR APPLICATION NUMBER: PCT/US03/40426  
; PRIOR FILING DATE: 2003-12-16  
; NUMBER OF SEQ ID NOS: 38  
; SEQ ID NO 17  
; LENGTH: 236  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is chimeric

## US-11-147-780-17

Query Match 72.4%; Score 475; DB 7; Length 236;  
Best Local Similarity 78.9%; Pred. No. 3.3e-30;  
Matches 97; Conservative 4; Mismatches 18; Indels 4; Gaps 1;

Qy 9 SFLLISASVIM---SRGQIVLSQSPAILASPGKVTMTCRASSSVSYMHYQKQPGSS 64  
Db 6 AFLASMFVSIATNAVAQIVLSQSPAILASPGKVTMTCRASSSVSYMHYQKQPGSS 65  
Qy 65 PKWIYGTSTLASGVPTRFSGSGTYSYLTISRVEADAATYCCQWSSNPFTFGSGTK 124  
Db 66 PKWIYAPSNLASGVPARFSGSGTYSYLTISRVEADAATYCCQWSSNPFTFGAGTK 125

Qy 125 LEI 127

Db 126 LEL 128

## RESULT 11

## US-11-107-028-28

; Sequence 28, Application US/11107028  
; Publication No. US20050276803A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAN, ANDREW C.  
; APPLICANT: GONG, QIAN  
; APPLICANT: MARTIN, FLAVIUS  
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion  
; FILE REFERENCE: P2112R1  
; CURRENT APPLICATION NUMBER: US/11/107,028  
; PRIOR FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US 60/563,263  
; PRIOR FILING DATE: 2004-04-16  
; NUMBER OF SEQ ID NOS: 52  
; SEQ ID NO 28  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Mus musculus

## US-11-107-028-28

Query Match 71.6%; Score 470; DB 7; Length 107;  
Best Local Similarity 87.6%; Pred. No. 4.2e-30;  
Matches 92; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Query Match 71.6%; Score 470; DB 7; Length 106;  
Best Local Similarity 87.6%; Pred. No. 4.2e-30;  
Matches 92; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 23 QIVLSQSPAILASPGKVTMTCRASSSVSYMHYQKQPGSSPKWIYGTSTLASGVPTR 82  
Db 1 QIVLSQSPAILASPGKVTMTCRASSSVSYMHYQKQPGSSPKWIYGTSTLASGVPAR 60

Qy 83 FSGSGGTYSYLTISRVEADAATYCCQWSSNPFTFGSGTKLEI 127

Db 61 FSGSGGTYSYLTISRVEADAATYCCQWSSNPFTFGAGTKLEL 105

## RESULT 12

## US-11-120-338-1

; Sequence 1, Application US/11120338  
; Publication No. US20050271658A1  
; GENERAL INFORMATION:  
; APPLICANT: BRUNETTA, PAUL G.  
; APPLICANT: GREWAL, IQBAL S.  
; APPLICANT: WALICKE, PATRICIA A.  
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE  
; FILE REFERENCE: P2079R2  
; CURRENT APPLICATION NUMBER: US/11/120,338  
; PRIOR FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: US 60/568,460  
; PRIOR FILING DATE: 2004-05-05  
; NUMBER OF SEQ ID NOS: 25  
; SEQ ID NO 1  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Mus musculus

## US-11-120-338-1

Query Match 71.6%; Score 470; DB 7; Length 107;  
Best Local Similarity 87.6%; Pred. No. 4.2e-30;  
Matches 92; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 23 QIVLSQSPAILASPGKVTMTCRASSSVSYMHYQKQPGSSPKWIYGTSTLASGVPTR 82  
Db 1 QIVLSQSPAILASPGKVTMTCRASSSVSYMHYQKQPGSSPKWIYGTSTLASGVPAR 60

Qy 83 FSGSGGTYSYLTISRVEADAATYCCQWSSNPFTFGSGTKLEI 127

Db 61 FSGSGGTYSYLTISRVEADAATYCCQWSSNPFTFGAGTKLEL 105

## RESULT 13

## US-11-106-820-1

; Sequence 1, Application US/11106820  
; Publication No. US20060002930A1  
; GENERAL INFORMATION:  
; APPLICANT: BRUNETTA, PAUL G  
; APPLICANT: SEWELL, KATHRYN L.  
; TITLE OF INVENTION: Treatment of Disorders  
; FILE REFERENCE: P2102R1  
; CURRENT APPLICATION NUMBER: US/11/106,820  
; PRIOR FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US 60/563,227  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 60/565,098  
; PRIOR FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 45  
; SEQ ID NO 1  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Mus musculus

## US-11-106-820-1

Query Match 71.6%; Score 470; DB 7; Length 107;  
Best Local Similarity 87.6%; Pred. No. 4.2e-30;  
Matches 92; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy	23	QIVLSOSPAILFASPGETVTMTCRASSSVIYMCNQKQPGSSPKWIIYGTSTLASGVPTR	82
Db	1	QIVLSOSPALLSASPGCKVTMTCRASSSVSYHHWTQQKPGSSPKWIIYAPSNILASGVPAR	60
Qy	83	FSGSGSGTYSYLTI SRVEAEDAATYYCQOWSSNPPTFGSGTKLEI	127
Db	61	FSGSGSGTYSYLTI SRVEAEDAATYYCQOWSFNPTPFCAGTKLEL	105

```

RESULT 14
US-11-143-077-1
; Sequence 1, Application US/11143077
; Publication NO. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-143-077-1

```

	Query Match	71.6%	Score 470	DB 7	Length 107
	Best Local Similarity	87.6%	Pred. No. 4.2e-30		
	Matches 92	Conservative 2	Mismatches 11	Indels 0	Gaps 0
Qy	23	QIVLSQSPAILFASPGFVTWTCRASSSVIYMCWNQKPGSSPKPWYIGTSTLASGVPT	82		
Db	1	QIVLSQSPAILSASFGKVTWTCRASSSVSYMHYQKPGSSPKPWYIAPNTLASGVPA	60		
Qy	83	FSGSGSGTYSLTIISRVAEDAAIYVQQQSSNPFTEGSGTKLEI	127		
Db	61	FSGSGSGTYSLTIISRVAEDAAIYVQQQSSNPFTEGAGTKLEI	105		

RESULT 15  
US-11-190-364-1  
; Sequence 1, Application US/11190364  
; Publication No. US20060024300A1  
; GENERAL INFORMATION:  
; APPLICANT: Adams ET AL.  
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof  
; FILE REFERENCE: P1990R3C1P1  
; CURRENT APPLICATION NUMBER: US/11/190,364  
; CURRENT FILING DATE: 2005-07-26  
; PRIOR APPLICATION NUMBER: US 60/434,115  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: US 60/536,163  
; PRIOR FILING DATE: 2003-12-01  
; PRIOR APPLICATION NUMBER: PCT/US03/40426  
; PRIOR FILING DATE: 2003-12-16  
; PRIOR APPLICATION NUMBER: US 11/147,780  
; PRIOR FILING DATE: 2005-06-07  
; NUMBER OF SEQ ID NOS: 38  
; SEQ ID NO 1  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-190-364-1

Query Match 71.6%; Score 470; DB 7; Length 107;  
Best Local Similarity 87.6%; Pred. No. 4.2e-30;  
Matches 92; Conservative 2; Mismatches 11; Indels

```

Qy 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNOQKPGSSPKPWITGCTSLASGVPT 82
Db 1 QIVLSQSPALISAPGCKVTMTCRASSSVSYMHYQOKPGSSPKPWIIYAPSNLASGVPAR 60
Qy 83 FSGSGGTSYSLIISRVEADAATYYCQOWSSNPFPTFGSGTKLEI 127
Db 61 FSGSGGTSYSLIISRVEADAATYYCQOWSFNPFPTFGACTKLEL 105

RESULT 16
US-11-147-780-1
; Sequence 1, Application US/11147780
; Publication No. US20060034835A1
; GENERAL INFORMATION:
; APPLICANT: Adams Et AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: F1990R3C1
; CURRENT APPLICATION NUMBER: US/11/147,780
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-147-780-1

```

	Query Match	71.68;	Score 470;	DB 7;	Length 107;
	Best Local Similarity	87.68;	Pred No. 4.2e-30;		
	Matches 92;	Conservative 2;	Mismatches 11;	Indels 0;	Gaps 0;
Qy	23	QIVLSQSPAILFASPGETVTMTCRASSSVLYMCWNQKPGSSPKPWITGTTSLASGVPTR	82		
Db	1	QIVLSQSPAILASPGSKVTMTCRASSSVYMWYQKPGSSPKPWIIYAPENLASGVPAR	60		
Qy	83	PSGSGSGTYSLSLITSRVAEADAATYYCQOWSSNPFTFGSGTKLEI	127		
Db	61	PSGSGSGTYSLSLITSRVAEADAATYYCQOWSFNPPTFGAGTKLEI	105		

```

RESULT 17
US-11-143-386-1
; Sequence 1, Application US/11143386
; Publication No. US20060051345A1
; GENERAL INFORMATION:
; APPLICANT: PROHNA, PAUL A.
; TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS
; FILE REFERENCE: P2134R1
; CURRENT APPLICATION NUMBER: US/11/143,386
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/576,993
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 1
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-143-386-1

```

	Query Match	71.6%	Score 470	DB 7	Length 107
	Best Local Similarity	87.6%	Pred. No. 4.2e-30		
	Matches 92	Conservative 2	Mismatches 11	Indels 0	Gaps 0
QY	23	QVLSQSPAILFASPGFTVTWTCRASSSVIYMCWNQKPGSGKPFWIYGTSTLASCVTR	82		
Db	1	QVLSQSPAILFASPGFTVTWTCRASSSVIYMCWNQKPGSGKPFWIYGTSTLASCVTR	60		
QY	83	PSGSGSGTYSLTLTISRVAEDAAATYYCQOWSSNPFPTGSGTGKLEI	127		



Db 61 FSGSGSGTSLTISRVEADATYYCQWSENPPTFGAGTKLEL 105  
|||||

## RESULT 18

US-11-193-440-89

; Sequence 89, Application US/11193440

; Publication No. US20060002939A1

## GENERAL INFORMATION:

; APPLICANT: Fischer, Gerald W.

; Schuman, Richard P.

; Wong, King

; Stinson, Jeffrey L.

TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND

CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM

POSITIVE BACTERIA

NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:

ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &amp;

DUNNER, LLP

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatenIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/193,440

FILING DATE: 01-Aug-2005

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/893,615

FILING DATE: 29-Jun-2001

ATTORNEY/AGENT INFORMATION:

NAME: Einaudi, Carol P.

REGISTRATION NUMBER: 32,220

REFERENCES/DOCKET NUMBER: 04995.0041-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 89:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 89:

US-11-193-440-89

Query Match 71.2%; Score 467; DB 7; Length 106;  
Best Local Similarity 88.8%; Pred. No. 7.1e-30;  
Matches 93; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCNQKPGSSPKPWIYGTSTLASGVPT 82

Db 1 QIVLSQSPAILFASPGETVTMTCRASSSVYMHYQKPGSSPKPWIATSNLASGVPT 60

QY 83 FSGSGSGTSLTISRVEADATYYCQWSENPPTFGGKLEI 127

Db 61 FSGSGSGTSLTISRVEADATYYCQWSENPPTFGGKLEI 105

## RESULT 19

US-11-250-411-92

; Sequence 92, Application US/11250411

; Publication No. US20060034838A1

## GENERAL INFORMATION:

; APPLICANT: SHITARA, KENYA

; APPLICANT: ITO, MIKITO

; APPLICANT: HANAI, NOBUO

; APPLICANT: KAWADA, YOKO  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: SHIBUYA, MASABUMI  
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY  
; FILE REFERENCE: 249-107  
; CURRENT APPLICATION NUMBER: US/11/250,411  
; CURRENT FILING DATE: 2005-10-17  
; PRIOR APPLICATION NUMBER: US/09/453,718  
; PRIOR FILING DATE: 1999-12-03  
; PRIOR APPLICATION NUMBER: 09/315,051  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/119,014  
; PRIOR FILING DATE: 1998-07-20  
; PRIOR APPLICATION NUMBER: PCT/JP97/04259  
; PRIOR FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 92  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein  
US-11-250-411-92

Query Match 70.4%; Score 462; DB 7; Length 128;

Best Local Similarity 72.4%; Pred. No. 2e-29;

Matches 92; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

QY 1 MDPQVQIFSFLLISASVIMRQIVLSQSPAILFASPGETVTMTCRASSSVIYMCNQK 60

Db 1 MDPQVQIFSFLLISASVIMRQIVLSQSPAILFASPGETVTMTCRASSSVIYMCNQK 60

QY 61 PGSSPKPWIYGTSTLASGVPTFRFSGSGTSLTISRVEADATYYCQWSENPPTFG 120

Db 61 PGKAPKLLIYDTSKLPFGVPSRPSGSGTDFLLISSLQPEDPAIYTCQWSENPPTFG 120

QY 121 SGTGLEI 127

Db 121 QGTKEI 127

## RESULT 20

US-11-107-028-34

; Sequence 34, Application US/11107028

; Publication No. US20050276803A1

## GENERAL INFORMATION:

; APPLICANT: CHAN, ANDREW C.

; APPLICANT: GONG, QIAN

; APPLICANT: MARTIN, FLAVIUS

; TITLE OF INVENTION: Method for Augmenting B Cell Depletion

; FILE REFERENCE: P2112R1

; CURRENT APPLICATION NUMBER: US/11/107,028

; CURRENT FILING DATE: 2005-04-15

; PRIOR APPLICATION NUMBER: US 60/563,263

; PRIOR FILING DATE: 2004-04-16

; NUMBER OF SEQ ID NOS: 52

; SEQ ID NO 34

; LENGTH: 106

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: sequence is synthesized

US-11-107-028-34

Query Match 70.3%; Score 461; DB 7; Length 106;

Best Local Similarity 86.5%; Pred. No. 2.1e-29;

Matches 90; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 24 IIVLSQSPAILFASPGETVTMTCRASSSVIYMCNQKPGSSPKPWIYGTSTLASGVPT 83

Db 2 IOLTQSPAILFASPGKVTMTCRASSSVIYHFWQKPGSSPKPWIATSNLASGVPT 61

Qy 84 SGSGGTSYSLTISRVEAEDATYYCQOWSSNPPTGSGTKLEI 127  
Db 62 SGSGGTSYSLTISRVEAEDATYYCQOWTSNPPTFGGKLEI 105

Search completed: March 20, 2006, 07:32:42  
Job time : 3.37968 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:31:52 ; Search time 22.5444 Seconds  
(without alignments)  
2353.772 Million cell updates/sec

Title: US-10-687-035-33

Perfect score: 656

Sequence: 1 MDPQVQIFSPLLISASVMS.....YCOQSSNPFTFGSGTKLRI 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	656	100.0	127	5	US-10-687-035-33
2	578	88.1	129	5	US-10-723-003-38
3	578	88.1	129	6	US-11-004-639-38
4	578	88.1	235	5	US-10-723-003-42
5	578	88.1	235	6	US-11-004-639-42
6	572	87.2	128	3	US-09-905-928-4
7	572	87.2	128	4	US-10-096-364-4
8	572	87.2	128	4	US-10-238-681-7
9	572	87.2	128	4	US-10-411-037-60
10	572	87.2	128	4	US-10-411-026-60
11	572	87.2	128	4	US-10-410-962-60
12	572	87.2	128	4	US-10-411-049-60
13	572	87.2	128	4	US-10-327-663-12
14	572	87.2	128	4	US-10-410-930-60
15	572	87.2	128	4	US-10-410-997-60
16	572	87.2	128	4	US-10-411-012-60
17	572	87.2	128	4	US-10-287-994-60
18	572	87.2	128	4	US-10-410-913-60
19	572	87.2	128	5	US-10-410-980-60
20	572	87.2	128	5	US-10-410-897-60
21	572	87.2	128	5	US-10-492-261-60
22	572	87.2	128	5	US-10-956-039-4
23	566	86.3	128	5	US-10-941-768A-46
24	566	86.3	266	4	US-10-207-655-11
25	566	86.3	266	4	US-10-053-530-11
26	566	86.3	266	6	US-11-089-511-11
27	566	86.3	266	6	US-11-089-190-11
28	566	86.3	266	6	US-11-089-511-11
29	566	86.3	266	6	US-11-088-570-11
30	566	86.3	266	6	US-11-088-569-11
31	566	86.3	266	6	US-11-088-693-11
32	566	86.3	266	6	US-11-089-367-11
33	566	86.3	266	6	US-11-089-368-11
34	566	86.3	267	5	US-10-627-556-214
35	566	86.3	268	5	US-10-627-556-212
36	566	86.3	268	5	US-10-627-556-244
37	566	86.3	422	4	US-10-207-655-34
38	566	86.3	422	4	US-10-207-655-152
39	566	86.3	422	4	US-10-053-530-34
40	566	86.3	422	5	US-10-627-556-693
41	566	86.3	422	6	US-11-089-511-34
42	566	86.3	422	6	US-11-089-190-34
43	566	86.3	422	6	US-11-088-570-34
44	566	86.3	422	6	US-11-088-737-34
45	566	86.3	422	6	US-11-088-569-34
46	566	86.3	422	6	US-11-088-693-34
47	566	86.3	422	6	US-11-089-367-34
48	566	86.3	422	6	US-11-089-368-34
49	566	86.3	482	4	US-10-207-655-33
50	566	86.3	482	4	US-10-207-655-150
51	566	86.3	482	5	US-10-627-556-691
52	566	86.3	482	6	US-11-089-511-33
53	566	86.3	482	6	US-11-089-190-33
54	566	86.3	482	6	US-11-088-570-33
55	566	86.3	482	6	US-11-088-737-33
56	566	86.3	482	6	US-11-088-569-33
57	566	86.3	482	6	US-11-088-693-33
58	566	86.3	482	6	US-11-089-367-33
59	566	86.3	482	6	US-11-089-368-33
60	566	86.3	482	6	US-10-207-655-235
61	566	86.3	498	4	US-10-207-655-22
62	566	86.3	499	4	US-10-207-655-15
63	566	86.3	499	4	US-10-207-655-16
64	566	86.3	499	4	US-10-207-655-17
65	566	86.3	499	4	US-10-207-655-18
66	566	86.3	499	4	US-10-053-530-15
67	566	86.3	499	4	US-10-053-530-16
68	566	86.3	499	4	US-10-053-530-17
69	566	86.3	499	5	US-10-627-556-689
70	566	86.3	499	6	US-11-089-511-15
71	566	86.3	499	6	US-11-089-511-16
72	566	86.3	499	6	US-11-089-511-17
73	566	86.3	499	6	US-11-089-190-15
74	566	86.3	499	6	US-11-089-190-16
75	566	86.3	499	6	US-11-088-570-15
76	566	86.3	499	6	US-11-088-570-16
77	566	86.3	499	6	US-11-088-570-17
78	566	86.3	499	6	US-11-088-570-18
79	566	86.3	499	6	US-11-088-570-19
80	566	86.3	499	6	US-11-088-570-20
81	566	86.3	499	6	US-11-088-570-21
82	566	86.3	499	6	US-11-088-570-22
83	566	86.3	499	6	US-11-088-570-23
84	566	86.3	499	6	US-11-088-570-24
85	566	86.3	499	6	US-11-088-570-25
86	566	86.3	499	6	US-11-088-570-26
87	566	86.3	499	6	US-11-088-570-27
88	566	86.3	499	6	US-11-088-570-28
89	566	86.3	499	6	US-11-088-570-29
90	566	86.3	499	6	US-11-088-570-30
91	566	86.3	499	6	US-11-088-570-31
92	566	86.3	499	6	US-11-088-570-32
93	566	86.3	499	6	US-11-088-570-33
94	566	86.3	499	6	US-11-088-570-34
95	566	86.3	500	4	US-10-207-655-240
96	566	86.3	500	4	US-10-207-655-274
97	566	86.3	500	4	US-10-207-655-352
98	566	86.3	500	4	US-10-207-655-385
99	566	86.3	500	4	US-10-207-655-386
100	566	86.3	500	4	US-10-207-655-387

## ALIGNMENTS

```
RESULT 1
US-10-687-035-33
; Sequence 33, Application US/10687035
; Publication No. US20050064518A1
; GENERAL INFORMATION:
; APPLICANT: Albione, Earl F.
; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
; TITLE OF INVENTION: CA 125/0772P AND METHODS OF USE THEREOF
; FILE REFERENCE: 6750-214-999
; CURRENT APPLICATION NUMBER: US/10/687,035
; CURRENT FILING DATE: 2003-10-15
; PRIOR FILING DATE: 2003-07-10
; PRIOR FILING DATE: 2003-07-10
; PRIOR FILING DATE: 2003-10-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 776.1 light chain polypeptide variable region (776.1L)
US-10-687-035-33

Query Match      100.0%; Score 656; DB 5; Length 127;
Best Local Similarity 100.0%; Pred. No. 5.9e-49;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60
Db      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60

Qy      61 PGSSPKPWIYGTSTLASGVPTFRSGSGTSLTISRVEADAATYCCQWSSNPPTFG 120
Db      61 PGSSPKPWIYGTSTLASGVPTFRSGSGTSLTISRVEADAATYCCQWSSNPPTFG 120

Qy      121 SGTGLEI 127
Db      121 SGTGLEI 127

RESULT 2
US-10-723-003-38
; Sequence 38, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 54906200200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2003-11-25
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-723-003-38

Query Match      88.1%; Score 578; DB 5; Length 129;
Best Local Similarity 90.6%; Pred. No. 3.2e-42;
Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60
Db      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60

Qy      61 PGSSPKPWIYGTSTLASGVPTFRSGSGTSLTISRVEADAATYCCQWSSNPPTFG 120
Db      61 PGSSPKPWIYGTSTLASGVPTFRSGSGTSLTISRVEADAATYCCQWSSNPPTFG 120

Qy      121 SGTGLEI 127
Db      121 SGTGLEI 127

RESULT 3
US-11-004-639-38
; Sequence 38, Application US/11004639
; Publication No. US20050232931A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 54906200200
; CURRENT APPLICATION NUMBER: US/11/004,639
; CURRENT FILING DATE: 2004-12-02
; PRIOR FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2003-11-25
; PRIOR FILING DATE: 2003-11-25
; PRIOR FILING DATE: 2003-06-13
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-004-639-38

Query Match      88.1%; Score 578; DB 6; Length 129;
Best Local Similarity 90.6%; Pred. No. 3.2e-42;
Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60
Db      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60

Qy      61 PGSSPKPWIYGTSTLASGVPTFRSGSGTSLTISRVEADAATYCCQWSSNPPTFG 120
Db      61 PGSSPKPWIYGTSTLASGVPTFRSGSGTSLTISRVEADAATYCCQWSSNPPTFG 120

Qy      121 SGTGLEI 127
Db      121 SGTGLEI 127

RESULT 4
US-10-723-003-42
; Sequence 42, Application US/10723003
; Publication No. US20040254108A1
; GENERAL INFORMATION:
; APPLICANT: MA, Jing
; APPLICANT: GUO, Yajun
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
; FILE REFERENCE: 54906200200
; CURRENT APPLICATION NUMBER: US/10/723,003
; CURRENT FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2003-11-25
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-723-003-38

Query Match      88.1%; Score 578; DB 5; Length 129;
Best Local Similarity 90.6%; Pred. No. 3.2e-42;
Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60
Db      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60

Qy      61 PGSSPKPWIYGTSTLASGVPTFRSGSGTSLTISRVEADAATYCCQWSSNPPTFG 120
Db      61 PGSSPKPWIYGTSTLASGVPTFRSGSGTSLTISRVEADAATYCCQWSSNPPTFG 120

Qy      121 SGTGLEI 127
Db      121 SGTGLEI 127
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; PRIOR APPLICATION NUMBER: CN 031292909  
; PRIOR FILING DATE: 2003-06-13  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 42  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-723-003-42

Query Match 88.1%; Score 578; DB 5; Length 235;  
Best Local Similarity 90.6%; Pred. No. 5.9e-42;  
Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;  
QY 1 MDFQVQIFPSLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQK 60  
DB 1 MDFQVQIFPSLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWFQK 60  
QY 61 PGSSPKPMIYGTSLASGVPTFRSGSGGTSYSLTISRVEADAATYCCQWSSNPFTFG 120  
DB 61 PGSSPKPMIYATNSLASGVPTFRSGSGGTSYSLTISRVEADAATYCCQWTSNPFTFG 120  
QY 121 SGTKEI 127  
DB 121 GGTKEI 127

## RESULT 5

US-11-004-639-42  
; Sequence 42, Application US/11004639  
; Publication No. US20050232931A1  
; GENERAL INFORMATION:  
; APPLICANT: MA, Jing  
; APPLICANT: GUO, Yajun  
; TITLE OF INVENTION: PREPARATION AND APPLICATION OF  
; TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS  
; FILE REFERENCE: 54906200200  
; CURRENT APPLICATION NUMBER: US/11/004,639  
; CURRENT FILING DATE: 2004-12-02  
; PRIOR APPLICATION NUMBER: US/10/723,003  
; PRIOR FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: CN 2003101199300  
; PRIOR FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: CN 031292909  
; PRIOR FILING DATE: 2003-06-13  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 42  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-11-004-639-42

Query Match 88.1%; Score 578; DB 6; Length 235;  
Best Local Similarity 90.6%; Pred. No. 5.9e-42;  
Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;  
QY 1 MDFQVQIFPSLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQK 60  
DB 1 MDFQVQIFPSLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWFQK 60  
QY 61 PGSSPKPMIYGTSLASGVPTFRSGSGGTSYSLTISRVEADAATYCCQWSSNPFTFG 120  
DB 61 PGSSPKPMIYATNSLASGVPTFRSGSGGTSYSLTISRVEADAATYCCQWTSNPFTFG 120  
QY 121 SGTKEI 127  
DB 121 GGTKEI 127

## RESULT 6

US-09-905-928-4  
; Sequence 4, Application US/09905928  
; Publication No. US20030021781A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Leonard, John E.  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Reff, Mitchell E.  
; APPLICANT: Rastetter, William H.  
; TITLE OF INVENTION: Therapeutic Application of Chimeric and  
; TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted  
; TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell Lymphoma  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince St.  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/905,928  
; FILING DATE: 17-JUL-2001  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/475,813  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/149,099  
; FILING DATE: 03-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/978,891  
; FILING DATE: 13-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-158  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-905-928-4

Query Match 87.2%; Score 572; DB 3; Length 128;  
Best Local Similarity 89.8%; Pred. No. 1e-41;  
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MDFQVQIFPSLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQK 60  
DB 1 MDFQVQIFPSLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWFQK 60  
QY 61 PGSSPKPMIYGTSLASGVPTFRSGSGGTSYSLTISRVEADAATYCCQWSSNPFTFG 120  
DB 61 PGSSPKPMIYATNSLASGVPTFRSGSGGTSYSLTISRVEADAATYCCQWTSNPFTFG 120  
QY 121 SGTKEI 127  
DB 121 GGTKEI 127

RESULT 7  
US-10-096-964-4  
; Sequence 4, Application US/10096964  
; Publication No. US20030082172A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; Hanna, Nabil  
; Leonard, John E.  
; Newman, Roland A.  
; Reff, Mitchell E.  
; Rastetter, William H.  
; TITLE OF INVENTION: Therapeutic Application of Chimeric and  
; Radiolabeled Antibodies to Human B Lymphocyte Restricted  
; Differentiation Antigen for the Treatment of B-Cell Lymphoma  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince St.  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/096,964  
; FILING DATE: 14-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,813  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/149,099  
; FILING DATE: 03-NOV-1993  
; APPLICATION NUMBER: US 07/978,891  
; FILING DATE: 13-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-158  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-096-964-4

Query Match 87.2%; Score 572; DB 4; Length 128;  
Best Local Similarity 89.8%; Pred. No. 1e-41;  
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MDFQVQIFPSLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60  
DB 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQOK 60  
QY 61 PGSSPKPMIYGTSTLAGVPTFRFGSGSGTYSLTISRVEADAATYYCQWMSNPPTFG 120  
DB 61 PGSSPKPMIYATSNLASGVPVRFSGSGSGTYSLTISRVEADAATYYCQWTSNPPTFG 120  
QY 121 SGTKLEI 127  
DB 121 GGTKLEI 127

RESULT 8

US-10-238-681-7  
; Sequence 7, Application US/10238681  
; Publication No. US20030147885A1  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON, DARRELL R.  
; APPLICANT: HANNA, NABIL  
; APPLICANT: LEONARD, JOHN E.  
; APPLICANT: NEWMAN, ROLAND A.  
; APPLICANT: REFF, MITCHELL E.  
; APPLICANT: RASTETTER, WILLIAM H.  
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND RADIO-LABELED  
; ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED  
; DIFFERENTIATION ANTIGEN FOR TREATMENT OF B CELL  
; TITLE OF INVENTION: LYMPHOMA  
; FILE REFERENCE: 37003/0291808  
; CURRENT APPLICATION NUMBER: US/10/238,681  
; CURRENT FILING DATE: 2002-09-11  
; PRIOR APPLICATION NUMBER: 08/921,060  
; PRIOR FILING DATE: 1997-08-29  
; PRIOR APPLICATION NUMBER: 08/149,099  
; PRIOR FILING DATE: 1993-11-03  
; PRIOR APPLICATION NUMBER: 07/978,891  
; PRIOR FILING DATE: 1992-11-13  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Murine sp.  
US-10-238-681-7

Query Match 87.2%; Score 572; DB 4; Length 128;  
Best Local Similarity 89.8%; Pred. No. 1e-41;  
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MDFQVQIFPSLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60  
DB 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQOK 60  
QY 61 PGSSPKPMIYGTSTLAGVPTFRFGSGSGTYSLTISRVEADAATYYCQWMSNPPTFG 120  
DB 61 PGSSPKPMIYATSNLASGVPVRFSGSGSGTYSLTISRVEADAATYYCQWTSNPPTFG 120  
QY 121 SGTKLEI 127  
DB 121 GGTKLEI 127

RESULT 9  
US-10-411-037-60  
; Sequence 60, Application US/10411037  
; Publication No. US2004004346A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: DePree, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; APPLICANT: Bove, Caryn  
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA  
; GALACTOSIDASE A  
; FILE REFERENCE: 040853-01-5082  
; CURRENT APPLICATION NUMBER: US/10/411,037  
; CURRENT FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: US 60/328,523  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25

```

; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-037-60

Query Match      87.2%; Score 572; DB 4; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVVTTCRASSSVIYMCNQOK 60
Db 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVVTTCRASSSVIYHWFQOK 60
QY 61 PGSSPKPWYGTSTLASGVPTRPSGSGSGTSYSLTISRVEADAATYCCQWSSNPPTFG 120
Db 61 PGSSPKPWYATSNLASGVVPRFSGSGSGTSYSLTISRVEADAATYCCQWTSNPPTFG 120
QY 121 SGTKLEI 127
Db 121 GGTKLEI 127

RESULT 11
US-10-410-962-60
; Sequence 60, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-962-60

Query Match      87.2%; Score 572; DB 4; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVVTTCRASSSVIYMCNQOK 60
Db 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVVTTCRASSSVIYHWFQOK 60
QY 61 PGSSPKPWYGTSTLASGVPTRPSGSGSGTSYSLTISRVEADAATYCCQWSSNPPTFG 120
Db 61 PGSSPKPWYATSNLASGVVPRFSGSGSGTSYSLTISRVEADAATYCCQWTSNPPTFG 120
QY 121 SGTKLEI 127
Db 121 GGTKLEI 127

RESULT 12
US-10-411-049-60
; Sequence 60, Application US/10411049
; Publication No. US20040082026A1
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; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePree, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; CURRENT FILING DATE: 2003-04-09
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 60
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-411-049-60

Query Match      87.2%; Score 572; DB 4; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQOK 60
Qy 61 PGSSPKPWIIYGTSLASGVPRFSGSGSGTSYSLTISRVEADAATYYCQWTSNPPTFG 120
Db 61 PGSSPKPWIIYATSLASGVPRFSGSGSGTSYSLTISRVEADAATYYCQWTSNPPTFG 120
Qy 121 SGTKEI 127
Db 121 GGTKEI 127

RESULT 13
US-10-327-663-12
; Sequence 12, Application US/10327663
; Publication No. US20040093621A1
; GENERAL INFORMATION:
; APPLICANT: Kenya SHITARA
; APPLICANT: Mikiko SAKURADA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Mitsuo SATOH
; APPLICANT: Ryosuke NAKANO
; TITLE OF INVENTION: ANTIBODY COMPOSITION WHICH SPECIFICALLY BINDS TO CD20
; FILE REFERENCE: 249-289
; CURRENT APPLICATION NUMBER: US/10/327,663
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: JP 2001-392753
; PRIOR FILING DATE: 2001-12-25
; PRIOR APPLICATION NUMBER: JP 2002-106948
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: JP 2002-319975
; PRIOR FILING DATE: 2001-11-01

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; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 12
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-327-663-12

Query Match      87.2%; Score 572; DB 4; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQOK 60
Qy 61 PGSSPKPWIIYGTSLASGVPRFSGSGSGTSYSLTISRVEADAATYYCQWTSNPPTFG 120
Db 61 PGSSPKPWIIYATSLASGVPRFSGSGSGTSYSLTISRVEADAATYYCQWTSNPPTFG 120
Qy 121 SGTKEI 127
Db 121 GGTKEI 127

RESULT 14
US-10-410-930-60
; Sequence 60, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePree, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5056
; CURRENT APPLICATION NUMBER: US/10/410,930
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 60
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-410-930-60

Query Match      87.2%; Score 572; DB 4; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQOK 60
Qy 61 PGSSPKPWIIYGTSLASGVPRFSGSGSGTSYSLTISRVEADAATYYCQWTSNPPTFG 120
Db 61 PGSSPKPWIIYATSLASGVPRFSGSGSGTSYSLTISRVEADAATYYCQWTSNPPTFG 120
Qy 121 SGTKEI 127
Db 121 GGTKEI 127

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Db 61 PGSSPKWYATNSLGVPRFSGSGTYSLSITSRVEADAATYCCQWTSNPPTFG 120  
121 SGTGLEI 127  
122 GGTKLEI 127

RESULT 15  
US-10-410-997-60  
; Sequence 60, Application US/10410997  
; Publication No. US20040126838A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: Defrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; APPLICANT: Bove, Caryn  
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF  
; FILE REFERENCE: 040853-01-5059  
; CURRENT APPLICATION NUMBER: US/10/410,997  
; CURRENT FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: US 60/328,523  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 60  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-410-997-60

Query Match 87.2%; Score 572; DB 4; Length 128;  
Best Local Similarity 89.8%; Pred. No. 1e-41;  
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MDFQVQIFPFLILISASVIMSRGOIVLSQSPAILFASPGETVTTTCRASSSVIYMCWNOOK 60  
Db 1 MDFQVQIISFLILISASVIMSRGOIVLSQSPAILFASPGETVTTTCRASSSVIYHWFQOK 60  
QY 61 PGSSPKWYATNSLGVPRFSGSGTYSLSITSRVEADAATYCCQWTSNPPTFG 120  
Db 61 PGSSPKWYATNSLGVPRFSGSGTYSLSITSRVEADAATYCCQWTSNPPTFG 120  
QY 121 SGTGLEI 127  
122 GGTKLEI 127

RESULT 16  
US-10-411-012-60  
; Sequence 60, Application US/10411012  
; Publication No. US20040132640A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: Defrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert

; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; APPLICANT: Bove, Caryn  
; TITLE OF INVENTION: GLYCOPERylation METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE  
; FILE REFERENCE: 040853-01-5051  
; CURRENT APPLICATION NUMBER: US/10/411,012  
; CURRENT FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: US 60/328,523  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 60  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-411-012-60

Query Match 87.2%; Score 572; DB 4; Length 128;  
Best Local Similarity 89.8%; Pred. No. 1e-41;  
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MDFQVQIFPFLILISASVIMSRGOIVLSQSPAILFASPGETVTTTCRASSSVIYMCWNOOK 60  
Db 1 MDFQVQIISFLILISASVIMSRGOIVLSQSPAILFASPGETVTTTCRASSSVIYHWFQOK 60  
QY 61 PGSSPKWYATNSLGVPRFSGSGTYSLSITSRVEADAATYCCQWTSNPPTFG 120  
Db 61 PGSSPKWYATNSLGVPRFSGSGTYSLSITSRVEADAATYCCQWTSNPPTFG 120  
QY 121 SGTGLEI 127  
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RESULT 17  
US-10-287-994-60  
; Sequence 60, Application US/10287994  
; Publication No. US20040137557A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: Defrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Bove, Caryn  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES  
; FILE REFERENCE: 040853-01-5052-00  
; CURRENT APPLICATION NUMBER: US/10/287,994  
; CURRENT FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 60/328,523  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17

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; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 128
; TYPE: PR
; ORGANISM: Mus musculus
US-10-287-994-60

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Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

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Qy 61 PGSSPKPMIYGTSTLASGVPTFRFSGSGSGTSYSLTISRVEADAATYTCQWSSNPPTFG 120
Db 61 PGSSPKPMIYATNLAGVPVRFSGSGSGTSYSLTISRVEADAATYTCQWSSNPPTFG 120
Qy 121 SGTKLEI 127
Db 121 GGTKLEI 127

RESULT 19
US-10-410-980-60
; Sequence 60, Application US/10410980
; Publication No. US20050031584A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: INTERLEUKIN-2: REMODELING AND GLYCOCONJUGATION OF IL-2
; FILE REFERENCE: 040853-01-5066
; CURRENT APPLICATION NUMBER: US/10/410,980
; PRIOR FILING DATE: 2003-04-09
; PRIOR FILING DATE: 2001-10-10
; PRIOR FILING DATE: 2001-10-10
; PRIOR FILING DATE: 2001-10-19
; PRIOR FILING DATE: 2002-06-07
; PRIOR FILING DATE: 2002-06-25
; PRIOR FILING DATE: 2002-07-17
; PRIOR FILING DATE: 2002-07-17
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 128
; TYPE: PR
; ORGANISM: Mus musculus
US-10-410-980-60

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Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

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Db 61 PGSSPKPMIYATNLAGVPVRFSGSGSGTSYSLTISRVEADAATYTCQWSSNPPTFG 120
Qy 121 SGTKLEI 127
Db 121 GGTKLEI 127

RESULT 20
US-10-410-997-60
; Sequence 60, Application US/10410897
; Publication No. US20050100982A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
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; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: FACTOR IX; REMODELING AND GLYCOCONJUGATION OF FACTOR IX
; FILE REFERENCE: 040853-01-5058
; CURRENT APPLICATION NUMBER: US/10/410,897
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-897-60

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Query Match      87.2%; Score 572; DB 5; Length 128;
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Qy      61 PGSSPKPWIIYGTSTLASGVPTFRSGSGGTSYSLTISRVEAEDAATYCCQWSSNPPTFG 120
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Qy      121 SGTKLEI 127
Db      121 GGTKLEI 127

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:30:27 ; Search time 6.76331 Seconds  
(without alignments)  
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**Title:** US-10-687-035-33

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

**Listing first 100 summaries**

Database : Issued Patents AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	572	87.2	128	2	US-08-475-8158-7	Sequence 7, Appl	
3	572	87.2	128	2	US-08-475-813-4	Sequence 4, Appl	
4	566	86.3	128	2	US-09-724-138-46	Sequence 46, Appl	
5	566	86.3	128	2	US-09-630-198-46	Sequence 46, Appl	
6	559	85.2	129	1	US-08-449-287-2	Sequence 2, Appl	
7	559	85.2	235	2	US-09-423-439-18	Sequence 18, Appl	
8	559	85.2	235	2	US-09-423-439-58	Sequence 58, Appl	
9	559	85.2	235	2	US-09-011-769A-23	Sequence 23, Appl	
10	558	85.1	235	2	US-09-238-741-2	Sequence 2, Appl	
11	548	83.5	128	2	US-08-619-491-2	Sequence 2, Appl	
12	548	83.5	128	4	PCT-US95-07302-2	Sequence 2, Appl	
13	543	82.8	128	1	US-07-946-421-26	Sequence 26, Appl	
14	543	82.8	235	1	US-08-303-569B-5	Sequence 5, Appl	
15	543	82.8	235	1	US-08-116-247-5	Sequence 5, Appl	
16	543	82.8	235	2	US-09-795-515-5	Sequence 5, Appl	
17	543	82.8	235	2	US-09-348-224-5	Sequence 5, Appl	
18	532	81.1	129	1	US-08-116-778B-2	Sequence 2, Appl	
19	532	81.1	129	1	US-08-438-562-2	Sequence 2, Appl	
20	532	81.1	129	1	US-08-483-528B-92	Sequence 92, Appl	
21	531	80.9	128	1	US-08-656-586-2	Sequence 2, Appl	
22	524	79.9	128	1	US-07-634-278-31	Sequence 31, Appl	
23	524	79.9	128	1	US-08-477-728-31	Sequence 31, Appl	
24	524	79.9	128	1	US-08-474-040-31	Sequence 31, Appl	
25	524	79.9	128	1	US-08-477-200-31	Sequence 31, Appl	
26	524	79.9	128	2	US-08-484-537-31	Sequence 31, Appl	
27	524	79.9	235	2	US-09-910-053-17	Sequence 17, Appl	

## ALIGNMENTS

RESULT 1  
US-08-476-275-4  
; Sequence 4, Application US/08476275  
; Patent No. 5776456  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Leonard, John E.  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Reff, Mitchell E.  
; APPLICANT: Rastetter, William H.  
; TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted  
; TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell  
; TITLE OF INVENTION: Lymphoma  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince St.  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,275  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/149,099  
; FILING DATE: 03-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/978,891  
; FILING DATE: 13-NOV-1992  
; NAME: Teskin, Robin L.  
; ATTORNEY/AGENT INFORMATION:  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-155  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-476-275-4

Query Match 87.2%; Score 572; DB 1; Length 128;  
Best Local Similarity 89.8%; Pred. No. 3.2e-50;  
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
  
Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60  
Db 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQOK 60  
  
Qy 61 PGSSPKPWYGTSTLASGVPFRFGSGSGTYSYLSITSRVEADAATYTCQOWSNPPTFG 120  
Db 61 PGSSPKPWYATSNLASGVPFRFGSGSGTYSYLSITSRVEADAATYTCQOWSNPPTFG 120  
  
Qy 121 SGTKEI 127  
Db 121 GGTKEI 127

RESULT 2  
US-08-475-815B-7  
; Sequence 7, Application US/08475815B  
; Patent No. 6399061  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON, DARRELL R.  
; APPLICANT: HANNA, NABIL  
; APPLICANT: LEONARD, JOHN E.  
; APPLICANT: NEWMAN, ROLAND A.  
; APPLICANT: REFF, MITCHELL E.  
; APPLICANT: RASTETTER, WILLIAM H.  
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND  
; TITLE OF INVENTION: RADIO LABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED  
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL  
; TITLE OF INVENTION: LYMPHOMA  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY WINTHROP  
; STREET: 1100 New York Avenue, N.W., Ninth FL.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,815B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/149,099  
; FILING DATE: 03-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/978,891  
; FILING DATE: 13-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 23522-0157  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-475-815B-7

Query Match 87.2%; Score 572; DB 2; Length 128;  
Best Local Similarity 89.8%; Pred. No. 3.2e-50;  
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
  
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Db 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQOK 60  
  
Qy 61 PGSSPKPWYGTSTLASGVPFRFGSGSGTYSYLSITSRVEADAATYTCQOWSNPPTFG 120  
Db 61 PGSSPKWYATSNLASGVPFRFGSGSGTYSYLSITSRVEADAATYTCQOWSNPPTFG 120  
  
Qy 121 SGTKEI 127  
Db 121 GGTKEI 127

RESULT 3

US-08-475-813-4  
; Sequence 4, Application US/08475813  
; Patent No. 6682734  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Leonard, John E.  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Reff, Mitchell E.  
; APPLICANT: Rastetter, William H.  
; TITLE OF INVENTION: Therapeutic Application of Chimeric and  
; Radiolabeled Antibodies to Human B Lymphocyte Restricted  
; Differentiation Antigen for the Treatment of B-Cell Lymphoma  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince St.  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,813  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/149,099  
; FILING DATE: 03-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/978,891  
; FILING DATE: 13-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-158  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-475-813-4

Query Match 87.2%; Score 572; DB 2; Length 128;  
Best Local Similarity 89.8%; Pred. No. 3.2e-50;  
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MDPQVOIFSLISASVIMSRGOIVLSQSPAILFASPGETVTTWCRTASSSVIYMCWNQOK 60  
Db 1 MDPQVOIFSLISASVIMSRGOIVLSQSPAILFASPGETVTTWCRTASSSVIYHFWQOK 60  
QY 61 PGSSPKPWIYGTSLASGVPTFRFSGSGSGTSYSLTISRVEADAATYCCQWSSNPPTFG 120  
Db 61 PGSSPKPWIYATSNLGSVPFRFSGSGSGTSYSLTISRVEADAATYCCQWSSNPPTFG 120  
QY 121 SGTKLEI 127  
Db 121 GGTKLEI 127

RESULT 4  
US-09-724-138-46  
; Sequence 46, Application US/09724138  
; Patent No. 6652852  
; GENERAL INFORMATION:

; APPLICANT: Robinson, Randy  
; APPLICANT: Liu, Alvin  
; APPLICANT: Ledbetter, Jeffrey  
; TITLE OF INVENTION: Chimeric Antibody with Specificity to Human B Cell Surface Anti-  
; FILE REFERENCE: PPL-001CN2  
; CURRENT APPLICATION NUMBER: US/09/724,138  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/630198  
; PRIOR FILING DATE: 2000-08-01  
; PRIOR APPLICATION NUMBER: US 09/021934  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: US 08/471984  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: US 07/665939  
; PRIOR FILING DATE: 1991-03-05  
; PRIOR APPLICATION NUMBER: US 07/195961  
; PRIOR FILING DATE: 1988-05-13  
; PRIOR APPLICATION NUMBER: US 07/016202  
; PRIOR FILING DATE: 1987-01-08  
; PRIOR APPLICATION NUMBER: PCT/US86/02269  
; PRIOR FILING DATE: 1986-10-27  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 46  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-724-138-46

Query Match 86.3%; Score 566; DB 2; Length 128;  
Best Local Similarity 88.2%; Pred. No. 1.3e-49;  
Matches 112; Conservative 4; Mismatches 11; Indels 0; Gaps 0;  
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Db 61 PGSSPKPWIYATSNLGSVPFRFSGSGSGTSYSLTISRVEADAATYCCQWSSNPPTFG 120  
QY 121 SGTKLEI 127  
Db 121 AGTKLEI 127

RESULT 5  
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; Sequence 46, Application US/09630198  
; Patent No. 6893625  
; GENERAL INFORMATION:  
; APPLICANT: Robinson, Randy  
; APPLICANT: Liu, Alvin  
; APPLICANT: Ledbetter, Jeffrey  
; TITLE OF INVENTION: Chimeric Antibody with Specificity to Human B Cell Surface Anti-  
; FILE REFERENCE: PPL-001CN  
; CURRENT APPLICATION NUMBER: US/09/630,198  
; CURRENT FILING DATE: 2000-08-01  
; PRIOR APPLICATION NUMBER: US 09/021934  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: US 08/471984  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: US 07/665939  
; PRIOR FILING DATE: 1991-03-05  
; PRIOR APPLICATION NUMBER: US 07/195961  
; PRIOR FILING DATE: 1988-05-13  
; PRIOR APPLICATION NUMBER: US 07/016202  
; PRIOR FILING DATE: 1987-01-08  
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; PRIOR FILING DATE: 1986-10-27  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 46

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; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-630-198-46

Query Match      86.3%; Score 566; DB 2; Length 128;
Best Local Similarity 88.2%; Pred. No. 1.3e-49;
Matches 112; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60
DB 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60
QY 61 PGSSPKPWIVGTSTLASGVPTFRSGSGGTSYSLTISRVEADAATYTCQWSSNPPTFG 120
DB 61 PGSSPKPWIVGTSTLASGVPTFRSGSGGTSYSLTISRVEADAATYTCQWSSNPPTFG 120
QY 121 SGTKLEI 127
DB 121 AGTKLEL 127

RESULT 6
US-08-449-287-2
; Sequence 2, Application US/08449287
; Patent No. 5877293
; GENERAL INFORMATION:
; APPLICANT: ADAIR, John Robert
; APPLICANT: BODMER, Mark William
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
; TITLE OF INVENTION: Their Production
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,287
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/154,389
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB91/01108
; FILING DATE: 05-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9014932.9
; FILING DATE: 05-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT GB90/02017
; FILING DATE: 21-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/110 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-449-287-2

Query Match      85.2%; Score 559; DB 1; Length 129;
Best Local Similarity 88.2%; Pred. No. 6.6e-49;
Matches 112; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60
DB 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60
QY 61 PGSSPKPWIVGTSTLASGVPTFRSGSGGTSYSLTISRVEADAATYTCQWSSNPPTFG 120
DB 61 PGSSPKPWIVGTSTLASGVPTFRSGSGGTSYSLTISRVEADAATYTCQWSSNPPTFG 120
QY 121 SGTKLEI 127
DB 121 GGTKLEI 127

RESULT 7
US-09-423-439-18
; Sequence 18, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423 439
; FILING DATE: 09-No. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-423-439-18

Query Match      85.2%; Score 559; DB 2; Length 235;
Best Local Similarity 88.2%; Pred. No. 1.4e-48;
Matches 112; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60
DB 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVMTTCRASSSVIYMCWNQOK 60
QY 61 PGSSPKPWIVGTSTLASGVPTFRSGSGGTSYSLTISRVEADAATYTCQWSSNPPTFG 120
DB 61 PGSSPKPWIVGTSTLASGVPTFRSGSGGTSYSLTISRVEADAATYTCQWSSNPPTFG 120
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Qy 121 SGTKEI 127  
Db 121 GGTKEI 127

## RESULT 8

US-09-423-439-58  
; Sequence 58, Application US/09423439  
; Patent No. 6339070  
; GENERAL INFORMATION:  
; APPLICANT: EMERY, Stephen Charles  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Winthrop, L.L.P.  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/423.439  
; FILING DATE: 09-May-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB98/01294  
; FILING DATE: 05-MAY-1998  
; APPLICATION NUMBER: GB 9709421.3  
; FILING DATE: 10-MAY-1997  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 235 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:  
US-09-423-439-58

Query Match 85.2%; Score 559; DB 2; Length 235;  
Best Local Similarity 88.2%; Pred. No. 1.4e-48;  
Matches 112; Conservative 1; Mismatches 14; Indels 0; Gaps 0;  
Qy 1 MDPQVQIFSPFLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQK 60  
Db 1 MDPQVQIFSPFLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWYQK 60  
Qy 61 PGSSPKRWIYGTSLASGVTPRFGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120  
Db 61 PGSSPKRWIYATNLASGVTPRFGSGSGTSYSLTISRVEADAATYCCQWSSKPFTFG 120  
Qy 121 SGTKEI 127  
Db 121 GGTKEI 127

## RESULT 9

US-09-011-769A-23  
; Sequence 23, Application US/09011769A  
; Patent No. 6436691  
; GENERAL INFORMATION:  
; APPLICANT: SLATER, Anthony M.  
; BLAKEY, David C.  
; DAVIES, David H.  
; HENNAM, John F.  
; HENNEQUIN, Laurent F.A.  
; MARSHAW, Peter R.  
; DOWELL, Robert I.

; TITLE OF INVENTION: Chemical Compounds  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pillsbury Madison & Sutro, LLP  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 1.44 Mb disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/011.769A  
; FILING DATE: 13-Feb-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB96/01975  
; FILING DATE: 13-AUG-1996  
; APPLICATION NUMBER: GB 9612295.7  
; FILING DATE: 12-JUN-1996  
; APPLICATION NUMBER: GB 9611019.2  
; FILING DATE: 25-MAY-1996  
; APPLICATION NUMBER: GB 9516810.0  
; FILING DATE: 16-AUG-1995  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 235 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-011-769A-23

Query Match 85.2%; Score 559; DB 2; Length 235;  
Best Local Similarity 88.2%; Pred. No. 1.4e-48;  
Matches 112; Conservative 1; Mismatches 14; Indels 0; Gaps 0;  
Qy 1 MDPQVQIFSPFLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQK 60  
Db 1 MDPQVQIFSPFLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWYQK 60  
Qy 61 PGSSPKRWIYGTSLASGVTPRFGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120  
Db 61 PGSSPKRWIYATNLASGVTPRFGSGSGTSYSLTISRVEADAATYCCQWSSKPFTFG 120  
Qy 121 SGTKEI 127  
Db 121 GGTKEI 127  
RESULT 10  
US-09-238-741-2  
; Sequence 2, Application US/09238741  
; Patent No. 6897044  
; GENERAL INFORMATION:  
; APPLICANT: BRASLAWSKY, GARY R.  
; APPLICANT: HANNA, NABIL  
; APPLICANT: HARIHARAN, KANDASAMY  
; APPLICANT: LABAREE, MICHAEL J.  
; APPLICANT: HUYNH, TRI B.  
; TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES  
; FILE REFERENCE: 23522.0584  
; CURRENT APPLICATION NUMBER: US/09/238.741  
; CURRENT FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: "Dimeric" Anti-CD20 Light Chain (Version 1)
US-09-238-741-2

Query Match      85.1%; Score 558; DB 2; Length 235;
Best Local Similarity 88.2%; Pred. No. 1.7e-48;
Matches 112; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILPASGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILPASGPKVTMTCRASSSVIYHWFQOK 60

Qy 61 PGSSPKWIYGTSTLASGVTRFSGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120
Db 61 PGSSPKWIYATSNLASGVTRFSGSGSGTSYSLTISRVEADAATYCCQWTSNPFTFG 120

Qy 121 SGTKLEI 127
Db 121 GGAKLEI 127

RESULT 11
US-08-619-491-2
; Sequence 2, Application US/08619491
; Patent No. 6210670
; GENERAL INFORMATION:
; APPLICANT: Berg, Ellen L.
; TITLE OF INVENTION: Cross-Reacting Monoclonal Antibodies
; TITLE OF INVENTION: Specific for E-Selectin and P-Selectin
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/619,491
; FILING DATE: 26-MAR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: WO PCT/US95/07302
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/259,963
; FILING DATE: 14-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 011823-005810US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-619-491-2

Query Match      83.5%; Score 548; DB 2; Length 128;
Best Local Similarity 85.8%; Pred. No. 8.4e-48;
Matches 109; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILPASGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILPASGPKVTMTCRASSSVIYHWFQOK 60

Qy 61 PGSSPKWIYGTSTLASGVTRFSGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120
Db 61 PGSSPKWIYATSNLASGVTRFSGSGSGTSYSLTISRVEADAATYCCQWTSNPFTFG 120

Qy 121 SGTKLEI 127
Db 121 GGAKLEI 127

RESULT 12
PCT-US95-07302-2
; Sequence 2, Application PC/TUS9507302
; GENERAL INFORMATION:
; APPLICANT: Berg, Ellen L.
; TITLE OF INVENTION: Cross-Reacting Monoclonal Antibodies
; TITLE OF INVENTION: Specific for E-Selectin and P-Selectin
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: PCT/US95/07302
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/259,963
; FILING DATE: 14-JUNE-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-005810PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-07302-2

Query Match      83.5%; Score 548; DB 4; Length 128;
Best Local Similarity 85.8%; Pred. No. 8.4e-48;
Matches 109; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILPASGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILPASGPKVTMTCRASSSVIYHWFQOK 60

Qy 61 PGSSPKWIYGTSTLASGVTRFSGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120
Db 61 PGSSPKWIYATSNLASGVTRFSGSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120

Qy 121 SGTKLEI 127
Db 121 SGTKLEI 127

RESULT 13
US-07-946-421-26
```

CORRESPONDENCE ADDRESS:  
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 58592052ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/303.569B  
APPLICATION NUMBER: US/08/303.569B  
FILING DATE: 07-SEP-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Trujillo, Doreen Yanko  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CARP-0032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-303-569B-5

Query Match 82.8%; Score 543; DB 1; Length 235;  
Best Local Similarity 85.0%; Pred. No. 5.7e-47;  
Matches 108; Conservative 5; Mismatches 14; Indels 0; Gaps 0

Qy	1	MDFOVQIFSELLISASVIMRGQIVLSQSPAILFPASGETVTMTCRASSSVIYMCWNOOK	60
Db	1	MDFOVQIFSELLISASVIMRGQIVLSQSPAILFPASGETVTMTCRASSSVIYMCWNOOK	60
Qy	61	PGSPKPKWIVGTSTLASGVPTFRPSGSGSGSYSLTISRVEAEDATYYCCQWSSNPFTFG	120
Db	61	SGTSPKRWIVDTSKLASGVPAHFRGSGSGSYSLTISRVEAEDATYYCCQWSSNPFTFG	120
Qy	121	SGTKLEI 127	
Db	121	SGTKLEI 127	

RESULT 15  
US-08-116-247-5  
Sequence 5, Application US/08116247  
Patent No. 5929212  
GENERAL INFORMATION:  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Zivin, Robert A.  
APPLICANT: Adair, John R.  
APPLICANT: Athwal, Diljeet S.  
TITLE OF INVENTION: CD3 Specific Recombinant Antibody  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5859212ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/116.247

;; FILING DATE: 435  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/743,377  
;; FILING DATE: 10-OCT-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Paintin, Francis A.  
;; REGISTRATION NUMBER: 19,386  
;; REFERENCE/DOCKET NUMBER: CARP-0011  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 568-3100  
;; TELEFAX: (215) 568-3439  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 235 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-116-247-5

Query Match 82.8%; Score 543; DB 1; Length 235;  
Best Local Similarity 85.0%; Pred. No. 5.7e-47;  
Matches 108; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60  
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCSASSSVIYNNWYQOK 60  
Qy 61 PGSSPKPWYGTSTLASGVPTFRFGSGSGTYSYLSITISRVEADAATYYCQWSSNPPTFG 120  
Db 61 SGTSPKRWIYDTSKLASGVPAHFRGSGSGTYSYLSITISGMEADAATYYCQWSSNPPTFG 120  
Qy 121 SGTKLEI 127  
Db 121 SGTKLEI 127

## RESULT 16

US-09-795-515-5  
; Sequence 5, Application US/09795515  
; Patent No. 6632927  
; GENERAL INFORMATION:  
; APPLICANT: Adair, John R.  
; APPLICANT: Athwal, Diljeet S.  
; APPLICANT: Emage, John S.  
; TITLE OF INVENTION: Humanised Antibodies  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6632927ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/795,515  
;; FILING DATE:

;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/846,658  
;; FILING DATE: 01-MAY-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Trujillo, Doreen Yanko  
;; REGISTRATION NUMBER: 35,719  
;; REFERENCE/DOCKET NUMBER: CARP-0057  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 568-3100  
;; TELEFAX: (215) 568-3439

;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 235 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-09-795-515-5

Query Match 82.8%; Score 543; DB 2; Length 235;  
Best Local Similarity 85.0%; Pred. No. 5.7e-47;  
Matches 108; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60  
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCSASSSVIYNNWYQOK 60  
Qy 61 PGSSPKPWYGTSTLASGVPTFRFGSGSGTYSYLSITISRVEADAATYYCQWSSNPPTFG 120  
Db 61 SGTSPKRWIYDTSKLASGVPAHFRGSGSGTYSYLSITISGMEADAATYYCQWSSNPPTFG 120  
Qy 121 SGTKLEI 127  
Db 121 SGTKLEI 127

## RESULT 17

US-09-348-224-5  
; Sequence 5, Application US/09348224  
; Patent No. 6750325  
; GENERAL INFORMATION:  
; APPLICANT: Jollieffe, Linda Kay  
; APPLICANT: Zivin, Robert Allan  
; APPLICANT: Adair, John Robert  
; APPLICANT: Athwal, Diljeet Singh  
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody  
; FILE REFERENCE: CARP0066  
; CURRENT APPLICATION NUMBER: US/09/348,224  
; CURRENT FILING DATE: 1999-07-06  
; EARLIER APPLICATION NUMBER: 08/116,247  
; EARLIER FILING DATE: 1993-09-03  
; EARLIER APPLICATION NUMBER: 07/743,377  
; EARLIER FILING DATE: 1991-10-04  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-348-224-5

Query Match 82.8%; Score 543; DB 2; Length 235;  
Best Local Similarity 85.0%; Pred. No. 5.7e-47;  
Matches 108; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60  
Db 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCSASSSVIYNNWYQOK 60  
Qy 61 PGSSPKPWYGTSTLASGVPTFRFGSGSGTYSYLSITISRVEADAATYYCQWSSNPPTFG 120  
Db 61 SGTSPKRWIYDTSKLASGVPAHFRGSGSGTYSYLSITISGMEADAATYYCQWSSNPPTFG 120  
Qy 121 SGTKLEI 127  
Db 121 SGTKLEI 127

## RESULT 18

US-08-116-778B-2  
; Sequence 2, Application US/08116778E  
; Patent No. 5830470  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, KAZUYASU



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; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 88..96
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
; US-08-438-562-2

Query Match      81.1%; Score 532; DB 1; Length 129;
Best Local Similarity 84.3%; Pred. No. 3.5e-46;
Matches 107; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQOK 60
Db 1 MHFQVQIFSFLLISASVIMSRGQIVLTQSPAIMSASPGKVTITCSASSSVSYMHWFQOK 60
Qy 61 PGSPKPMIYGTSTLASGVPTFRFSGSGSGTSYSLTISRVEAEDAATYYCQWSSNPFTFG 120
Db 61 PGTSPLMIYSTNLASGVTPARFSGSGSGTSYSLTISRMEADAATYYCQORSYPYTFG 120
Qy 121 SGTKEI 127
Db 121 GGTKEI 127

RESULT 20
US-08-483-528B-92
; Sequence 92, Application US/08483528B
; Patent No. 5939532
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, NAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08483,528B
; FILING DATE: 07-JUN-95
; CLASSIFICATION: 536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -22...-1
; IDENTIFICATION METHOD: BY SIMILARITY WITH KNOWN SEQUENCE TO TO AN
; IDENTIFICATION METHOD: ESTABLISHED CONSENSUS
; FEATURE:
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; NAME/KEY: domain
; LOCATION: 24..33
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 49..55
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
; FEATURE:
; NAME/KEY: domain
; LOCATION: 88..96
; IDENTIFICATION METHOD: BY SIMILARITY
; IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
; IDENTIFICATION METHOD: CONSENSUS
; OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
; US-08-483-528B-92

Query Match      81.1%; Score 532; DB 1; Length 129;
Best Local Similarity 84.3%; Pred. No. 3.5e-46;
Matches 107; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

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Db 1 MHFQVQIFSFLLISASVIMSRGQIVLTQSPAIMSASPGKVTITCSASSSVSYMHWFQOK 60
Qy 61 PGSPKPMIYGTSTLASGVPTFRFSGSGSGTSYSLTISRVEAEDAATYYCQWSSNPFTFG 120
Db 61 PGTSPLMIYSTNLASGVTPARFSGSGSGTSYSLTISRMEADAATYYCQORSYPYTFG 120
Qy 121 SGTKEI 127
Db 121 GGTKEI 127

Search completed: March 20, 2006, 07:31:34
Job time : 7.76331 secs
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:28:19 ; Search time 45.9655 Seconds  
(without alignments)  
1213.978 Million cell updates/sec

Title: US-10-687-035-33

Perfect score: 656

Sequence: 1 MDPQVQIFSLISASVIMS.....YCOQWSNPFTFGSGTKLEI 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq\_21.\*

- 1: Geneseqp1990s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	656	100.0	127	8	ADS94334
2	579	88.3	145	2	AAR15323
3	579	88.3	145	2	AAR32127
4	578	88.1	129	9	ADV22494
5	578	88.1	129	9	ADV98557
6	578	88.1	235	9	ADV92498
7	578	88.1	235	9	ADV98561
8	572	87.2	128	2	AAR55214
9	572	87.2	128	6	ABR55872
10	572	87.2	128	6	ABU08393
11	572	87.2	128	7	ADC66268
12	572	87.2	128	7	ADB85686
13	572	87.2	128	7	ADE73083
14	572	87.2	128	7	ADF60660
15	572	87.2	128	8	ADN49732
16	572	87.2	128	8	ADU74408
17	572	87.2	128	9	ADZ59908
18	572	87.2	235	5	AAE27925
19	572	87.2	235	6	ABB82834
20	567	86.4	500	9	ADY21925
21	566	86.3	128	1	AAAP70628
22	566	86.3	128	1	AAAP94781
23	566	86.3	128	2	AAW10243
24	566	86.3	128	2	AAW10589

25	566	86.3	128	2	AAW16344	Aaw16344 2H7 light
26	566	86.3	128	2	AAW41071	Aaw41071 Mouse 2H7
27	566	86.3	128	2	AAW47514	Aaw47514 Mouse 2H7
28	566	86.3	128	2	AAW47521	Aaw47521 Mouse 2H7
29	566	86.3	128	2	AAW89541	Aaw89541 Mouse ant
30	566	86.3	128	4	AAW89093	Aaw89093 2H7 light
31	566	86.3	128	7	ADC65029	Adc65029 Immunoglo
32	566	86.3	266	5	ABG31021	Abg31021 Mouse sin
33	566	86.3	266	7	ADD25450	Add25450 Binding d
34	566	86.3	266	7	ADM42725	Adm42725 Synthetic
35	566	86.3	266	9	ABE95393	Aeb95393 Mouse 2H7
36	566	86.3	266	9	ABE94427	Aeb94427 Mouse ant
37	566	86.3	267	9	ADY21839	Ady21839 Human ant
38	566	86.3	268	9	ADY21869	Ady21869 Human ant
39	566	86.3	268	9	ADY21837	Ady21837 Human ant
40	566	86.3	422	5	ABG31032	Abg31032 Synthetic
41	566	86.3	422	7	ADD25591	Add25591 Binding d
42	566	86.3	422	7	ADD25473	Add25473 Binding d
43	566	86.3	422	7	ADM42748	Adm42748 2H7scfv-C
44	566	86.3	422	9	ABE95416	Aeb95416 Mouse 2H7
45	566	86.3	422	9	ABE94450	Aeb94450 Mouse ant
46	566	86.3	426	9	ADY22144	Ady22144 Antibody
47	566	86.3	426	9	ABE95423	Aeb95423 Mouse 2H7
48	566	86.3	426	9	ABE94457	Aeb94457 Mouse ant
49	566	86.3	482	5	ABG31031	Abg31031 Synthetic
50	566	86.3	482	7	ADD25472	Add25472 Binding d
51	566	86.3	482	7	ADD25589	Add25589 Binding d
52	566	86.3	482	7	ADM42747	Adm42747 2H7-CD154
53	566	86.3	482	9	ABE95415	Aeb95415 Mouse 2H7
54	566	86.3	482	9	ABE94449	Aeb94449 Mouse ant
55	566	86.3	486	9	ADY22142	Ady22142 Antibody
56	566	86.3	486	9	ABE95425	Aeb95425 Mouse 2H7
57	566	86.3	486	9	ABE94456	Aeb94456 Mouse ant
58	566	86.3	498	7	ADD25674	Add25674 Binding d
59	566	86.3	498	9	ADY21647	Ady21647 Antibody
60	566	86.3	499	5	ABG31026	Abg31026 Synthetic
61	566	86.3	499	5	ABG31027	Abg31027 Synthetic
62	566	86.3	499	5	ABG31025	Abg31025 Synthetic
63	566	86.3	499	7	ADD25587	Add25587 Binding d
64	566	86.3	499	7	ADD25454	Add25454 Binding d
65	566	86.3	499	7	ADD25456	Add25456 Binding d
66	566	86.3	499	7	ADD25455	Add25455 Binding d
67	566	86.3	499	7	ADM42731	Adm42731 2H7scfv-I
68	566	86.3	499	7	ADM42729	Adm42729 2H7scfv-I
69	566	86.3	499	7	ADM42730	Adm42730 2H7scfv-I
70	566	86.3	499	9	ABE95397	Aeb95397 Mouse hum
71	566	86.3	499	9	ABE95398	Aeb95398 Mouse hum
72	566	86.3	499	9	ABE95399	Aeb95399 Mouse hum
73	566	86.3	499	9	ABE94431	Aeb94431 Mouse ant
74	566	86.3	499	9	ABE94433	Aeb94433 Mouse ant
75	566	86.3	499	9	ABE94432	Aeb94432 Mouse ant
76	566	86.3	500	7	ADD25826	Add25826 Binding d
77	566	86.3	500	7	ADD25837	Add25837 Binding d
78	566	86.3	500	7	ADD25713	Add25713 Binding d
79	566	86.3	500	7	ADD25836	Add25836 Binding d
80	566	86.3	500	7	ADD25824	Add25824 Binding d
81	566	86.3	500	7	ADD25827	Add25827 Binding d
82	566	86.3	500	7	ADD25835	Add25835 Binding d
83	566	86.3	500	7	ADD25828	Add25828 Binding d
84	566	86.3	500	7	ADD25825	Add25825 Binding d
85	566	86.3	500	7	ADD25679	Add25679 Binding d
86	566	86.3	500	7	ADD25791	Add25791 Binding d
87	566	86.3	500	9	ADY21783	Ady21783 Antibody
88	566	86.3	500	9	ADY21891	Ady21891 Antibody
89	566	86.3	500	9	ADY21764	Ady21764 Antibody
90	566	86.3	500	9	ADY21793	Ady21793 Antibody
91	566	86.3	500	9	ADY21915	Ady21915 Antibody
92	566	86.3	500	9	ADY21997	Ady21997 Antibody
93	566	86.3	500	9	ADY21787	Ady21787 Antibody
94	566	86.3	500	9	ADY21931	Ady21931 Antibody
95	566	86.3	500	9	ADY21993	Ady21993 Antibody
96	566	86.3	500	9	ADY21683	Ady21683 Antibody
97	566	86.3	500	9	ADY21785	Ady21785 Antibody

98 566 86.3 500 9 ADY21789 Antibody  
99 566 86.3 500 9 ADY21653 Antibody  
100 566 86.3 500 9 ADY21933 Antibody

ALIGNMENTS

RESULT 1  
AD94334  
ID ADS94334 standard; protein; 127 AA.  
XX  
AC ADS94334;  
XX  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Antibody 776.1 light chain variable region (776.1L) SEQ ID NO:33.  
XX  
KW antibody; antigen-binding antibody fragment;  
KW cell-associated CA 125/O772P; monoclonal antibody; cytostatic;  
KW immunostimulant; mediator of lysis; tumour; cell proliferative disorder;  
KW cancer; cervical cancer; uterine cancer; breast cancer; lung cancer;  
KW ovarian cancer.  
XX  
OS Synthetic.  
XX  
PN WO2004035537-A2.  
XX  
XX  
PD 29-APR-2004.  
XX  
XX 15-OCT-2003; 2003WO-US032945.  
XX  
PR 16-OCT-2002; 2002US-0418828P.  
PR 10-JUL-2003; 2003US-0485986P.  
XX  
XX (EURO-) EUROCELLIQUE SA.  
XX  
XX Albone EF, Soltis DA;  
XX  
XX WPI; 2004-357171/33.  
DR N-PSDB; ADS94343.  
XX  
XX Novel isolated antibody, or antigen-binding antibody fragment binding  
PT with cell-associated CA 125/O772P polypeptide relative to shed CA  
PT 125/O772 polypeptide, useful for ameliorating cervical or ovarian cancer.  
XX  
PS Claim 32; SEQ ID NO 33; 153pp; English.

XX The present invention describes an isolated antibody, or an antigen-  
XX binding antibody fragment (I), that preferentially binds cell-associated  
XX CA 125/O772P polypeptide relative to shed CA 125/O772 polypeptide. Also  
XX described: (1) a monoclonal antibody (II) produced by hybridoma 4E7; (2)  
XX as deposited in (II); (4) an isolated nucleic acid molecule (III)  
XX comprising a nucleotide sequence that encodes a variable chain region of  
XX (I); (5) a pharmaceutical composition comprising an antibody or an  
XX antigen-binding antibody fragment that preferentially binds cell-  
XX associated CA 125/O772P polypeptide relative to shed CA 125/O772P  
XX polypeptide, and a carrier; (6) a pharmaceutical composition comprising a  
XX monoclonal antibody or an antigen-binding monoclonal antibody fragment  
XX that preferentially binds cell-associated CA 125/O772P polypeptide  
XX relative to shed CA 125/O772P polypeptide, and a carrier; (7) an article  
XX of manufacture (IV) comprising packaging material and a composition  
XX comprising an antibody, or an antigen-binding antibody fragment that  
XX preferentially binds cell-associated CA 125/O772P relative to shed CA  
XX 125/O772P, and a carrier contained within the packaging material, and  
XX composition in a form suitable for administration to a subject; (8) a  
XX fusion polypeptide (V) comprising an antibody, or an antigen-binding  
XX antibody fragment, which preferentially binds cell-associated CA  
XX 125/O772P relative to shed CA 125/O772P operably linked to a heterologous  
XX agent; (9) ameliorating (M1) a symptom of a CA 125/O772P-related disorder  
XX; (10) a monoclonal antibody (VI) chosen from 325.1, 621.1, 633.1, 654.1,  
XX 725.1, 8G9, 7F10, 8A1, 8AC3, 15C9, 8E3, 8B5, 7G10, 16C7, 7H1, 16H9,

CC 7A11, 4E7, 117.1, 368.1, 446.1, 501.1, and 776.1 or its antigen-binding  
CC antibody fragment; (11) an antibody or antigen binding antibody fragment  
CC that competes with (VI); and (12) a pharmaceutical composition comprising  
CC (VI) and a carrier. (I) has cytostatic activity, and can be used as an  
CC immunostimulant and a mediator of lysis of positive tumour cell. (I) is  
CC useful for ameliorating a symptom of a CA 125/O77P-related disorder which  
CC is a cell proliferative disorder such as cancer, cervical or uterine  
CC cancer, breast or lung cancer or ovarian cancer. (V) is useful  
CC diagnostically for monitoring the development or progression of cancer or  
CC tumour as part of clinical testing procedure. The present sequence  
CC represents an antibody light chain variable region amino acid sequence,  
CC which is used in the exemplification of the present invention.  
XX  
SQ Sequence 127 AA;

Query Match 100.0%; Score 656; DB 8; Length 127;  
Best Local Similarity 100.0%; Pred. No. 1.3e-40;  
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MDFQVOIFSPFLTISASVIMSRGOIVLSQSPAILFASPGETVMTCRASSSVIYMCWNQOK 60  
Db 1 MDFQVOIFSPFLTISASVIMSRGOIVLSQSPAILFASPGETVMTCRASSSVIYMCWNQOK 60  
Qy 61 PGSSPKPWIYGTSTLASGVPTFRFSGSGTSTSLTISRVEAEDAATYCCQWSSNPFTFG 120  
Db 61 PGSSPKPWIYGTSTLASGVPTFRFSGSGTSTSLTISRVEAEDAATYCCQWSSNPFTFG 120  
Qy 121 SGTKLEI 127  
Db 121 SGTKLEI 127

RESULT 2  
AAR15323  
ID AAR15323 standard; protein; 145 AA.

XX AAR15323;  
XX  
XX 24-OCT-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 16-MAR-1992 (first entry)  
XX  
DE IL-2 chimeric antibody light chain.  
XX Interleukin-2; immunosuppressant.  
XX  
XX Homo sapiens.  
XX Mus musculus.  
XX Chimeric.  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..22 /note= "signal peptide"  
FT Peptide 23..117 /note= "V-region"  
FT Peptide 118..128 /note= "J1-region"  
FT Peptide 129..145 /note= "C-region"  
XX  
XX EP460674-A.  
XX  
XX 11-DEC-1991.  
XX  
XX 06-JUN-1991; 91EP-00109303.  
XX  
XX 08-JUN-1990; 90DE-04018442.  
XX  
XX (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX Weidlu U, Kaluza B, Knapp W;  
XX WPI; 1991-363168/50.  
DR



DR N-PSDB; AAQ15115.  
XX New recombinant DNA encoding chimeric antibody - with human constant and  
PT non-human variable regions, esp. directed against interleukin 2 receptor.  
PT  
XX Disclosure; Page 12; 24pp; German.  
XX  
CC The sequence is that of the interleukin-2 (IL-2) chimeric antibody light  
CC chain, coded by clone 215. Antibodies against IL-2 receptors are useful  
CC as immunosuppressants, and are much less immunogenic than mouse or rat  
CC antibodies. See also AAR15321-R15326. (Updated on 25-MAR-2003 to correct  
CC PI field.) (Updated on 24-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 145 AA;  
Query Match 88.3%; Score 579; DB 2; Length 145;  
Best Local Similarity 89.8%; Pred. No. 6.2e-35;  
Matches 114; Conservative 4; Mismatches 9; Indels 0; Gaps 0;  
QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNOOK 60  
DB 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNOOK 60  
QY 61 PGSSPKPWYGTSTLASGVPTRFSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120  
DB 61 PGSSPKPWIQATSNLAFGVPSRFSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120  
QY 121 SGTKLEI 127  
DB 121 SGTKLEI 127  
RESULT 3  
AAR32127  
ID AAR32127 standard; protein; 145 AA.  
AC AAR32127;  
XX 25-MAR-2003 (revised)  
DT 10-MAR-2003 (revised)  
DT 02-JUN-1993 (first entry)  
XX  
DE Anti-IL2R-alpha antibody M-215 light chain variable region.  
XX immunosuppression; tissue transplantation; graft; L chain; V region;  
KW T-helper cell inhibition; transplant rejection; Mab;  
KW interleukin-2 receptor.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..22  
FT Region /label= signal  
FT Region 23..116  
FT Region /label= Variable-region  
FT Region 117..128  
FT Region /label= J4-region  
FT Region 129..145  
FT /label= start\_of\_Constant\_region  
XX  
PN DE4143214-A1.  
XX  
XX 28-JAN-1993.  
XX  
PF 30-DEC-1991; 91DE-04143214.  
XX  
XX 25-JUL-1991; 91DE-04124759.  
XX  
PA (BOEP ) BOEHRINGER MANNHEIM GMBH.  
XX  
PI Weidle U, Scheuer W, Kaluza B, Riethmüller G;  
XX WPI; 1993-037582/05.  
DR

DR N-PSDB; AAQ36613.  
XX Synergistic antibody compsn. for use as immunosuppressant - comprises  
PT monoclonal anti-CD4 antibodies and monoclonal anti-IL2R alpha- or anti-  
PT IL2R beta antibodies.  
XX  
PS Example 1; Page 15; 18pp; German.  
XX  
CC This sequence is from the light chain variable region of an anti-IL2R  
CC alpha monoclonal antibody. The antibody is only weakly inhibitory on its  
CC own. When anti-IL2R alpha antibodies which are strongly inhibitory on  
CC their own are used with anti-CD4 antibodies which are also strongly  
CC inhibitory, their immunosuppressive properties are improved; they  
CC synergistically inhibit T-helper cell proliferation to effectively  
CC inhibit transplant rejection at low doses without significantly reducing  
CC the general immune response. No such synergistic effect is observed with  
CC the weakly inhibitory Mab M-215. See AAQ36607-Q36616. (Updated on 10-MAR-  
CC 2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 145 AA;  
Query Match 88.3%; Score 579; DB 2; Length 145;  
Best Local Similarity 89.8%; Pred. No. 6.2e-35;  
Matches 114; Conservative 4; Mismatches 9; Indels 0; Gaps 0;  
QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNOOK 60  
DB 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNOOK 60  
QY 61 PGSSPKPWYGTSTLASGVPTRFSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120  
DB 61 PGSSPKPWIQATSNLAFGVPSRFSGSGTSYSLTISRVEADAATYCCQWSSNPFTFG 120  
QY 121 SGTKLEI 127  
DB 121 SGTKLEI 127  
RESULT 4  
ADV92494  
ID ADV92494 standard; protein; 129 AA.  
AC ADV92494;  
XX  
DT 10-MAR-2005 (first entry)  
XX  
DE 2B8 light chain variable region protein.  
XX  
KW Antibody engineering; chimeric antibody; cytostatic; gene therapy;  
KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;  
KW breast cancer; hepatocellular carcinoma.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..22  
FT Region /label= Signal peptide  
FT Region 23..129  
FT /note= "Light chain variable region gene (VL)"  
FT Protein 23..129  
FT /note= "Mature 2B8 light chain variable region protein"  
XX  
PN US2004254108-A1.  
XX  
XX 16-DEC-2004.  
PD  
XX 26-NOV-2003; 2003US-00723003.  
PF  
XX 13-JUN-2003; 2003CN-00129290.  
PR 25-NOV-2003; 2003CN-01119930.  
XX  
XX (MAJ/J) MA J.  
PA

PA (GUOY/) GUO Y.  
 XX Ma J, Guo Y;  
 PI WPI; 2005-030218/03.  
 XX N-PSDB; ADV92493.  
 DR  
 XX  
 PT New chimeric protein comprises an Flt3 ligand and a proteinous or  
 PT peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,  
 PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.  
 XX  
 XX Claim 23; SEQ ID NO 38; 158pp; English.  
 PS  
 CC The present invention relates to a chimeric protein having a Flt3 ligand  
 CC (FL) or its biologically active fragment and a proteinous or peptidyl  
 CC tumoricidal agent. The invention is useful for treating malignancy,  
 CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a  
 CC vaccine for eliciting an immune response. The invention is also useful in  
 CC gene therapy. The present sequence is the 2B8 light chain variable region  
 CC protein.  
 XX  
 SQ Sequence 129 AA;  
 Query Match 88.1%; Score 578; DB 9; Length 129;  
 Best Local Similarity 90.6%; Pred. No. 6.5e-35;  
 Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCNQOK 60  
 DB 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWFQOK 60  
 QY 61 PGSSPKPWIYGTSLASGVPTFRFSGSGTYSLSLTISRVEADAATYCCQWSNPPTFG 120  
 DB 61 PGSSPKPWIYATNLASGVPTFRFSGSGTYSLSLTISRVEADAATYCCQWTSNPPTFG 120  
 QY 121 SGTKLEI 127  
 DB 121 GGTKLEI 127  
 RESULT 5  
 ADV98557  
 ID ADV98557 standard; protein; 129 AA.  
 XX  
 AC ADV98557;  
 XX  
 DT 24-MAR-2005 (first entry)  
 DE Novel chimeric protein-related 2B8 light chain protein SeqID38.  
 XX  
 KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;  
 KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.  
 XX  
 OS Homo sapiens.  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 XX WO2005001048-A2.  
 XX  
 XX 06-JAN-2005.  
 XX  
 XX 04-JUN-2004; 2004WO-US017765.  
 XX  
 XX 13-JUN-2003; 2003CN-00129290.  
 PR 25-NOV-2003; 2003CN-01119930.  
 PR 26-NOV-2003; 2003US-00723003.  
 PR 28-NOV-2003; 2003TW-00133577.  
 XX  
 XX (SYMB-) SYMBIGENE ACQUISITION CO INC.  
 PA  
 XX Ma J, Guo Y;  
 PI WPI; 2005-075540/08.  
 XX

DR N-PSDB; ADV98556.  
 XX  
 PT New chimeric protein for preventing or treating neoplastic conditions,  
 PT e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an  
 PT Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal  
 PT agent.  
 XX  
 XX Example 5; SEQ ID NO 38; 147pp; English.  
 PS  
 CC This invention relates to a novel chimeric protein comprising an Flt3  
 CC ligand, or its biological fragment, and a proteinous or peptidyl  
 CC tumoricidal agent. The invention may be useful for the production of  
 CC compounds with a cytostatic activity or a vaccine. The composition and  
 CC methods are useful for preventing or treating neoplastic conditions, such  
 CC as melanoma, breast cancer or hepatocellular carcinoma. The present  
 CC sequence is that of a protein which is related to the chimeric proteins  
 CC of the invention.  
 XX  
 SQ Sequence 129 AA;  
 Query Match 88.1%; Score 578; DB 9; Length 129;  
 Best Local Similarity 90.6%; Pred. No. 6.5e-35;  
 Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCNQOK 60  
 DB 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWFQOK 60  
 QY 61 PGSSPKPWIYGTSLASGVPTFRFSGSGTYSLSLTISRVEADAATYCCQWSNPPTFG 120  
 DB 61 PGSSPKPWIYATNLASGVPTFRFSGSGTYSLSLTISRVEADAATYCCQWTSNPPTFG 120  
 QY 121 SGTKLEI 127  
 DB 121 GGTKLEI 127  
 RESULT 6  
 ADV92498  
 ID ADV92498 standard; protein; 235 AA.  
 XX  
 AC ADV92498;  
 XX  
 DT 10-MAR-2005 (first entry)  
 DE Anti-CD20 chimeric antibody light chain protein.  
 XX  
 KW Antibody engineering; chimeric antibody; cytostatic; gene therapy;  
 KW vaccine; gastrointestinal disease; immune response; melanoma; malignancy;  
 KW breast cancer; hepatocellular carcinoma.  
 XX  
 OS Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 FT Peptide 1..22  
 FT /label= Signal peptide  
 FT Region 23..129  
 FT /note= "Light chain variable region gene (VL)"  
 FT Region 130..235  
 FT /note= "Human kappa chain constant cdna (CL)"  
 XX  
 XX US2004254108-A1.  
 DN  
 XX 16-DEC-2004.  
 PD  
 XX 26-NOV-2003; 2003US-00723003.  
 PF  
 XX 13-JUN-2003; 2003CN-00129290.  
 PR 25-NOV-2003; 2003CN-01119930.  
 PR  
 XX (MAJJ/) MA J.  
 XX (GUOY/) GUO Y.  
 XX

PI Ma J, Guo Y;  
 XX WPI; 2005-030218/03.  
 DR N-PSDB; ADV92497.  
 XX  
 XX New chimeric protein comprises an Flt3 ligand and a proteinous or  
 PT peptidyl tumoricidal agent, useful for treating malignancy or neoplasm,  
 PT e.g. melanoma, breast cancer, or hepatocellular carcinoma.  
 XX  
 XX Claim 23; SEQ ID NO 42; 158pp; English.  
 XX  
 XX The present invention relates to a chimeric protein having a Flt3 ligand  
 CC (FL) or its biologically active fragment and a proteinous or peptidyl  
 CC tumoricidal agent. The invention is useful for treating malignancy,  
 CC neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a  
 CC vaccine for eliciting an immune response. The invention is also useful in  
 CC gene therapy. The present sequence is the anti-CD20 chimeric antibody  
 CC light chain protein.  
 XX  
 XX Sequence 235 AA;  
 SQ  
 Query Match 88.1%; Score 578; DB 9; Length 235;  
 Best Local Similarity 90.6%; Pred. No. 1.2e-34;  
 Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCNQK 60  
 DB 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQK 60  
 QY 61 PGSSPKPWYGTSTLASGVPTFRSGSGSGTYSLTISRVEAEADATYCCQWSSNPPTFG 120  
 DB 61 PGSSPKPWYATNLASGVPTFRSGSGSGTYSLTISRVEAEADATYCCQWTSNPPTFG 120  
 QY 121 SGTKLEI 127  
 DB 121 GGTKLEI 127  
 RESULT 7  
 ADV98561  
 ID ADV98561 standard; protein; 235 AA.  
 XX  
 AC ADV98561;  
 XX  
 XX 24-MAR-2005 (first entry)  
 DT  
 DE Novel chimeric protein-related anti-CD20 light chain protein SeqID42.  
 XX  
 KW protein engineering; pharmaceutical; cytostatic; vaccine; cancer;  
 KW neoplasm; melanoma; breast tumor; hepatocellular carcinoma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005001048-A2.  
 XX  
 XX 06-JAN-2005.  
 PD  
 XX 04-JUN-2004; 2004WO-US017765.  
 PF  
 XX 13-JUN-2003; 2003CN-00129290.  
 PR 25-NOV-2003; 2003CN-01119930.  
 PR 26-NOV-2003; 2003US-00723003.  
 PR 28-NOV-2003; 2003TW-00133577.  
 XX  
 PA (SYMB-) SYMBIGENE ACQUISITION CO INC.  
 XX  
 XX Ma J, Guo Y;  
 PI WPI; 2005-075540/08.  
 DR N-PSDB; ADV98560.  
 XX  
 XX New chimeric protein for preventing or treating neoplastic conditions,  
 PT e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an

PT Flt3 ligand or its fragment, and a proteinous or peptidyl tumoricidal  
 PT agent.  
 XX  
 PS Example 5; SEQ ID NO 42; 147pp; English.  
 XX  
 CC This invention relates to a novel chimeric protein comprising an Flt3  
 CC ligand, or its biological fragment, and a proteinous or peptidyl  
 CC tumoricidal agent. The invention may be useful for the production of  
 CC compounds with a cytostatic activity or a vaccine. The composition and  
 CC methods are useful for preventing or treating neoplastic conditions, such  
 CC as melanoma, breast cancer or hepatocellular carcinoma. The present  
 CC sequence is that of a protein which is related to the chimeric proteins  
 CC of the invention.  
 XX  
 SQ Sequence 235 AA;  
 Query Match 88.1%; Score 578; DB 9; Length 235;  
 Best Local Similarity 90.6%; Pred. No. 1.2e-34;  
 Matches 115; Conservative 2; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCNQK 60  
 DB 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYHWFQK 60  
 QY 61 PGSSPKPWYGTSTLASGVPTFRSGSGSGTYSLTISRVEAEADATYCCQWSSNPPTFG 120  
 DB 61 PGSSPKPWYATNLASGVPTFRSGSGSGTYSLTISRVEAEADATYCCQWTSNPPTFG 120  
 QY 121 SGTKLEI 127  
 DB 121 GGTKLEI 127  
 RESULT 8  
 AAR55214  
 ID AAR55214 standard; protein; 128 AA.  
 XX  
 AC AAR55214;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 01-FEB-1995 (first entry)  
 XX  
 DE Murine variable region light chain from 2B8.  
 XX  
 KW B cell lymphoma chimeric antibody; CD20; peripheral blood cells;  
 KW cell lysis.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO9411026-A2.  
 XX  
 PD 26-MAY-1994.  
 XX  
 PF 12-NOV-1993; 93WO-US010953.  
 XX  
 PR 13-NOV-1992; 92US-00978891.  
 PR 03-NOV-1993; 93US-00149099.  
 XX  
 PA (IDEC-) IDEC PHARM CORP.  
 XX  
 XX Anderson DR, Rastetter WH, Hanna N, Leonard JB, Newman RA;  
 PI Reff ME;  
 XX  
 XX WPI; 1994-183162/22.  
 DR N-PSDB; AAQ65630.  
 XX  
 XX Treating B cell lymphoma with chimeric antibody - against CD20, causing  
 PT rapid depletion of peripheral B cells, also new antibodies and  
 PT hybridomas.  
 XX  
 PS Disclosure; Fig 4; 101pp; English.  
 XX  
 XX The sequence is the murine variable region light chain derived from

CC murine anti-CD20 monoclonal antibody 2B5. See also AA065629-35. (Updated  
CC on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct  
CC PI field.)  
XX  
SQ Sequence 128 AA;  
Query Match 87.2%; Score 572; DB 2; Length 128;  
Best Local Similarity 89.8%; Pred. No. 1.8e-34;  
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MDFQVQIFSPLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQOK 60  
DB 1 MDFQVQIISPLLISASVIMSRGQIVLSQSPAILFASPGKVWTCRASSSVIYHWFQOK 60  
QY 61 PGSSPKPWIYGTSLASGVPTFRFSGSGSGTSYSLTISRVEADAATYCCOWSSNPPTFG 120  
DB 61 PGSSPKPWIYATSNLASGVPTFRFSGSGSGTSYSLTISRVEADAATYCCOWTSNPPTFG 120  
QY 121 SGTKLEI 127  
DB 121 GGTKLEI 127  
RESULT 9  
ABR55872  
ID ABR55872 standard; protein; 128 AA.  
XX AC ABR55872;  
XX 02-SEP-2003 (first entry)  
XX Anti-CD20 antibody light chain variable region.  
XX Peptide remodeling; glycoconjugation; glycosyltransferase; glycan; CD20;  
KW antibody; mouse.  
XX Mus musculus.  
XX WO2003031464-A2.  
XX 17-APR-2003.  
XX 09-OCT-2002; 2002WO-US032263.  
XX 10-OCT-2001; 2001US-0328523P.  
XX 19-OCT-2001; 2001US-0344692P.  
XX 28-NOV-2001; 2001US-0334233P.  
XX 28-NOV-2001; 2001US-0334301P.  
XX 07-JUN-2002; 2002US-0387292P.  
XX 25-JUN-2002; 2002US-0391777P.  
XX 17-JUL-2002; 2002US-0396594P.  
XX 16-AUG-2002; 2002US-0404249P.  
XX 28-AUG-2002; 2002US-0407527P.  
XX (NEOS-) NEOSE TECHNOLOGIES INC.  
XX De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;  
XX WPI; 2003-449162/42.  
XX N-PSDB; ACC78894.  
XX Remodeling a peptide, by removing a saccharyl subunit from the peptide to  
FT form truncated glycan, and adding or deleting glycosyl groups to a  
PT peptide and/or adding modifying group of a peptide to remodel the  
PT peptide.  
XX Example; Fig 82B; 900pp; English.  
XX The invention relates to a cell-free, in vitro method of remodeling a  
CC peptide. The method involves removing a saccharyl subunit from the  
CC peptide, thus forming a truncated glycan, and contacting the truncated  
CC glycan with at least one glycosyltransferase and at least one glycosyl  
CC donor under conditions suitable to transfer at least one glycosyl donor

CC to the truncated glycan, thus remodeling the peptide. Conjugates can be  
CC formed between a granulocyte colony stimulating factor (G-CSF) peptide,  
CC interferon alpha peptide, interferon beta peptide, Factor VIIa peptide,  
CC Factor IX peptide, follicle stimulating hormone peptide, erythropoietin  
CC (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)  
CC peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-Pi)  
CC peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA)  
CC peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha  
CC receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-  
CC glycoprotein IIb/IIIa monoclonal antibody peptide, chimeric anti HER2  
CC antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-  
CC CD20 antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide,  
CC insulin peptide, hepatitis B surface antigen (HbsAg), human growth  
CC hormone (HGH) peptide, and a modifying group, where the modifying group  
CC is covalently attached to the peptide through an intact glycosyl linking  
CC group. The method is useful for a cell-free, in vitro method of  
CC remodeling the above mentioned peptides. The present sequence represents  
CC the murine anti-CD20 antibody light chain mature variable region  
XX  
SQ Sequence 128 AA;

Query Match 87.2%; Score 572; DB 6; Length 128;  
Best Local Similarity 89.8%; Pred. No. 1.8e-34;  
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MDFQVQIFSPLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQOK 60  
DB 1 MDFQVQIISPLLISASVIMSRGQIVLSQSPAILFASPGKVWTCRASSSVIYHWFQOK 60  
QY 61 PGSSPKPWIYGTSLASGVPTFRFSGSGSGTSYSLTISRVEADAATYCCOWSSNPPTFG 120  
DB 61 PGSSPKPWIYATSNLASGVPTFRFSGSGSGTSYSLTISRVEADAATYCCOWTSNPPTFG 120  
QY 121 SGTKLEI 127  
DB 121 GGTKLEI 127

## RESULT 10

ABU08393  
ID ABU08393 standard; protein; 128 AA.

XX AC ABU08393;

XX 11-JUN-2003 (first entry)

DT Murine anti-CD20 antibody light chain variable region.

DE B cell lymphoma; chimeric anti-CD20 antibody; cytostatic; mouse; VL;  
KW expression vector; murine; light chain; variable region.

XX Mus sp.

XX Key Location/Qualifiers  
FH Peptide 1..22

FT Protein /label= signal\_peptide

FT 23..128  
/label= Mature\_anti-CD20\_antibody\_VL\_region

XX US2002197255-A1.

XX 26-DEC-2002.

XX 25-JUL-2001; 2001US-00911703.

XX 07-JUN-1995; 95US-00475813.

XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Hanna N, Leonard JE, Newman RA, Reff ME;  
PI Rastetter WH;

XX WPI; 2003-352746/33.

DR N-PSDB; ABX94206.  
 XX Treating B cell lymphoma in humans, comprises administering  
 PT immunologically active, chimeric anti-CD20 antibodies and/or radiolabeled  
 PT anti-CD20 antibodies to the human.  
 XX Example; Fig 4; 51pp; English.  
 XX The present invention relates to a method for treating B cell lymphoma.  
 CC The method comprises administering at a first administration period, an  
 CC immunologically active, mouse/human chimeric anti-CD20 antibody and/or  
 CC administering, at a second administration period, a radiolabeled anti-  
 CC CD20 antibody, to the human subject. The invention also discloses  
 CC expression vectors that may be used in the method of the present  
 CC invention. The method is useful for treating B cell lymphoma in humans.  
 CC The present sequence represents murine anti-CD20 antibody light chain  
 CC variable region  
 XX Sequence 128 AA;  
 SQ Query Match 87.2%; Score 572; DB 6; Length 128;  
 Best Local Similarity 89.8%; Pred. No. 1.8e-34;  
 Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 MDFQVQIFPFLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWNQOK 60  
 DB 1 MDFQVQIIIFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWNQOK 60  
 QY 61 PGSSPKPWYGTSTLASGVPTFRSGSGSGTYSLTISRVEAEDAATYCCOWSSNPPTFG 120  
 DB 61 PGSSPKPWYATNSLAVGVPFRSGSGSGTYSLTISRVEAEDAATYCCOWTSNPPTFG 120  
 QY 121 SGTKLEI 127  
 DB 121 GGTKLEI 127  
 RESULT 12  
 ADE85686  
 ID ADE85686 standard; protein; 128 AA.  
 XX AC ADE85686;  
 XX DT 29-JAN-2004 (first entry)  
 XX DE Murine immunoglobulin light chain variable region.  
 XX KW B cell lymphoma; anti-CD20; peripheral B cell; C2B8;  
 XX KW immunoglobulin light chain variable region; mouse; antibody.  
 XX OS Mus sp.  
 XX PN US2003147885-A1.  
 XX PD 07-AUG-2003.  
 XX PF 11-SEP-2002; 2002US-00238681.  
 XX PR 13-NOV-1992; 92US-00978891.  
 XX PR 03-NOV-1993; 93US-00149099.  
 XX PR 29-AUG-1997; 97US-00921060.  
 XX PA (IDEC-) IDEC PHARM CORP.  
 XX PI Anderson DR, Hanna N, Leonard JE, Newman RA, Reff ME;  
 PI Rastetter WH;  
 XX DR WPI; 2003-897520/82.  
 XX DR N-PSDB; ADE85696.  
 XX PT Treating B cell lymphoma by administering an anti-CD20 antibody and at  
 XX PT least one chemotherapeutic agent.  
 XX PS Example; SEQ ID NO 7; 52pp; English.  
 XX The invention relates to an improved method for treating B cell lymphoma  
 CC comprising administering an anti-CD20 antibody. The improvement comprises  
 CC administering at least one chemotherapeutic agent. The antibody causes a  
 CC substantial depletion of peripheral B cells. The antibody is chimeric  
 CC anti-CD20 or C2B8. The method is useful for treating B cell lymphoma.

DR N-PSDB; ABX94206.  
 XX Treating B cell lymphoma in humans, comprises administering  
 PT immunologically active, chimeric anti-CD20 antibodies and/or radiolabeled  
 PT anti-CD20 antibodies to the human.  
 XX Example; Fig 4; 51pp; English.  
 XX The present invention relates to a method for treating B cell lymphoma.  
 CC The method comprises administering at a first administration period, an  
 CC immunologically active, mouse/human chimeric anti-CD20 antibody and/or  
 CC administering, at a second administration period, a radiolabeled anti-  
 CC CD20 antibody, to the human subject. The invention also discloses  
 CC expression vectors that may be used in the method of the present  
 CC invention. The method is useful for treating B cell lymphoma in humans.  
 CC The present sequence represents murine anti-CD20 antibody light chain  
 CC variable region  
 XX Sequence 128 AA;  
 SQ Query Match 87.2%; Score 572; DB 6; Length 128;  
 Best Local Similarity 89.8%; Pred. No. 1.8e-34;  
 Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 MDFQVQIFPFLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWNQOK 60  
 DB 1 MDFQVQIIIFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWNQOK 60  
 QY 61 PGSSPKPWYGTSTLASGVPTFRSGSGSGTYSLTISRVEAEDAATYCCOWSSNPPTFG 120  
 DB 61 PGSSPKPWYATNSLAVGVPFRSGSGSGTYSLTISRVEAEDAATYCCOWTSNPPTFG 120  
 QY 121 SGTKLEI 127  
 DB 121 GGTKLEI 127  
 RESULT 11  
 ADC66268  
 ID ADC66268 standard; protein; 128 AA.  
 XX AC ADC66268;  
 XX DT 18-DEC-2003 (first entry)  
 XX DE Mouse anti-CD20 antibody light chain variable region.  
 XX KW immunosuppressant; cytostatic; antibody; CD20;  
 XX KW N-glycoside bond complex sugar chain; fucose; N-acetylglucosamine;  
 XX KW sugar chain; cancer; immune disorder.  
 XX OS Mus musculus.  
 XX PN WO2003055993-A1.  
 XX PD 10-JUL-2003.  
 XX PF 25-DEC-2002; 2002WO-JP013534.  
 XX PR 25-DEC-2001; 2001JP-00392753.  
 XX PR 09-APR-2002; 2002JP-00106948.  
 XX PR 01-NOV-2002; 2002JP-00319975.  
 XX PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX PI Shitara K, Sakurada M, Uchida K, Shinkawa T, Satoh M, Nakano R;  
 XX DR WPI; 2003-559274/52.  
 XX DR N-PSDB; ADC66267.  
 XX PT Antibody binding to CD20 and having Fc-bound sugar chains of low fucose  
 XX PT content for treatment of cancer and immune disorders.

CC This sequence represents a murine immunoglobulin light chain variable  
 CC region used in the method of the invention.

XX  
 SQ Sequence 128 AA;  
 Query Match 87.2%; Score 572; DB 7; Length 128;  
 Best Local Similarity 89.8%; Pred. No. 1.8e-34;  
 Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 MDFQVQIFSPFLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQOK 60  
 DB 1 MDFQVQIIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWFQOK 60  
 QY 61 PGSSPKPWYIYGTSLASGVPTFRSGSGTYSYSLTISRVEADAATYCCQWSSNPPTFG 120  
 DB 61 PGSSPKPWYIYATNLASGVPTFRSGSGTYSYSLTISRVEADAATYCCQWTSNPPTFG 120  
 QY 121 SGTKLEI 127  
 DB 121 GGTKLEI 127

## RESULT 13

AD73083  
 ID ADE73083 standard; protein; 128 AA.

XX AC ADE73083;

XX DT 29-JAN-2004 (first entry)

XX DE Murine FUT8-related sequence.

XX KW Antiallergic; Anti-inflammatory; Immunosuppressive; Antibacterial;  
 KW Antiviral; Cytostatic; enzyme; alpha 1,6-fucosyltransferase; tumour;  
 KW allergy; inflammation; autoimmune disease; circulatory disorder;  
 KW viral infection; bacterial infection; murine.

XX OS Mus musculus.

XX PN WO2003085107-A1.

XX PD 16-OCT-2003.

XX PF 09-APR-2003; 2003WO-JP004507.

XX PR 09-APR-2002; 2002JP-00106953.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Yamane N, Satoh M, Mori K, Yamano K;

XX DR WPI; 2003-833570/77.

XX DR N-PSDB; ADE73068.

XX PT Cells with reduced or absent alpha 1,6-fucosyltransferase activity for  
 PT treatment of tumors, allergy, inflammation, autoimmune disease,  
 PT circulatory disorders, and viral and bacterial infection.

XX PS Example 6; Page 164-165; 187pp; Japanese.

XX CC The present invention relates to cells with modified sugar chain  
 CC modifying enzyme activity. The enzyme activity of binding the 1-position  
 CC of fucose to the 6-position of an N-acetylglucosamine at the reducing end  
 CC of a complex N-glycoside linked sugar chain via an alpha-bond is absent  
 CC or less than in the parent cell. The sugar chain modifying enzyme is  
 CC preferably alpha 1,6-fucosyltransferase (ADE73052-ADE73053 and ADE73055-  
 CC ADE73056). The invention is useful for the treatment and prevention of  
 CC tumours, allergy, inflammation, autoimmune disease, circulatory  
 CC disorders, and viral and bacterial infection. The present sequence was  
 CC used in an example from the invention.

XX SQ Sequence 128 AA;

Query Match 87.2%; Score 572; DB 7; Length 128;  
 Best Local Similarity 89.8%; Pred. No. 1.8e-34;  
 Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDFQVQIFSPFLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQOK 60  
 DB 1 MDFQVQIIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWFQOK 60  
 QY 61 PGSSPKPWYIYGTSLASGVPTFRSGSGTYSYSLTISRVEADAATYCCQWSSNPPTFG 120  
 DB 61 PGSSPKPWYIYATNLASGVPTFRSGSGTYSYSLTISRVEADAATYCCQWTSNPPTFG 120  
 QY 121 SGTKLEI 127  
 DB 121 GGTKLEI 127

## RESULT 14

AD760660  
 ID ADF60660 standard; protein; 128 AA.

XX AC ADF60660;

XX DT 12-FEB-2004 (first entry)

XX DE Protein related to the invention #1.

XX KW Cytostatic; antiallergic; immunomodulator; cardiant; virucide;  
 KW antibacterial; drug; antibody; lectin; N-acetylglucosamine; fucose;  
 KW tumour; allergy; inflammation; autoimmune disease; circulatory system;  
 KW viral; bacterial; infection; CCR4.

XX OS Mus musculus.

XX PN WO2003084569-A1.

XX PD 16-OCT-2003.

XX PF 09-APR-2003; 2003WO-JP004503.

XX PR 09-APR-2002; 2002JP-00106949.

XX PA (KYOW ) KYOWA HAKKO KOGYO KK.

XX PI Niwa R, Shitara K;

XX DR WPI; 2003-812676/76.

XX DR N-PSDB; ADF60645.

XX PT Drugs containing antibody compositions produced by cells tolerant to  
 PT lectin recognizing specific sugar-chain structure, useful in screening  
 PT and treating patients not suitable for drugs not derived from these  
 PT cells.

XX PS Example 2; SEQ ID NO 6; 157pp; Japanese.

XX CC The invention relates to a drug containing as the active ingredient, an  
 CC antibody composition produced by cells tolerant to a lectin recognising a  
 CC sugar-chain structure in which an alpha-bond is formed between the 6-  
 CC position of N-acetylglucosamine at the reducing end of an N-glycoside  
 CC bond-type complex sugar chain and the 1-position of fucose. The drugs are  
 CC useful in screening and treating patients not suitable for drugs not  
 CC derived from these cells. They are particularly useful as diagnostics,  
 CC preventives or remedies for diseases accompanying tumour, allergy or  
 CC inflammation, autoimmune diseases, diseases of the circulatory system,  
 CC and viral or bacterial infections. In a method from the invention, a CCR4  
 CC gene was used for constructing a vector (CAG-CCR4/pcDNA3) for producing a  
 CC transfectant EL-4 cell (ATCC TIB-39) to express chimeric CCR4. Antibody-  
 CC dependent cytotoxicity of the thus produced antibody composition was  
 CC confirmed. The current sequence represents a protein related to the  
 CC invention.

XX SQ Sequence 128 AA;

```
Query Match      87.2%; Score 572; DB 7; Length 128;
Best Local Similarity 89.8%; Pred. No. 1.8e-34;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDFQVQIFPSLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQOK 60
DB 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWFQOK 60
QY 61 PGSSPKPWYIGTSLASGVPTFRSGSGSGTSYSLTISRVEADAATYCCOWSSNPPTFG 120
DB 61 PGSSPKPWYIATNSLASGVPTFRSGSGSGTSYSLTISRVEADAATYCCOWSSNPPTFG 120
QY 121 SGTKLEI 127
DB 121 GGTKLEI 127

RESULT 15
ADN49732
ID ADN49732 standard; protein; 128 AA.
XX
AC ADN49732;
XX
DT 15-JUL-2004 (first entry)
XX
DE Mature variable light chain anti-CD20 murine antibody protein SeqID 60.
XX
KW mouse; murine; antibody; erythropoietin; EPO; glycoconjugation;
KW glycoPEGylated EPO peptide; anaemia; antianemic; haematocrit level;
KW kidney dialysis; haematology; CD20.
XX
OS Mus musculus.
XX
PN WO2004033651-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031974.
XX
PR 09-OCT-2002; 2002WO-US032263.
XX
PR 05-NOV-2002; 2002US-00287994.
XX
PR 06-JAN-2003; 2003US-00360770.
XX
PR 19-FEB-2003; 2003US-00360779.
XX
PR 09-APR-2003; 2003US-00410945.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
XX
DR WPI; 2004-399848/37.
XX
DR N-PSDB; ADN49731.
XX
PT Novel erythropoietin peptide comprising one or more glycans, having
PT glycoconjugate molecule covalently attached to peptide, useful for
PT treating anemia in mammal such as human.
XX
PS Disclosure; SEQ ID NO 60; 1018pp; English.
XX
CC This invention relates to novel erythropoietin (EPO) peptides and the
CC remodelling and glycoconjugation of these naturally occurring peptides
CC thereof. Specifically, each EPO peptide comprises one or more glycans and
CC has a glycoconjugate molecule such as polyethylene glycol (PEG) attached
CC to it. Accordingly, the present invention provides glycoPEGylated EPO
CC peptides that have either monoantennary, biantennary or triantennary
CC glycans covalently attached thereto. As such, these peptides are useful
CC for the treatment of anaemia, and hence exhibit antianemic activities
CC working to increase haematocrit levels in mammals, in particular in
CC humans i.e. increasing the relative volume of blood occupied by
CC erythrocytes. Furthermore, EPO therapy can be used to treat kidney
CC dialysis patients. This polypeptide is a human protein sequence related
CC to the field of haematology, given in an exemplification of the
CC invention.

XX
SQ Sequence 128 AA;
XX
Query Match      87.2%; Score 572; DB 8; Length 128;
Best Local Similarity 89.8%; Pred. No. 1.8e-34;
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDFQVQIFPSLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQOK 60
DB 1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYHWFQOK 60
QY 61 PGSSPKPWYIGTSLASGVPTFRSGSGSGTSYSLTISRVEADAATYCCOWSSNPPTFG 120
DB 61 PGSSPKPWYIATNSLASGVPTFRSGSGSGTSYSLTISRVEADAATYCCOWSSNPPTFG 120
QY 121 SGTKLEI 127
DB 121 GGTKLEI 127

RESULT 16
ADU74408
ID ADU74408 standard; protein; 128 AA.
XX
AC ADU74408;
XX
DT 10-FEB-2005 (first entry)
XX
DE Mouse anti-CD20 light chain variable region.
XX
KW Hemostatic; Hepatotropic; Antianemic; Cytostatic; Osteopathic;
KW Antibacterial; Respiratory-Gen.; Antiinflammatory; Nephrotropic;
KW Antiinfertility; Antitubercular; Tuberculostatic; protein engineering;
KW bleeding; factor VIII deficiency; factor IX deficiency; liver cirrhosis;
KW infertility; anemia; end-stage renal disease; acute myelogenous leukemia;
KW osteoporosis; pulmonary fibrosis; tuberculosis.
XX
OS Mus musculus.
XX
PN WO2004099231-A2.
XX
PD 18-NOV-2004.
XX
PF 09-APR-2004; 2004WO-US011494.
XX
PR 09-APR-2003; 2003US-00410897.
XX
PR 09-APR-2003; 2003US-00410913.
XX
PR 09-APR-2003; 2003US-00410930.
XX
PR 09-APR-2003; 2003US-00410945.
XX
PR 09-APR-2003; 2003US-00410962.
XX
PR 09-APR-2003; 2003US-00410980.
XX
PR 09-APR-2003; 2003US-00410997.
XX
PR 09-APR-2003; 2003US-00411012.
XX
PR 09-APR-2003; 2003US-00411026.
XX
PR 09-APR-2003; 2003US-00411037.
XX
PR 09-APR-2003; 2003US-00411043.
XX
PR 09-APR-2003; 2003US-00411044.
XX
PR 09-APR-2003; 2003US-00411049.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI De Frees S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
XX
DR WPI; 2004-833698/82.
XX
DR N-PSDB; ADU74407.
XX
CC Cell-free in vitro method of remodeling peptide comprising poly(ethylene
CC glycol) useful for generating glycopeptide suitable for therapeutic uses
CC in mammal, involves addition or deletion of glycosyl groups to peptide.
XX
PS Disclosure; SEQ ID NO 60; 1024pp; English.
XX
CC The invention relates to a cell-free in vitro method (M1) of remodeling a
```

CC peptide comprising poly(ethylene glycol). (M1) is useful for remodeling  
CC protein to generate glycopeptide having desired glycosylation pattern  
CC suitable for therapeutic use in mammal. (M1) is useful for remodeling  
CC peptides chosen from immunoglobulin, erythropoietin, tissue-type  
CC activator peptide, etc. (M1) is useful for remodeling (a) G-CSF which is  
CC useful for treating acute myeloid leukemia (AML), non-myeloid cancer  
CC patient receiving bone marrow transplant, (b) factor VII for treating  
CC bleeding episode, factor VIII deficiency, factor IX deficiency, liver  
CC cirrhosis, (c) FSH for patients undergoing intrauterine insemination, in  
CC vitro fertilization and for infertile patient, (d) EPO for treating  
CC anemia, anemic patients having chronic renal insufficiency and end stage  
CC renal disease, anemic patient undergoing dialysis, (e) GM-CSF for  
CC treating acute myelogenous leukemia, (f) IFN-gamma for treating malignant  
CC osteoporosis, pulmonary fibrosis, tuberculosis, cryptococcal meningitis,  
CC etc. The glycopeptide produced using (M1) has specific customized or  
CC desired glycosylation pattern. (M1) allows efficient production of  
CC improved therapeutic moiety. The present sequence represents the amino  
CC acid sequence of a protein remodelled in the present invention  
XX  
SQ Sequence 128 AA;  
Query Match 87.2%; Score 572; DB 8; Length 128;  
Best Local Similarity 89.8%; Pred. No. 1.8e-34;  
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MDFQVQIIFLLISASVIMSRGQIVLSQSPAILFASPGETVWTTCRASSSVIYMCWNOOK 60  
DB 1 MDFQVQIIFLLISASVIMSRGQIVLSQSPAILFASPGETVWTTCRASSSVIYHFWQOK 60  
QY 61 PGSSPKPWIYGTSTLASGVPTFRFSGSGGTSYSLTISRVEADAATYCCQWSSNPPTFG 120  
DB 61 PGSSPKPWIYATNSLNSGVPTFRFSGSGGTSYSLTISRVEADAATYCCQWTSNPPTFG 120  
QY 121 SGTKEI 127  
DB 121 GGTKEI 127  
RESULT 17  
ADZ59908  
ID ADZ59908 standard; protein; 128 AA.  
XX  
XX ADZ59908;  
AC  
XX  
XX 30-JUN-2005 (first entry)  
DT  
DE Fucosyltransferase 8 (alpha (1,6) fucosyltransferase.  
XX  
XX cytosolic; antiinflammatory; immunosuppressive; vasotropic; virucide;  
KW antibacterial; drug discovery; cell culture; immune disorder; cancer;  
KW neoplasm; inflammation; autoimmune disease; allergy; antiallergic;  
KW viral infection; infection; bacterial infection;  
KW Fucosyltransferase 8 (alpha (1,6) fucosyltransferase.  
XX  
XX Mus musculus.  
XX  
XX WO200503740-A1.  
XX  
XX 21-APR-2005.  
XX  
XX 08-OCT-2004; 2004WO-JP015315.  
XX  
XX 09-OCT-2003; 2003JP-00350166.  
XX  
XX (KYOWA) KYOWA HAKKO KOGYO KK.  
XX  
XX Nakano R, Satoh M, Iida S, Urakubo M, Kusunoki M, Kinoshita S;  
PI Ohnuki N;  
XX  
XX WPI; 2005-346214/35.  
XX  
XX Novel cell that is neutralized to serum-free medium and carrying knockout  
PT of gene encoding enzyme involved in carbohydrate modification, useful for

PT manufacturing glycoprotein composition useful in treating, e.g. cancer.  
XX  
XX Disclosure; Page 122-123; 135pp; Japanese.  
XX  
CC The invention describes a cell (I) that is neutralized to a serum-free  
CC medium and carrying a knockout genome gene encoding an enzyme which  
CC participates in a sugar chain modification, where fucose is linked by an  
CC alpha linkage at the 1-position to the 6-position of N-acetylglucosamine  
CC at the reducing end of an N-glycoside-binding complex sugar chain. Also  
CC described are: a neutralization (M1) method of cell to the serum free  
CC medium; cloning, after making neutralizing cell to the serum free medium  
CC by (M1); a cell having a knockout genome gene encoding the enzyme  
CC which is involved in the carbohydrate modification that is neutralized to  
CC the serum free medium; and a cloned cell strain, comprising having a  
CC knocked out genome gene encoding the enzyme which is involved in the  
CC carbohydrate modification that is neutralized to the serum free medium.  
CC (I) is useful for manufacturing a glycoprotein composition, which  
CC involves culturing (I) in a culture medium and collecting the accumulated  
CC glycoprotein composition from the culture medium. The glycoprotein  
CC composition is useful in drug discovery and for treating immunological  
CC disease such as cancer, inflammatory disease, autoimmune disease, the  
CC allergy, circulatory disorder, virus or bacterial infection. This is the  
CC amino acid sequence of a polypeptide used in the creation of host cells  
CC capable of producing glycoprotein compositions useful in drug discovery.  
XX  
SQ Sequence 128 AA;  
Query Match 87.2%; Score 572; DB 9; Length 128;  
Best Local Similarity 89.8%; Pred. No. 1.8e-34;  
Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
QY 1 MDFQVQIIFLLISASVIMSRGQIVLSQSPAILFASPGETVWTTCRASSSVIYMCWNOOK 60  
DB 1 MDFQVQIIFLLISASVIMSRGQIVLSQSPAILFASPGETVWTTCRASSSVIYHFWQOK 60  
QY 61 PGSSPKPWIYGTSTLASGVPTFRFSGSGGTSYSLTISRVEADAATYCCQWSSNPPTFG 120  
DB 61 PGSSPKPWIYATNSLNSGVPTFRFSGSGGTSYSLTISRVEADAATYCCQWTSNPPTFG 120  
QY 121 SGTKEI 127  
DB 121 GGTKEI 127  
RESULT 18  
AAE27925  
ID AAE27925 standard; protein; 235 AA.  
XX  
XX AAE27925;  
AC  
XX 27-DEC-2002 (first entry)  
DT  
DE Human C2B8 antibody light chain protein.  
XX  
XX Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;  
KW neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;  
KW non-Hodgkin's lymphoma; haematologic malignancy; tumour.  
XX  
XX Homo sapiens.  
XX  
XX WO200260955-A2.  
XX  
XX 08-AUG-2002.  
XX  
XX 29-JAN-2002; 2002WO-US002373.  
XX  
XX 29-JAN-2001; 2001US-0264318P.  
XX  
XX 16-NOV-2001; 2001US-0331481P.  
XX  
XX (IDEC-) IDEC PHARM CORP.  
XX  
XX Braslawsky GR, Hanna N, Chinn P;  
XX



DR WPI; 2002-698547/75.  
 DR N-PSDB; AAD45754.  
 XX  
 PT Novel domain deleted CC49 antibody reactive with tumor associated antigen  
 PT -72, or C2B8 antibody reactive with CD20, useful for treating  
 PT myelosuppressed patient suffering from a neoplastic disorder.  
 XX  
 PS Example 1; Fig 3B; 74pp; English.  
 XX  
 CC The present invention relates to domain deleted CC49 or C2B8 antibodies.  
 CC Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain  
 CC deleted sequence in which CH2 domain has been deleted and are reactive  
 CC with tumor associated antigen (TAG)-72. The C2B8 antibodies are reactive  
 CC with CD20 and comprise a heavy chain having a sequence of a derived  
 CC domain deleted C2B8 construct where the CH2 domain has been deleted.  
 CC Sequences of the invention are useful for imaging a neoplasm. They are  
 CC also useful for treating myelosuppressed patients suffering from  
 CC neoplastic disorder such as haematologic neoplasm, preferably non-  
 CC Hodgkin's lymphoma. Antibodies of the invention are also used to treat  
 CC neoplastic disorder, colon cancer and haematologic malignancy. They are  
 CC useful for reducing tumour size, inhibiting tumour growth and/or  
 CC prolonging the survival time of tumour-bearing animals and for treating  
 CC tumours. The present sequence is human C2B8 light chain protein. This  
 CC sequence is used in the exemplification of the invention  
 XX  
 SQ Sequence 235 AA;  
 Query Match 87.2%; Score 572; DB 5; Length 235;  
 Best Local Similarity 89.8%; Pred. No. 3.2e-34;  
 Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 MDPQVQIFSPILLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCNQOK 60  
 DB 1 MDPQVQIIFSPILLISASVIMSRGQIVLSQSPAILFASPGKVWTCRASSSVIYHFWQOK 60  
 QY 61 PGSSPKPWYIGTSLASGVPTFRSGSGSGTYSLSLTISRVEAEDAATYCCQWSNPPTFG 120  
 DB 61 PGSSPKPWYATNSLASGVPTFRSGSGSGTYSLSLTISRVEAEDAATYCCQWSNPPTFG 120  
 QY 121 SGTKLEI 127  
 DB 121 GGTKLEI 127  
 RESULT 19  
 ABB82834  
 ID ABB82834 standard; protein; 235 AA.  
 AC ABB82834;  
 XX  
 DT 31-MAR-2003 (first entry)  
 XX  
 DE Antibody C2B8 light chain.  
 XX  
 CC C2B8; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;  
 KW vscrotic; immunomodulator; protozoacide; antidiabetic; nephrotropic;  
 KW thymimetic; hepatotropic; haemostatic; antileprotic; antibacterial;  
 KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;  
 KW dermatological; immunosuppressive; antiinflammatory.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200296948-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 XX 29-JAN-2002; 2002WO-US0002374.  
 XX  
 PR 29-JAN-2001; 2001US-0264318P.  
 PR 16-NOV-2001; 2001US-0331481P.  
 PR 21-DEC-2001; 2001US-0341858P.  
 XX  
 PA (IDEC-) IDEC PHARM CORP.

XX Braslawsky GR, Hanna N, Chinn P, Hariharan K;  
 XX WPI; 2003-140446/13.  
 DR N-PSDB; ABZ24018.  
 XX  
 PT Novel dimeric antibody useful for treating immune disorder and neoplastic  
 PT disorder, has several non-covalently associated monomeric subunits.  
 XX  
 PS Example 1; Fig 3B; 78pp; English.  
 XX  
 CC The invention relates to a dimeric antibody (I) comprising several  
 CC monomeric subunits, where the monomeric subunits are non-covalently  
 CC associated. (I) is useful for treating a disorder, especially immune  
 CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,  
 CC resistant Hodgkin's disease high grade, low grade and intermediate grade  
 CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),  
 CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular  
 CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,  
 CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic  
 CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,  
 CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,  
 CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small  
 CC cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a  
 CC detailed description of the various uses of (I)). The present sequence  
 CC represents the antibody C2B8 light chain  
 XX  
 SQ Sequence 235 AA;  
 Query Match 87.2%; Score 572; DB 6; Length 235;  
 Best Local Similarity 89.8%; Pred. No. 3.2e-34;  
 Matches 114; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 MDPQVQIFSPILLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCNQOK 60  
 DB 1 MDPQVQIIFSPILLISASVIMSRGQIVLSQSPAILFASPGKVWTCRASSSVIYHFWQOK 60  
 QY 61 PGSSPKPWYIGTSLASGVPTFRSGSGSGTYSLSLTISRVEAEDAATYCCQWSNPPTFG 120  
 DB 61 PGSSPKPWYATNSLASGVPTFRSGSGSGTYSLSLTISRVEAEDAATYCCQWSNPPTFG 120  
 QY 121 SGTKLEI 127  
 DB 121 GGTKLEI 127  
 RESULT 20  
 ADY21925  
 ID ADY21925 standard; protein; 500 AA.  
 AC ADY21925;  
 XX  
 DT 05-MAY-2005 (first entry)  
 XX  
 DE Antibody fusion 2H7 VH L1L5-IgG1 (CSSS-S)H-K290QCH2-CH3.  
 XX  
 CC Antibacterial; Virucide; Antiparasitic; Fungicide; Immunotherapy;  
 KW antibody engineering; cancer; neoplasm; cytostatic; immune disorder;  
 KW graves disease; antithyroid; endocrine disease; hashimoto's disease;  
 KW immunosuppressive; rheumatoid arthritis; antiarthritic; antirheumatic;  
 KW inflammation; musculoskeletal disease; systemic lupus erythematosus;  
 KW antiinflammatory; dermatological; dermatological disease;  
 KW metabolic disorder; sjogrens syndrome; ocular disease;  
 KW thrombocytopenic purpura; hemostatic; hematological disease;  
 KW multiple sclerosis; neuroprotective; neurological disease;  
 KW myasthenia gravis; muscular-gen.; bacterial infection; fungal infection;  
 KW fungicide; viral infection; virucide; parasitic infection; antiparasitic;  
 KW fusion protein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO2005017148-A1.

```

XX
SQ      Sequence 500 AA;

Query Match      86.4%; Score 567; DB 9; Length 500;
Best Local Similarity 88.2%; Pred. No. 1.6e-3;
Matches 112; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY      1 MDFQVQFSPILLISASVIMRGQIVLSQSPAILLFPASPGETVTMTTCRASSSVIYMCNQOK 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 MDFQVQFSPILLISASVILARGQIVLSQSPAILLASPGEKVTMTTCRASSSVSYMHVYQOK 60

QY      61 PGSSPKPWIVGTSTLASGVTRSGSGSGTYSLSLTISRVEADAATYTCQWSSNPFTFG 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      61 PGSSPKPWIVAPSNLASGVPARFSGSGSGTYSLSLTISRVEADAATYTCQWSSNPFTFG 120

QY      121 SGTKLEI 127
      :|||||:
DB      121 AGTKLEI 127

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Search completed: March 20, 2006, 07:35:40  
Job time : 48.9655 secs

24-FEB-2005.

24-DEC-2003; 2003WO-US041600.

26-JUL-2003; 2003US-00627556.

(TRUB-) TRUBION PHARM INC.

Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

WPI; 2005-182370/19.

N-PSDB; ADY21924.

New non-naturally occurring single chain protein comprising polypeptides with binding domain, connecting regions and N-terminally truncated immunoglobulin, having immunological activity, useful for neutralizing infectious agent.

Disclosure; Page 383; 590pp; English.

The invention relates to a non-naturally occurring single chain protein (I) comprising a first polypeptide having a binding domain polypeptide capable of binding to a target molecule, the binding domain polypeptide comprising a heavy chain variable region, which comprises an amino acid substitution or deletion at one or more amino acid residues, a second polypeptide comprising a connecting region attached to the first polypeptide, and a third polypeptide comprising an N-terminally truncated immunoglobulin heavy chain constant region polypeptide attached to the second polypeptide, where the non-naturally occurring single-chain protein is capable of an immunological activity. Also included are reducing a target cell population in a subject (involving administering to the subject a protein that is less than 150 kD, which involves treating the target cell population with a first protein or peptide that binds to cells within the target cell population, and treating the target cell population with a second protein or peptide that capable of at least one of binding an Fc receptor, inducing target cell apoptosis, or fix components, where the first protein or peptide molecule is directly connected to the second protein or peptide molecule or, optionally, the first protein or peptide molecule and the second protein or peptide molecule are linked by a third protein or peptide molecule, and where the protein molecule is not an antibody, a member of the TNF family or the TNF receptor family, and is not conjugated with a bacterial toxin, a cytotoxic drug, or a radioisotope), depleting cells in an animal (involving administering a modified IgE protein into the blood stream of an animal), a polynucleotide that encodes the polypeptide of the invention, a cell containing the polynucleotide, a recombinant vector capable of expressing the polypeptide, expressing the polypeptide, a composition comprising the polypeptide) in combination with one or more additional therapeutic compounds, displaying recombinant molecules (which molecules include a native or engineered immunoglobulin heavy chain variable region, the improvement comprising an immunoglobulin heavy chain region that includes one or more mutation, substitution, alteration, and/or deletion at one or more amino acid residue corresponding to positions 9, 10, 11, 12, 108, 110, and 112 in the heavy chain variable region) and a non-naturally occurring single chain antigen-binding protein comprising protein having a mutation chosen from a list given in the specification. The polypeptides of the invention comprise single chain antibodies (scFv, with or without mutated residues) linked via an immunoglobulin hinge region (wild-type or mutants where the cysteines are changed to serines/prolines and denoted (SSS-P/H), (CSC-S/H etc) to an immunoglobulin (IgG, IgE or IgA) heavy chain constant region (CH) which may also have mutations in CH2 (e.g. T256N) or a truncated CH3 (e.g. T4 CH3, a 4 amino acid deletion). The polypeptide may be further linked to a non-antibody protein such as the transmembrane and cytoplasmic tail (TN/CT) of caspase-3, caspase-8 or CD80. The fusion polypeptides are useful for neutralization of an infectious agent (where the infectious agent is a bacterium, a virus, a parasite, or a fungus) and also for treatment of cancer, immune disorders, Grave's disease, Hashimoto's disease, rheumatoid arthritis, systemic lupus erythematosus, Sjogren's syndrome, thrombocytopenic purpura, multiple sclerosis and myasthenia gravis. The present sequence represents a fusion protein of the invention.